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(NL); WEZEL GILLES PHILIPPUS
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AL049587 Streptomy
AX089416 Sequence
AL049863 Streptomy
AX007216 Sequence
D50051 Streptomyce
AL159139 Streptomyce
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AL05040 Streptomy
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AL096823 Streptomy
AF195770 Streptomy
AX007220 Sequence
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AX00728 Sequence
AX00738 Streptomy
AX137778 Streptomy
AX3333 S.albus bet
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AR103043 Sequence
AR103044 Sequence
AR103045 Sequence
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D87846 Streptomyce
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/db_xref="taxon:1911"
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LMFLCHR36_07
D87847
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AX089416
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                            July 18, 2002, 07:33:10 ; Search time
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Maximum Match 100%
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/codon_start=1
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/product="ssgA"
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/protein_id="CAC07384.1"
/db_xref="G1:9995083"
/db_xref="G1:9995083"
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GDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTA
PLVARLDRTDKLYMGCGHTLGGGHTLGDFDRDLGGRTA
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Cloning and characterization of a gene involved in regulation of
sporulation and cell division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
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Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                  Length 438
                                                of Streptomyces griseus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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complete cds
                                                                                                                                                                                                Score 438; DB 6;
Pred. No. 2.3e-47;
0; Mismatches 0;
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DNA for ssgA,
                                    /gene="ssgA"
/note="strain ATTC
                                                                                                                                                                                                tch 100.0%; al Similarity 100.0%; 438; Conservative 0
              /gene="ssgA"
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/translation="MMSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAF
GRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRT
DKLVPLGGEHTLGDFDGNLEDALGRILAEEQNAG"
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                                                                                      4 (bases 1 to 1513)
Shinichi, K. and Ensign, J.
Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus
Unpublished (1995)
5 (bases 1 to 1513)
Shinichi, K.
                                                                                                                                                                                                       Direct Submission
Submitted"(06-APR-1995) Kawamoto Shinichi, National Food Research
Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)
Location/Qualiflers
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Kawamoto, S., Watanabe, H., Hesketh, A., Ensign, J.C. and Ochi, K. Expression analysis of the ssgA gene product, associated with sporulation and cell division in Streptomyces griseus Microbiology (Reading, England) 143 (Pt 4), 1077-1086 (1997) 97286526
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hilarity 100.0%; Pred. No. 1.7e-47;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ssgA"
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                                                                                                                                                                                                                                                                                                     /organism="Streptomyces
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385. 389
392. 802
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As by DNA linear BCT 01-NOV-2000 Streptomyces netropsis SsgA (ssgA) gene, complete cds. AF195772
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GDAPVTWAFCRELLLDGINRPSGDGDYHIAPTDPEGLSDVSIRLQVGADRALFRAGAP
PLVAFLLDRTRSVPLGQEGTLGDFEDSLEAALGKILABEGNAG"
158 c 142 g 68 t
                                                                                                                                                                                                                              Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 438)
van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces netropsis ssgA gene
Unpublished
2 (bases 1 to 438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces griseus SsgA; possible
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   gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg
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Pred. No. 2.9e-33;
0; Mismatches 69
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Submitted (18-OCT-1999) Biochemistry,
9502, Leiden 2300 RA, Netherlands
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAG28483.1"
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division protein"
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                                                                                                                                                       AF195772.1 GI:11066162
                                                                                                                                                                                      Streptomyces netropsis. Streptomyces netropsis
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84.2%;
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
filamentous microorganisms
UNIV LEIDEN (NL); KRAAL BARRND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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RELLLGGLNSPSGDGDVHIGPPEPEGLGDVHTRLQVGADRALFRAGTAPLVAFLDRTD
RLYPLGQEHTLGDFDGNLEDALGRILAEEQNAG"
139 c 142 9 66 t
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100.0%; Pred. No. 2.2e-43;
ive 0; Mismatches 0;
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Sequence 3 from Patent WO0000613.
AX007218
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/gene="ssgA"
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
Actinomycetales; Streptomycineae; Streptomyces.

Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
But EIDER (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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                                                                        361 CAGACTCTGGGTGACTTCGAGGACAGCCTGGAGGCCGCGCTCGGCAAGATCCTCGCCGAG
                                              cacacgetgggtgacttcgacggcaacetggaggacgcactggggccgcatectcgccgag
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151 c 131 g 62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Streptomyces netropsis"
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AX007224
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83.3%;
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AUTHORS
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Complement(~1. 289)

Gene="SCO11.01c"

Complement(~1. 289)

Gene="SCO11.01c"

Complement(~1. 289)

Gene="SCO11.01c"

Job as: unknown function, previously sequenced as

TR:053870 (EMBL:037580), S.coelicolor hypothetical protein

ORF5 downstream of phosphotyrosine protein phosphatase

(159 aa). Weak similarity to the N-terminus of TR:06988

(EMBL:AL023797) Streptomyces coelicolor hypothetical

protein (172 aa), fasta scores; opt: 158 z-score: 206.4

E(): 0.00036, 46.28 identity in 65 aa overlap. Continues

as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcriptional regulator, len: 301 aa; previously sequenced as TR:053869 (EMBL:037580) S.coelicolor lysR-like protein (301 aa). Highly similar to SW:ARAB_STRAT (EMBL:037580), arab, Streptomyces antibioticus transcriptional regulatory protein (301 aa), fasta socres; opt: 1581 z-score: 1813.2 E(): 0, 80.3% identity in 300 aa overlap. Similar to many other transcriptional regulators. Contains probable helix-turn-helix motif at aa 17-38 (Score 1659, +4.84 SD). Contains Pfam match to PF00126 HTH_I. Bacterial regulatory helix-turn-helix protein, lysR family and PS00044 Bacterial regulatory proteins, lysR family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTVRPVVKRTARAVLLDGDHLILIKRTKPGVDPYWVTPGGGVEPDDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDEVHVLVATPHWAERAGVEDVRDTDASALKHVPVVEVHESLPFVGRYWASVFDARPA
SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
RTGTLAMPHIARAHEWLLRARADWN"
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RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAETGLEDDSTLRTLHLAGPPEFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERALPALGELTGEDGQAFALRASFGNAEETLEGLAAGHHDLAIGTTRPRGALHTATPL
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/protein_id="CAB46957.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="sequence corresponding to EMBL: U37580 from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="overlap with Streptomyces coelicolor cosmid H24 (EMBL-AL049826) from 41528 to 41625" complement (360, .1265) /gene="SCQ11.02c"
                                        ď
                              overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions. Cosmid 011 Cosmid 011 lies between H24 and D78 on the Asel-Q genomic restriction fragment.
   It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(831. .1256)
/gene="SCQ11.02c"
/note="MatCh to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"
complement(1125. .1217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(360. .1265)
/gene="SCQ11.02c"
/note="SCQ11.02c, abaB, probable_lysR-family
                                                                                                                                                                                                                           /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/label=SCO11.01c
/product="hypothetical protein"
/protein_id="CAB46956.1"
/db_xref="G1:5457268"
                                                                                                                                                                                                                                                                              /db_xref="taxon:100226"
/clone="cosmid Q11"
complement(1. .289)
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                                                                                                                                                           Location/Qualifiers
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/label=abaB
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                                                                                                                                                                                                                                                                /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                               complement(1.
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sequenced clone.
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yearna synthese/lyse, len: 392 as previously sequenced as SW:CYSA_STRCO (EMBL:U37580), cysA, S.coelicolor putative cystathionine gamma-lyses (392 as) previously sequenced as SW:CYSA_STRCO (EMBL:U37580), cysA, S.coelicolor putative cystathionine gamma-lyses (392 as). Similar to many e.g. SW:MEGL_PSEPU (EMBL:D8854), mdeA, Pseudomonas putida methionine gamma-lyses (398 as), fasta scores; opt: 608 z-score: 653.6 E(): 4.5e-29, 36.9% identity in 404 as overlap. Highly similar to TR:053668 (EMBL:X91393) Streptomyces antibioticus hypothetical protein found upstream of the abaB gene (232 as) (87.1% identity in 232 as overlap). Contains Pfam match to PF01053 Cys_Met_Meta_PP, Cys/Met metabolism PLP-dependent enzyme and PS008688 Cys/Met metabolism enzymes pyridoxal-phosphate attachment site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGVETLVFASGWAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IETPSNPGLDVCDVRRLVEAAHAGGALVÄVDNTLATPLGQRPLELGÄDFSVASGTKQL
TRGDVLLGYVAGRDAGAMAAVRRWKT VAG IPGOMEAVLAHRETATLĞLKVDGDST
ALKVAGALRTRPETTGLRY PGLPDDPSHKASQQMLRYGCVVSFTLFSRARADRELDA
LRLVEGATSFGGVRSTAERRGKWGGDAVPEGFTRLSVGAEDPDDLLAALLLRALDETTE
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to PF01451 LMWPc, Low molecular weight phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWHEGEGADPRTEAVLADHGYGLDHAARQFQQSWFSRLDLVVALDAGHLRALRRLAPT
ERDAAKVRLLRSYDFAVAGGDLDVPDFYYGGRDGFEECLEWVEAASTGLLAAVREQVE
GRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTYRVCFVCTGNICRSPMAEAVFRARVEDAGLGHLVEADSAGTG
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                                                                                                                                                  complement(1518. .2696)
/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
/note="PS00044 Bacterial regulatory proteins, lysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-tyrosine-phosphatase, len: 164 aa; previously sequenced as SW:PTPA_STRCO (EMBL:U37580), ptpA, S.coelicolor low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15441;
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/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=cysA
/product="putative cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00868 Cys/Met metabolism enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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77.6%; Pred. No. 9.9e-28;
iive 0; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=ptpA
/product="low molecular weight
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-synthase/lyase"
/protein_id="CAB46958.1"
/db_xref="G1:5457270"
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/db_xref="G1:5457271"
                                                            .2696)
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/gene="SCQ11.04c"
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                                                                                      /gene="SCQ11.03c"
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/transl_table=11
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                                                            complement (1518.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                     /note="cysA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ptpA"
                               signature
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Best Local Similarity 77.6
Matches 340; Conservative
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/gene="ssgA"
/note="similar to Streptomyces griseus SsgA; possible cell
division protein"
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van Wezel,G.P., Rousseau,C. and Kraal,B.
Cloning and sequencing of the Streptomyces goldeniensis ssgA gene Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                       306 accgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacac 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2. (bases 1 to 408)
van Wazel,G.P.
Direct Submission
Submitted (18-OCT-1999) Biochemistry, University of Leiden, 9502, Lidden 2300 RA, Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                   66 tattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttcca
                                                                                                                                                                                     ccttcccggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggtgggct
                                                                                                                                                                                                                                                                                                                                           6 cgagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcgttccg
                                                                                                                                                                                                                                                     121 cereceggagaegececeggecacereggererreggegergaacregregaggagr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF195770 408 bp DNA linear BCT O.
Streptomyces goldeniensis SsgA (ssgA) gene, complete cds.
AF195770
                                                                                   ö
                                                       Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..408
/organism="Streptomyces goldeniensis"
/db_xref="ATCC:21386"
/db_xref="taxon:121022"
                                                       Score 265; DB 1; L
Pred. No. 2.7e-25;
0; Mismatches 105;
 80
  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces goldeniensis. Streptomyces goldeniensis
 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF195770.1 GI:11066158
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                                                       60.5%;
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/note="similar to Streptomyces griseus SsgA; possible cell
division protein"
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RELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTD
QGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
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Streptomyces albus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 566)
van Wezell, G.P., Rousseau, C. and Kraal, B.
cloning and sequencing of the Streptomyces albus ssgA gene
Unpublished
                                                                                                                                          5624
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Submitted (18-OCT-1999) Biochemistry, University of Leiden,
9502, Leiden 2300 RA, Netherlands
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                                                                                                                                atgcgcgagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcg
                                                         ttccgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacg
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/organism="Streptomyces albus"
/db_xref="taxon:1888"
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van Wezel, G.P.
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01-NOV-2000

Box

Gaps

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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 407)

Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 5 06-JAN-2000;
UNIV LEIDEN (NL); KRAL BARRND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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RELLIDGGERRECGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPLGGERSLADFDALLDEALDRILAEEQNAG"
135 c 145 g 77 t
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Streptomyces albus G
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/note="strain ATCC of Streptomyces albus
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Pred. No. 1.3e-24;
0; Mismatches 92;
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                                                                                                                                                                                  Query Match 59.3%;
Best Local Similarity 77.4%;
Matches 315; Conservative
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/transl_table=11
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/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFG
RELLINGGRRPCGDGDVHIAAADPEFRGEVIIRLQVGSDQAMFRVGTAPLVAFLDRID
rtyptcgrRSLADALDBALDBALDRILABEDNAG"
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Patent: WO 0000613-A 7 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS VAN (NL)
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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/gene="ssgA"
/note="strain ATCC of Streptomyces goldeniensis"
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                                                                                                                                                                                   Length 408;
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/db_xref="taxon:121022"
                                                                                                                                                                                Score 260.8; DB 1;
Pred. No. 1e-24;
0; Mismatches 92;
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strand)

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasts -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Kroph et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/Ggl.bin/framePlot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapp between neighbouring submissions.

Cosmid El9A lies between and overlapps cosmids E6 and E56 on the ASEI-E genomic restriction fragment.
Submitted (16-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCE19A.01, hypothetical protein, partial CDS, len:
>31 aa; unknown function, similar to members of the alkyl
hydroperoxide reductase C/thiol-specific antioxidant
family e.g. TR:053226 (EMBL-AL021185), bcp, Mycobacterium
tuberculosis bacterioferritin comigratory protein (157
aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06,
63.3% identity in 30 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                 coelicolor sequencing at The Sanger Centre is funded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"hypothetical protein"
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/baxef=161:5531350"
/translation="IVVDEGGKVERALYNVRATGHVAKIIKDLGI"

    .35284
    /organism="Streptomyces coelicolor A3(2)"

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/db_xref="taxon:100226"
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/db.xref="G1:99508"
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1 (bases 1 to 35284)
1 (bases 1 to 4000 to 400
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Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ACCGTCGATCCGTACGCGGTGCGGTGCGCTTCCACCTCCCCGGAGACGCCCCGGTCACC 120
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James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
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                  /transl_table=11
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Seeger, K. and Harris, D.
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ilarity 74.2%;
Conservative
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Matches 302; Conserv
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/product="hypothetical protein"
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/db_xref="G1:5531354"
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AAGAHGVVKMGTAIQVVIGTDADPIAAEIEDHM"
oomplement(2385. 2489)
/gene="SCE19A.05c"
/note="Pfam match to entry PF00367 PTS_EIIB,
phosphotransferase system, EIB, score 43.00, E-value
unknown function, similar to parts of many sugar permeases e.g. TR:P96159 (EMBL:U65013), malx, Vibrio furnissii PTS (phosphoenolpyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 217 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 29-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCE19A.06"
/note="SCE19A.06, possible PTS transmembrane component,
len: 431 aa; similar to many PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20123 GTGGAACGCGAGCTGGAGCTCAGGCTCGTCGTCGCCCGAGAGGGGCATTCCGGTGCCG 20182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20243 TCCGGCCACCGGTGCACTGGACGTTCGCCGGGGACCTTCTGGTGGAGGGCGTCTTCCGG 20302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20303 CCGTCCGGGCACGGGAACGTGCGGGTGTGGCCGTCGAAGACGGAGGGCCCGCAGCGTCGTA 20362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20363 cresresescreasecesacesacescesacescereseasesceceaesescescesasses 20422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20423 TCGGCCTGGCTGGAGCGGACCCTGCGGGCGGTGCCGCGGGGACCGAGGGCGCGCAGCTC 20482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           giggagetecgatacgaggteggegatecgtatgeeateeggatgaegtteeacetteee 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 ggcgatgcccctgtgacctgggcgttcggccgcgagctgctggtggacgggctcaacagc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcgttccgtattccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20183 GCCGGGCTCGGCTACCACACGACGATCCCTACGCGGTGCACATCACCTTCCACATCGAC
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Streptomyces coelicolor cosmid L2.
AL137778
AL137778
acetyltransferase; acyltransferase; adenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 113.4; DB 1;
Pred. No. 2.1e-06;
0; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2660. .3955
/gene="SCE19A.06"
2660. .3955
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                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          llarity 55.4%;
Conservative
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Best Local S
Matches 219
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/protein_id="CAB50984.1"
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ADAIADSVTELQQAVENADDPTQWEESLNSIDKNLDRIGDGTDNTDVNKAVDDLGKAV
DNVRYSVBKNDEPTPLSPVTDAAGELTKVCTP"
COMplement(1201. .1233)
/gene="SCG19A.03c"
/note="SCG19A.03c"
/note="SG00013 Prokaryotic membrane lipoprotein lipid
attachment site"
complement(1454. .2191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1454. .2191)
/gene="SCE19A.04c"
/note="SCE19A.04c, rph, probable ribonuclease PH, len: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"putative ribonuclease PH"

/protein_id="CABSO985.1"

/db_xref="G1:6531353"

/translation="MSRIDGRPPQQLRPVIIERGWSKHAEGSVLVSFGDTKVLCNASV

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TEGYPRWRKGSGEGWYTAEYAMLPRATNTRGDRESYKGRIGGRTHEISRLIGRSLRAV
IDYRALGENTVVLDCDVLQADGGTRTAATTGAYVALADAVAMAQGRKLIKANRKPLTG

TVSAVSVGIVDGTPLLDLRYEEDVRAATTGAYVALGDGRFVEVQGTAEAEBFRADELN

TLLDLATAGCTELAELQRRALDATLER"
                                                                                                                                                                                                                                                                                                                TGVTFAENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARMAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGQLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jobe "SCEL9A.03C, possible secreted protein, len: 134 aa; unknown function, probable CDS suggested by GC frameplot, positional base preference and amino acid composition. Contains probable W. terminal signal sequence and appropriately positioned PSO0013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                         /translation="MTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                As; highly similar to many e.g. SW:RNPH_ECOLI (EMBL:X00781), rph, Escherichia coli ribonuclease PH (238 ab., fasta scores; opt: 916 z-score: 1116.8 E(): 0, 60.8% identity in 240 aa overlap. Contains Pfam match to entry PF01138 RNBse_PH, 3' excribonuclease family and PS01277 Ribonuclease PH signature"
     z-score: 743.6 E(): 0, 52.0% identity in 200 aa overlap. Similar to SW:YGGV_ECOLI (EMBL:U28377), yggV, Escherichia coli hypothetical protein (197 aa) (49.5% identity in 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF01138 RNase_PH, 3'
exoribonuclease family, score 266.70, E-value 3.1e-76"
complement(1805. 1843)
/gene="SCE19A.04c"
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/gene="SCE19A.05c"
complement(2268. .2501)
/gene="SCE19A.05c"
/note="SCE19A.05c, hypothetical protein, len: 77 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="PS01277 Ribonuclease PH signature"
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/db_xref="GI:5531351"
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/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                   complement(892, 1296)
/gene="SCE19A.03c"
complement(892, 1296)
/gene="SCE19A.03c"
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/label=SCE19A.03c
                                                                                                                                                                              /label=SCE19A.02c
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                                                                                                                                                   /transl_table=11
                                                                                                                      /codon_start=1
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                                                                                              overlap)"
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us-09-749-185-1.rge

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identical to previously sequenced SW.RELA_STRCO
(EMBL:X87267) Streptomyces coelicolor GTP
pyrophosphokinase (EC 2.7.6.5) RelA_847 as and highly
similar to SW.RELA_STRAT (EMBL.AF072829) Streptomyces
antibioticus RelA_protein_841 as; fasta scores; opt: 4969
z-score: 4906.2 E(): 0; 90.3% identity in 848 as overlap
and to SW.RELA_CORGL (EMBL.AF038651) Corynebacterium
glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA_760
as; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.7%
identity in 774 as overlap. Conteins Pfam match to entry
PF01842 AcT, AcT domain and match to Prosite entry PS00017
ATP/GTP-binding site motif A (P-loop)"
//transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / resultance = "CAPT pyrophosphokinase"
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FKDYIAMPKRNMYQSLHTYUGPGGKRVELQIRTFDHHRRAPKIGTAHARRAPVFGR
FKDYIAMPKRNMYQSLHTYUGPGGKRVELQIRTFDHHRRAPKIGTAHARRAPVFGR
ASKVRTDARSGKGRKDDHNNDMAALRQLLDWQKETEDDFGELESLBFDLSRREFYE
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//note="previously sequenced region SW:SCS
                                                                                                                                                                            AVDHIREQVDAHHAVGDLEALRARLDOLVALVETRREEKKAQRAKGSDEARGAKEALV
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FRACIDAQREEARRIKERLYSEREALSNSTDWGPTAARYBOLMSEWKAAGRAQREHEDD
LWMRFRGAQDYVFFARKSSVFARDAGOSENIKLKEELVTEARKLYVTDLKSSRAAFR
SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGGFTRRAVPRA"
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AAGAGPSRDWIGFVKSPRARNKIRAWFSKERRDEAIEGGKDAIVRAMRKQNLPIQRIL
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GG"
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                                                                                                                                          /translation="SWQAGSPEEALAYFERKYEGLVVEIGLLEKRVKTTDLSAKDAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     len: 847 aa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="previously sequenced region SW:SCAPTRELA EMBL:X87267 S.coelicolor apt & relA genes" complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="relA"
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1010: 1150
/note="SCL2.02"
/note="SCL2.02, unknown, len: 46 aa"
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/gene="relA"
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complement(1229. .3772)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The more also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Rucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp. CAUTION: We may not have predicted the initiation of the product of the program of bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SCL2.01, hypothetical protein, len: >328 aa; similar to TR:033236 (EMBL:298209) Mycobacterium tuberculosis hypothetical 49.8 kD protein MTCY174.11, len: 450 aa; fasta scores: opt: 843 z-score: 874.7 E(): 0; 45.9% identity in 296 aa overlap. Contains possible coiled-coils region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
Submitted (28-JAN-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CEB10 ISA E-mail: barrell@Sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 38640)
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                          Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                                                                                                                                                                     for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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/clone="cosmid L2"
              Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seeger, K.J. and Harris, D. Unpublished
3 (bases 1 to 38640)
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/partial
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                                                              ORGANISM
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AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                          TITLE
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                   SOURCE
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/traislation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
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NLMLRELGGPAAVTRVRSLGDRVTRLDRWEPELNSAEPGRYTDTTSPRAITRTYGRL
VLGDALNPRDRRLLYSWLLANTTSGDRERAGLEDDWTLGGRYGTNNDAGVTWP
PGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG"
                                                                                                                                                                                                                                      BCT 26-APR-1993
                                                                                                                                                                                                                                                                                                                   beta-lactamase.
Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1410)
Dehottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J.,
Erpicum, T., Frere, J.-M. and Ghuysen, J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                    35359 CACCGGCACTTCGATCTCGATCAGGAGCTCTCGCACATCCTGGCGGAAAGCTAGGGCGGG 35418
      cacacgetgggtgacttcgacggcaacctggaggacgcactgggccgcatcetcgccgag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 gagetetegtteegtatteeggtggageteegataegaggteggegateegtatgeeate 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 oggatgacgttccaccttcccggcgatgcccctgtgacctgggcgttcggccgcgagctg 171
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S.albus beta-lactamase gene, complete cds.
M28303
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Eur. J. Biochem. 166, 345-350 (1987)
87275916
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Best Local Similarity 64.0%; Pred. No. 0.00
Matches 137; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="beta-lactamase"
/protein_id="AAA26775.1"
/db_xref="G1:153339"
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/gene="beta-lactamase"
/note="inverted repeat"
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540 c 496 g 1
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SOURCE
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                                                                                                         /gene="apt"//gene="apt"/gene="apt"/gene="apt"/gene="apt"/gene="apt"/gene="apt"/gene="scl2.04c, apt, adenine phosphoribosiltransferase, len: 182 aa; identical to previously sequenced SW.APT_SGNO (EMBL:887267) Streptomyces coelicolor adenine phosphoribosyltransferase (EC 2.4.2.7) Apt, 182 aa and highly smilar to SW.APT_ECOLI (EMBL:M14040) Escherichia coli adenine phosphoribosyltransferase (EC 2.4.2.7) Apt, 183 aa; fasta scores: opt: 600 z-score: 682.8 E(): 1.2e-30; 54.8 identity in 168 aa overlap. Contains Pfam match to entry PF00156 Pribosyltran, Phosphoribosyl transferase domain and match to Prosite entry PS00103 purine/pyrimidine phosphoribosyl transferases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MADYPEPGVVFKDITPLLADPGAFAALTDALAEAAGRTGATKVV
GLEARGFILGAPVALRAGLGFIPVRKAGKLPGATLSQAYDLEYGSAEIEVHAEDLTAG
DRVLVVDDVLATGGTAEASLELIRRAGAEVAGLAVLMELGFLGGRARLEPALAGAPLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="apt"
/note="Pfam match to entry PF00156 Pribosyltran,
Phosphoribosyl transferase domain, score 150.30, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             len: 373 aa; identical to previously sequenced
SW:SECF_STRCO (EMBL:X85969) Streptomyces coelicolor
protein-export membrane protein SecF, 373 aa and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCTCCACCGTCCCACCGGCACCGCGACGTCCGTGTCTGGCCGTCCCGCAGTCACGGC 35238
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EMBL:X87267 S.coelicolor apt & relA genes" complement(3956. .4453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00103 Purine/pyrimidine phosphoribosyl
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                                                                                                                                                                                                                                                                                                                                                                                                   /product="adenine phosphoribosiltransferase"
/protein_id="CaB70916.1"
/db_xref="G1:6822210"
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Pred. No. 1.2e-05;
0; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transferases signature"
complement(4468. 4503)
complement(4501. .5622)
/gene="secF"
/gene="secF"
                                                                                          complement(3956. .4453)
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/translation="IGARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
VRARILQRAAGNPLALVELPRAAQGISPPLDDLPLTQRLETAFASRTDSLTRECRTFL
LVLAAEPTAPLNQLLDVASRLAGSEVTVYALQEAVDAGLVVLTGRTPERHPLARSAI
TYATVADRLSTHRALAETLEGSPGRRLVHLAAATLGPDDELAGQLERFADDAGKRGG
LAAAVPALRQAGELVHPPRRQTGLLVRAAELASEINDRVQAGILLNRADLAEFGPTER
RRLMLVSDKAAFEPDEPQRRIQDMIDAAAGAFDVGSTSVAENLLWRAAARCFFQDGDA
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/gene="SC8A11.03"
/gene="SC8A11.03, possible regulator, len: 156 aa; similar to TR:09S2F7 (EMBLAL096852) Streptomyces coelicolor putative regulator SCE19A.24, 142 aa; fasta scores: opt: 272 z-score: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                                                                                                                                                                                                                                        'note "nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGSMAIGDVGRATRYLAQAASVWRSQGRLGLLARSLAGSWPRLYLGQLAQAREESAE
GIALAEETGEWIVWLGLKATSALTAVLRGEREAAARSVRELRAHSLFPVMPFASVMAQ
OVEGLLALFDSRAVEAYDALARAFDKTDPHYHSTSRWLLVPDLVDAAAAAGRNEQARE
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QHGRRLRRQRRNVDARKPLRLARDEFDRVGAQPWADMAREQLRAAGESDGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (fragment), len: >750 aa, similar to TR:09S124 (EMBL.AL109747) Streptomyces coelicolor probable transcriptional regulator SCJ21.13, 919 aa; fasta scores: opt: 818 z-score: 913.7 E(): 0; 32.6% identity in 775 aa overlap. Contains Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family and match to Prosite entry PS00622 Bacterial regulatory proteins, luxR family signature. Also contains a possible helix-turn helix motif at residues 699. 720 (+3.25 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2093. [2176]
/gene="SCBAll.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative transcriptional regulator (fragment)"
/protein_id="CAC01573.1"
/db_xref="GI:9716212"
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Jone-"SCBA11.01"

/note-"Pfam match to entry PF00196 GerE, Bacterial

/note-"Pfam match in entry PF00196 GerE, Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC8All.01"
/note="SC8All.01, possible transcriptional regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTVTVDOVRAEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
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/transl_table=11
/product="hypothetical protein SCBAll.02c"
/protein_id="CAC01574.1"
/db_xref="G1:9716213"
                                                                     /organism="Streptomyces coelicolor A3(2)"
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/gene="SC8A11.02c"
complement(2184. .2453)
/gene="SC8A11.02c"
/note="SC8A11.02c" unknown, len: 89 aa"
                                                                                                                                    /db_xref="taxon:100226"
                                                                                                                                                                          /clone="cosmid 8A11"
      Location/Qualifiers
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2787. 3257
                                                                                                                                                                                                                                     /gene="SC8A11.01"
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                                                                                                        /strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CBIO ISA E-mail: Barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
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The length in codons is given for each CDS.

The highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot Program of Blibb et al., Gene 30:157-66(1984) as implemented at
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Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
Ast of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web
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Cost are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).
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Jun/cg1-bin/frameplot.pl. CAUTION: We may not have predicted the
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Bacteria; Firmicutes; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteridae; St
                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                            DNA
232 cccgagggcctcggagatgtccacatccggctcc 265
                                                                                                                                                                                                                                                                 Streptomyces coelicolor cosmid 8A11. AL391041
                                                                  181 rccrcccrcaccccrcrcraracccccc 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
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Saunders, D.C. and Harris, D.
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SC8A11
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gene CDS

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3076 CCGCGTGGCTCCAGGTCAACGCACACGGTGACATAGCCATCTTCAGCCTGCCCGTCCCGG 3135
                                                                                                                                                                                                                                                                                                                                                                                                                           248 atgtecacatecggetecaggteggegeggacegtgegetgtteegggeggggaeggeae
                                                                                                                                                                                                                                                                                                                                          308 cgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 tgggtgacttcgacggcaacct 389
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/gene="SC8A11.04c; probable secreted peptidase, len: 1253
aa; similar to TR:09RL54 (EMBL:A1121596) Streptomyces
aa; similar to TR:09RL54 (EMBL:A1121596) Streptomyces
coelicolor probable secreted peptidase SCF51A.10, 1245 aa;
fasta scores: opt: 1877 z-score: 1848.3 E(): 0; 37.24
identity in 1300 aa overlap, to TR:095684 (EMBL:D83672)
Streptomyces albogriseolus subtilisin-like protease, 1102
aa; fasta scores: opt: 1365 z-score: 1380.6 E(): 0; 33.48
identity in 1268 aa overlap and to Streptomyces coelicolor
probable secreted peptidase Scandilisto, 1239 aa; fasta
scores: opt: 1835 z-score: 1467.4 E(): 0; 46.9% identity
in 1279 aa overlap. Contains Pfam matches to entries
PF00008 Peptidase_S8, Subtilase family and PF02225 PA, PA
domain and matches to Prosite entries PS00136 Serine
proteases, subtilase family, aspartic acid active site,
PS00137 Serine active site, Also contains possible
nettive site and PS00138 Serine proteases, subtilase
family, serine active site. Also contains possible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative secreted peptidase"
/product="putative secreted peptidase"
/db.xref="c1:9116215"
/translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPAPA
/translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVYPPAPAPA
GSGALDERLENVYTPGTAARSGGAHWTVSGDTYVYPDAAPYL
GSGALDERLENVYTPLLBGYDDARABELLITYTTOTAARSLGGARTPEGARETELS
IRGAAISAEHSRAADFWISLTGTGDAAAGGSAARSATSGGRLAGGIAKVWLDGKVRAT
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HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSGGRAVEYRQDISLLGQ
PLGIVPTQVRAQGELTSWYTADDDVRWVSFASRPDLGGRGVARSYEPRSTTRETWFAP
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                                                                                                                                                                       /translation="MSGDHHGVQAQHSAAQALLPLSLCLSQMTGALEWEDVPAEFRYD
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                                                                                                                                                                                                       PDHPLLVTIRFAPEGAPPVTWHVGRDLLHEGLRTTSGLGDVQVWADTPTDRETAWLQV
NAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
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TPLPLVQLDYAVAVDLSGRAHRRTELIVTASHLEGAAGAGAIRTATVEVSYDDGATWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry PF02225 PA, PA domain, score 19.00, E-value 0.058"
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Pred. No. 0.0087;
0; Mismatches 148; Indels
                               /product="putative regulator"
/protein_id="CAC01575.1"
/db_xref="GI:9716214"
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/qene="SC8A11.04c"
                                                                                                                                                                                                                                                                                            complement(3297. .7058)
/gene="SC8A11.04c"
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/trans1_table=11
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Matches 174;
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3 (bases I to 37245)
Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Direct Submission
Submitted (07-APR-1999) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell6sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 70H, UK
NORMAY 10, 2000 this sequence version replaced gi:4584464.
                                                                                                                                                                                                                   BCT 05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                 ABC transporter; amino acid permease; BCCT family; carboxypeptidase; D-amino acid oxidase; ddah, dimethylarginine dimethylaminohydrolase; dehydrogenase; efflux protein; endonuclease; enoyl CoA hydratase; IPP isomerase; metallopeptidase; oxidoreductase; racemase; regulator; thiolase; transferase. Streptomyces coelicolor A3(2)
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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
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Actinomycetales; Streptomycineae; Streptomyces.
Actinomycetales; Streptomycineae; Streptomyces.
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Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                              SC5F2A 37245 bp D1 Streptomyces coelicolor cosmid 5F2A.
3196 GGCTCGGAACCGACGCCTTCCT 3217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 37245)
Oliver, K. and Harris, D.
Unpublished
                                                                                                                                                                                                                                                                                                                                          AL049587.2 GI:7768282
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complement(976. 3234)

complement(976. 3234)

/gene="SC5F2A.02c"
/note="SC5F2A.02c"
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (adg, qt, ttq or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the sequence way NoT be the entire insert of the sequence do it may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAHGWETLEVDPADDCPDSVFVEDAVVVFRNVALITRPGAESRRAETAGVEEAVARLG
SVNWWWEGFTLDGGDVLKIGDTITVGRGGRTWAAGVQQLRAREPLGARVVAVPVSK
VLHIKSAVTALPDGTYJGHTPLTDVPSLFPPRLDVPBESGAHVVLLGGSRLLMAASAP
KTAELLADLGHEPVLVDIGEFEKLEGCVTCLSVRLRELYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MSEFISITGARENNLQDVTLRIPKGRLTVFTGVSGSGKSSVVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIAVESRRQLNETFTWFVRNRLPKYERPHADALEGLTPAIVVDQRPVGGHSRSTVGTM
TDIHSVLRVLFSRHGTPGAGGATAYSFNDPSGMCPGCDGLGRRVQPDWDRILDPARSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTWSTEYEGLADRFERLYLKRDLSGMSERTRDLVRGFLVEARCPDCGGARLNAAALAS
RIDGHSIADCSRMQITDLIAVLRGIDDPVALPVAGAAVAALERVEAIGLGYLSLDRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MPSKKALVRRPSPRLAEGLVTHVEREKVDHGLALEQWDAYVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adgavrfppfaagtwogotytnteeldtgkpvgdftaaerafimrgrpgskvtvsgsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCSF2A.01c, ddah, dimethylarginine dimethylaminohydrolase, len: 258 as; hydrolyses dimethylaminohydrolase, len: 258 as; hydrolyses asymmetrically methylated arginine with preference for dimethylated arginine over monomethylated arginine (experimental). Similar to TR:D1038106 (EMBL:AB001915) NG,NG-dimethylarginine dimethylathaninohydrolase from Homo Sapiens (286 as) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 as overlap)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="dimethylarginine dimethylaminohydrolase"
/protein_id="CAB40668.1"
/db_xreff="GI:4584465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .37245
/organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Nominal overlap with cosmid 4C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="UvrA-like ABC transporter"
/protein_id="CAB40669.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS-PROT:09X7M4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref-"taxon:100226"
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/gene="SC5F2A.01c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="cosmid 5F2A"
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                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/label=ddah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ddah
                                                                                                                                                                                                                                                                                                                                                                                Cosmid 5F2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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CDS

gene CDS

FEATURES

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/product="putative ABC transporter"
/product="putative ABC transporter"
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/doxnolation="guideli
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complement(3245...4879)

/gene="SC5F2A.03c, probable ABC transporter, len: 544aa;
/note="SC5F2A.03c, probable ABC transporter, len: 544aa;
similar to many involved in antibiotic resistance egs.
TR:054381 (EMBL:X9146) from the lincomycin-production
TR:054381 (EMBL:X9146) from the lincomycin-production
gene cluster of Streptomyces lincolnensis 78-11 (578 aa)
fasta scores; opt: 1624, z-score: 1696.3, E(): 0, (50.38
identity in 541 aa overlap). Contains two Pfam matches to ps000017 ATP/GTP-binding site motif A (P-loop)
and Prosite match to Ps00211 ABC transporters family
signature. Also contains a possible coiled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //gene="SC5F2A".035

//oote="Pfam match to entry PF00005 ABC_tran, ABC

transporter score 122.30, E-value 9e-33"

complement(3743. 3766)

/gene="SC5F2A.03c"

/note="PS00017 ATP/GTP-binding site motif A (P-loop)."

complement(4232. 4783)

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/note="Pfam match to entry PF00005 ABC_tran, ABC

transporter, score 143.80, E-value 3.1e-39"

complement(4403. 4447)

/gene="SC5F2A.03c"

/note="PS00211 ABC transporters family signature."

/note="PS05F2A.03c"

/note="PS05F2A.03c"

/note="PS05F2A.03c"
                                           VVEHDPDV TALADHVVDMGPRAGADGGRVVFEGTPAGLAASDTLTGRCLGRRTAVKDT
VRAPTGELWVKGAERHNLREVTVAFPTGVLTAVTGVAGSGKSTLVAELTGAHPDAVVV
                                                                                                                                        DOSA IGISARSTPATY LGIMDTVRK VFAR ETGAEPGFFSFNSAGACGTCEGRGIIHTD
LAFMDPVTTTCHDCEGRRFREEVLRLTVDGRSVADV LAMTAGQALGFFSDPGVRRRLR
                                                                                                                                                                                                                               ALRDVGLTYLTLGQPLSTLSGGERQRIKLATRLHRTGAVYVLDEPTTGLHMSDVEGLL
ALLDRLVDAGNTVVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
ATLSGGEGQRLKTVRHLGSSLTGMTY IFDEPSVGLHPRDVGRLGDLLLRLRDKGNTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="rfam match to entry PF00005 ABC_tran, ABC transporter, score 35.60, E-value 4e-08."
complement(3118. 3141)
/gene="SCSF2A.02c"
/note="SCSF2A.02c"
complement(3245. 4879)
                                                                                                                                                                                                                                                                                                                                                                                                                                 /,joure="pfam match to entry PF00005 ABC_tran, ABC transporter, score 101.40, E-value 1.7e-26." complement(1759. 1782)
/gene="ps00017 APP/GTP-binding site motif A (P-loop)."
/gene="ps00017 APP/GTP-binding site motif A (P-loop)."
/gene="gs05F2A.02c" .3162)
                                                                                                                                                                                                                                                                                                                                                                  /gene="SC5F2A.02c"
/note="Dfa"
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/label=SC5F2A.03c
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/gene="SC5F2A.04"
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                                                                                                                                                                                                                                                                                                                                          STAEHLRRATRR"
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4942. .5850

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196 agoggogacggogatgtgcacatoggocogacogagocogagggootoggagatgtocac 255
                                                                                                                                                                                                               256 atccggctccaggtcggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtg 315
                                                                                                                                                                                                                                                        316 gegilectegaceggaceggacaagelegigeegeleggecaggageacaegeleggigae 375
Query Match 18.4%; Score 80.8; DB 1; Length 37245; Best Local Similarity 54.5%; Pred. No. 0.031; Matches 216; Conservative 0; Mismatches 162; Indels 18; Gaps
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1 atgcgcgagtcggttcaagc.....aggagcagaacgccggctga 438
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Streptomyces grise	Streptomyces grise	Streptomyces netro	Streptomyces golde	Streptomyces albus	S. spinosa DNA fra	S. spinosa DNA fra	Streptomyces grise	Streptomyces nours
SUMMARIES			ΙD		AAZ49727	AAZ49728	AAZ49731	AAZ49730	AAZ49729	AAF88315	AAF88312	AAZ49727	AAD17184
			DB		21	21	21	21			22	21	22
			re Match Length DB]	1 1 1	438	407	407	407	407	45624	.50000	438	65140
	dР	Query	Match		100.0	92.9	68.1	59.3	54.6	17.6	17.6	13.4	12.6
			Score		438	407	298.2	259.8	239	77.2	77.2	58.6	55.2
		Result	No.		-	7	· E	4	S	ر د	7	ω υ	6

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53.4 12.2 1313 22 AAR74867 53.4 12.2 1981 20 AAR37294 53.4 12.2 1981 20 AAR37295 53.4 12.2 1981 20 AAR37296 50.4 11.5 10.5 12 AAR6314 50.4 11.5 10.9 12 AAR6314 60.4 11.5 58857 1 AAR6314 60.4 11.1 58857 1 AAR8316 60.4 11.1 58857 1 AAR8316 60.6 11.3 7536 21 AAR8316 60.6 11.3 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5	υ	13	40		4.2	1549 407		AAQ88151 AAZ49728	,	Aanthomonas L-giut Streptomyces grise
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	PR		JUN-19	:86	98	EP-0202	148.			
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, runinant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
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mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agonist; antagonist; biomass; ds.

    271 ggcgcggaccgtgcgctgttccgggcggggacggcaccgctggtggcgttcctcgaccgg
    241 ggcgcggaccgtgcgctgttccgggcggggacggcaccgctggtggggttcctcgaccgg

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Matches 407; Conservative
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                                                                                                                                               Streptomyces griseus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acggcaccgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggag 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gggeteaacageeegageggegaeggegatgtgeacateggeeegaeegageeegaggge 240
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                                                                                                                                                                                                       enhancing fragmentation in filamentous improve their liquid culturing properties
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Pred. No. 1.8e-75;
0; Mismatches 0;
           ORG WETENSCHAPPELIJK ONDERZO
                                                                Luiten RGM;
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                                                                                                                                                                                                                                                                                         Claim 1; Page 27; 60pp; English.
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Best Local Similarity 100.
Matches 438; Conservative
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           (NEWE-) NEDERLANDSE
                                                                                                                     WPI; 2000-147269/13.
P-PSDB; AAY44649.
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241 ggcgcggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc 300
61 acccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgctgtgacc 120
                         tgggcgttcggccgcgagctgctgctgctggacgggctcaacagcccgagcggcgacggcgat
                                     gtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggtc
                                                                                                                        ggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcgaccgg
                                                                                              181 giccacategeceegacegaeeegagggeeigteggaegieteeateeggeieeaggig
                                                                                                                                                                        acggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                                                                                                                                                                                                                                                                                                                                           ssqA; liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                      gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 437
                                                                                                                                                                                                                                            gaggccgcgctcggcaagatcctcgccgaggagcagaacgccggctg 407
                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces goldeniensis ssgA gene.
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                                                                                                                                                                                            ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bloinsecticide; receptor agent; antagonist; blomass; ds.
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1e-48;
            gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 437
                         63 A; 151 C; 131 G; 62 T; 0 other;
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NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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SsgA_protein
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1..405
                                                                                                                                                                      Streptomyces netropsis ssgA gene.
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                                                                                               BP.
                                                                                             AAZ49731 standard; DNA; 407
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(first entry)

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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive
mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; hypocholesterolaemic agent; ruminant growth promoter; ATCC 21386; bioinsecticide; receptor agent; antagonist; bioinsecticide; receptor agents; antagonist; bioinsess; ds.
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/label= SsgA_protein
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P-PSDB; AAY44651.
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Score 298.2; Di Pred. No. 1e-48 0; Mismatches

Query Match 68.1%; Best Local Similarity 83.3%; Matches 339; Conservative (

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Wezel GP,
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AAF88315/c
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                                                                                                                                                91 gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgacc 150
                                                                                                                                                            301 acggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctc 360
agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                         Gaps
                                                                                                          90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; berbicide; antiparasitic agent; ruminant growth promoter; ATCC 3004; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                                                                                                                                               gtgcacatcggcccgaccgaggcctcggaggtctccacatccggctccaggtc
                                                                                                          31 atgagetteetegteteegaggagetetegtteegtatteeggtggageteegag
                                                                                                                     tgggcgttcggccgcgagctgctggacgggctcaacagcccgagcggcgacggcgat
                                                                                                                                                                                                                                                  181 gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                                                                                                                                                                                                                                                                                                             acggacaagetcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                         .<u>`</u>
                                                                    DB 21; Length 407;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                391 gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 437
                                                                                                                                                                                                                                                                                                                                                            Sequence 407 BP; 56 A; 135 C; 145 G; 71 T; 0 other;
                                                                            Pred. No. 2.3e-41;
0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIJKSUNIV LEIDEN.
NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                   59.3%; Score 259.8;
.larity 77.4%; Pred. No. 2.3s
Conservative 0; Mismatches
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1..405
/*tag= a
/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces albus G ssgA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ49729 standard; DNA; 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces albus G.
                                                                             Best Local Similarity
Matches 315; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200000613-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-2000
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                                                                    Query Match
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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, envigent inhibitors, antimigraine agents, herbicides, antiparaslic agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 accgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgcccggtcacc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 tgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggggacggcgac 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 greggegateegtatgecateeggatgaegtteeacetteeeggegatgeeetgtgaee 150
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transgenic plant; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 atgagetteetegteteegaggagetetegtteegtatteeggtggageteegataegag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taggecgtteggecgegagetgetgetggaegggeteaacagecegageggegat
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                                                                                     Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 407 BP; 57 A; 150 C; 139 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 239; DB 21;
Pred. No. 2.2e-37;
0; Mismatches 105;
                                                                                                                                                                              Disclosure; Fig 5; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF88315 standard; DNA; 45624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.68;
74.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 302; Conservative
2000-147269/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                               P-PSDB; AAY44650
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DE19957268-A1.

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhammose to a spinosyn or polyketide adding forosamine or trombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express (II) ame that have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying any angent of the section of the correspondence of the corresp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression clones in a gene bank. Cells transformed with (I) may produce (II) at shgniftcoantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21100 CACGGCACGTGCTCGCCACCATCATCTTCAACCTGGTAGCCCCGGCGGTGTGATCGCG 21041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21040 CCAGTCGCGTGGAGCTGCGGAACGACAGCCGCAATCCGTACGAGAACTC 20981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10200 CTGATCGCCGAGGCAGGCGAAGGCGATGTGCGGATCGGCC---CTCGACGGGTTTTCCG 20864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggagatgiccacaiccggciccaggicggcgggaccgigcgcigitccgggggggacg 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 45624;
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                                                                                                                                                                                                                                                                                                                Salas JA;
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                                                                                                                                                                                                                                                                                                                Velten R,
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                                                                                                                                                                                                                                                                                                                Froede R,
                                                                                                                     99DE-1057268
                                                                                                                                                                                99DE-1040596
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                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-267102/28
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                                                                                                                                                                                                                                                 (FARB ) BAYER AG.
                                                                                                                     29-NOV-1999;
                                                                                                                                                                                   27-AUG-1999;
                                                          08-MAR-2001
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Matches 209;
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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II): (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of the corresponding derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   markers for sequencing of the Saccharopolyspora spinosa genome. (II) are marcolldes with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24525 cacggcacggtgctcgccaccatgatcttcaacctggtagccccggcgggtgtgatcgcg 24584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24585 ccagtcggcgtggagctgcggtacgacagccgcaatccgtacgagatctccatgaagctc 24644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 cacetteceggegatgeceetgtgacetggggegtteggeegegagetgetgetggaeggg 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 egegagteggtteaageagaggteatgatgagetteetegteteegaggagetetegtte 63
                                                                                                                                                                                                           Forosamine; trimethylrhamnose; polyketide synthase; biosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forosamine, trimethylrhamnose and polyketide synthase biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50000 BP; 8484 A; 16290 C; 16535 G; 8691 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.6%; Score 77.2; DB 22;
51.0%; Pred. No. 1.8e-06;
ive 0; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Velten R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 14-31; 354pp; German.
                                                                                                                                                                 S. spinosa DNA fragment SEQ ID 1.
                                       AAF88312 standard; DNA; 50000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Froede R,
                                                                                                                                                                                                                                 spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                           99DE-1057268.
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                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                               Saccharopolyspora spinosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 209; Conserva
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                                                                                                                         28-AUG-2001
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                                                                               AAF88312;
               AAF88312
RESULT
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20743 CGGTGGATGAACGTCGACGAGGTGCTGAGCTGCTCTCGCACAACCT 20694

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Sequence 438 BP; 68 A; 145 C; 153 G; 72 T; 0 other;
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                                                                         Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyketide
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           24645 aacgtaggcacggacggtcaggtggactgggtgatcgcccgcgacctgctggccgacggg 24704
                                                            ctgatcgccgaggcaggcgaaggcgatgtgcggatcggcc---ctcgacggggttttccg 24761
                                                                                                           999ttggtcgtgatcgagatgagctcgccgtcgggggcaggcctccttcgaggtgaatgct 24821
                                                                                                                                                           gaccagettgeggaettettgaacgacacetacgacgtggtegaacetggtgatgaacae 24881
                                                                                                                                                                                                                                                                                                                                                                   ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigratine agent; herbicide; antiparasitic agent; ruminant growth promoter, ATCC 23345; bioinsecticide; receptor agent; antagonist; blomass; ds.
                                   ggagatgtccacatccggctccaggtcggcgcggaccgtgcgctgttccggggcgggacg
                                                                                                                                    gcaccgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                          24882 cggtggatgaacgtcgacgaggtgctgagccagctgctctcgcacaacct 24931
                                                                                                                                                                                 364 acgctgggtgacttcgacggcaacctggaggacgcactgggccgcatcct 413
(UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "SsgA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
31..438
                                                                                                                                                                                                                                                                                                                                              Streptomyces griseus ssgA gene-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 27; 60pp; English.
                                                                                                                                                                                                                                                                     AAZ49727 standard; DNA; 438 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-NL00395
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                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces griseus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999;
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                                                                                                                                                                                                                                                                                              AAZ49727;
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                                                                                                                                         ggtggagetecgatacgaggteggegatecgtatgecatecggatgaegttecaeettee 131
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                                                                                                                                                                                                                                                                               192 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt 251
                                                                                                                                                                                                                                                                                                             311
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                                       Gaps
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                                                                     12 ggttcaagcagaggtcatgatgagcttcctccgtaggaggtctccgtattcc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                     268 CCTGGAGCCGGATGTGGACATCTCCGAGGCCCTTCGGGCTCGGGCCGATGTGCACAT
                                                                                                                                                                                                                                                                                                                                                 312 ggtggcgttcctcgaccggacggacaagctcgtgccgctcgggccaggagcacacgctggg
                                                                                                                                                                                                                                                                                                                                                                                 148 TCACAGGGGCATCGCCGGGAAGGTGGAACGTCATCCGGATGGCATACGGATCGCCGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKS; macrolide; nystatin; PKS gene cluster;
                                     ö
 Length 438;
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                                     0; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "NysD2 partial protein"
/note= "CDS does not include stop codon"
complement (1056..2576)
   DB 21;
 Score 58.6; DB 2 Pred. No. 0.0075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "NysB protein"
16550..49840
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50260..51015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "NysE protein"
51405..54305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antifungal; antiblotic; nys1; ds.
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13.4%;
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6952..16530
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                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces noursel
 Query Match
Best Local Similarity
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50786 aggocatogagacotacogotgocogocogacogtoacogocogocogotgacogtoo 50845
                                                                                        50963 aggeceeggegateategatetgeteegggegeacetegeeggeaaeggetagegggege 51022
                                                                                                                                                  acggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggc 262
                                                                                                                                                                                                                                                                         togaccggacggacaagctcgtgccgctcggc-caggagcacacgctgggtgacttcgac 381
                                                                                                                                                                                                              gatacgaggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccc
                                                           50846 tcaccggcgaccgcgacccgaagacctccctggacgaggccga---ggcgtggcgcggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
                                                                                                                                                                                                                                                                                                                                                       /note= "CDS does not include start codon"
complement (59045..60241)
                                                                                                                                                                                                                                                                                                                                     382 ggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaac 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "CDS does not include start codon"
complement (60238..61296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces noursei nystatin PKS gene cluster DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "NysI complete protein"
34792.51099
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= g
'product= "NysD2 complete protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120628 121308
/*tag= h
/product= "NysR4 (long) protein"
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complement (58786..58980)
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51155..57355
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "NysM protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "NysN protein"
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6337..34771
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD17186 standard; DNA; 125401
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/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) ensyme involved in the blosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursel nysl DNA of nystatin PKS gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130,
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135, AAE10136, AAE10137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nystatin polyketide synthase polynucleotides and polypeptides useful as antibiotics and antifungals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strom
                                                                                                                                                 /*tag- j
/product= "NysR4 (short) protein"
/note= "cDS does not include start codon"
61736..62497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.6%; Score 55.2; DB 22; Length Best Local Similarity 49.3%; Pred. No. 0.03; Matches 201; Conservative 0; Mismatches 203; Indels
                                                                          "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                          start codon"
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letta H, Gulliksen O;
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SINTEF STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                            /product= "NysR5 protein"
/note= "CDS does not include
complement (62551..63615)
                                                                                                                                                                                                                                                                                             /note= "CDS does not include 63765..64961
               "NysRl protein"
                                                          'product- "NysR2 protein"
                                                                                                                      product= "NysR3 protein'
                                                                                                                                                                                                                                                                                       'product "ORF2 protein"
                                                                                                                                                                                                                                                                                                                                                   /product= "ORF1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 116-151; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellingsen TE, Sletta H,
   /*tag= g
/product= "Nys
54329..57190
                                                                          /note= "CDS a
57180..59963
                                                                                                                                      60415..61047
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10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
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DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
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(DZIE/)
(ZOTC/)
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Gaps

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Length 65140;

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16-AUG-2001

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Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode; insect; polyketide; polyketide synthase; PKS; extender module; nititator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase;
                                                                                        DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes
                                                                                                                                                                                                                                                                                       'note "Protein involved in transcription control"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= spnI
/note= "Spinosyn biosynthesis protein I"
complement (17749..18501)
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                                                                                                                                                                                                                                                                                                                                                                                           /note= "Spinosyn biosynthesis complement (4168..5325)
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7083..8450
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//octe= "Spinosyn biosynthesis
/967..10427
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complement (12696..13547)
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/note= "Spinosyn biosynthesis
complement (5363..6751)
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10436..11434
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complement (11530..12492)
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complement (14799..16418)
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16556..17743
                                                                                                                                                                                                                                                                                                                                           /note= "Keto acyl reductase"
complement (3416..4165)
                                                                                                                                                                                                                                     Location/Qualifiers
complement (1135..1971)
            AAZ21501 standard; DNA; 80161 BP
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/product= ORFL16
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                                                                (first entry)
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AAZ21501
               2,
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                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursel nystatin PKS gene cluster DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 gatacgaggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccc 142
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                                                                                                                                                                                                                                                                        WPI; 2001-557614/62.
P-PSDB; AAE10143, AAE10144, AAE10145, AAE10146, AAE10147, AAE10148.
AAE10149, AAE10150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.6%; Score 55.2; DB 22; Best Local Similarity 49.3%; Pred. No. 0.029; Matches 201; Conservative 0; Mismatches 203;
                                                                                                                                                                                                                                  Fjaervik E, Brautase
letta H, Gulliksen O;
                                                                                       NORGES TEKNISK NATURVITENSKAPELIGE.
EF STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 188-254; 266pp; English
                                                                                                                                                                                                                                                Sletta H,
                                                             2000GB-0009387.
          08-FEB-2001; 2001WO-GB00509.
                                    2000GB-0002840.
2000GB-0008786.
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                                                                                                                                                                                                                                                Ellingsen TE,
                                                                                                                             SINVENT AS.
DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
                                                                                                                  ALPHARMA AS.
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                                                             14-APR-2000;
                                    08-FEB-2000;
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(BRAU/) I
(STRO/)
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                                                                                                                                         (DZIE/)
(ZOTC/)
(SEKU/)
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(SINV-)
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/note= "Acyl carrier protein domain (ACP4): part of
extender module 4"
                                                                                                                                                                                                                                                    of
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/note= "Dehydratase domain (DH5): part of extender
module 5"
49226..49771
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/note= "Acyl carrier protein domain (ACP3): part e
extender module 3"
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//product= spnD
/note= "Spinosyn biosynthesis protein D"
45077..46348
//*tag= ap
/note= "Beta-ketosynthase domain (KS5): part of
extender module 5"
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Pred. No. 0.035;
0; Mismatches 132; Indels 3;
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/note= "Beta-ketoreductase domain (KR3): part
extender module 3"
39790..40035
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/note= "Beta-ketoreductase domain (KR4): part
extender module 4"
44431..44676
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extender module 5"
50009..50254
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/note= "Beta-ketosynthase domain (KS3): part
extender module 3"
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/note= "Beta-ketosynthase domain (KS4): part
extender module 4"
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/note= "Acyl transferase domain (AT3): part
extender module 3"
38992..39528
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/note= "Acyl transferase domain (AT5): part
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47753..48310
         /note= "Spinosyn biosynthesis protein C" 35518..36786
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extender module 4"
43615..44157
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Best Local Similarity 52.1%;
Matches 147; Conservative
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/note= "Acyl carrier protein domain (ACPi): part of the
initiator module"
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/note= "Acyl carrier protein domain (ACP2): part of
35419..4631
/*tag= af
                                                                                                                                                                                                                                                               /note= "Beta-ketosynthase domain (KS1): part of the initiator module" 22692...23669
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/note= "Acyl carrier protein domain (ACP1): part of
extender module 1"
38916..35374
                                                                                                                                                                                                                                                                                                                                 the
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/note= "Beta-ketoreductase domain (KR2): part of
extender module 2"
34886..30295
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/note= "Beta-ketoreductase domain (KR1): part of
extender module 1"
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/note= "Beta-ketosynthase domain (KS2): part of
extender module 2"
30629..31621
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/note= "Acyl transferase domain (AT1): part of
initiator module"
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extender module 1"
27582..28121
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'note= "Acyl transferase domain (AT2): part
    extender module 2"
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/note= "Enoyl reductase domain (ER2): part
extender module 2"
                                                                                                                                                                                                    /note= "Spinosyn biosynthesis protein A"
/transl_except= (Pos:26940..26942, aa:Pro)
11126..22379
/*tag= r
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             /note= "Spinosyn biosynthesis protein H"
complement (18541..19713)
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/note= "Beta-ketosynthase domain (KS1):
extender module 1"
25683..26684
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/note= "Dehydratase domain (DH2): part
module 2"
                                                                    /note= "Spinosyn biosynthesis protein
20168..20995
                                                                                                                                   'note= "Spinosyn biosynthesis protein
!!!!..28898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Spinosyn biosynthesis protein
                                            /*tag= o
/product= spnG
                                                                                                                         SpnF
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/product= spnH
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29024..30295
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398 cactgggccgcatcctcgccgaggagcagaacgccg
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46.9%;
                                                                                       DNA; 407
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                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                              1..405
/*tag=
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                                                                                                                                                                                                                                                                         Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147269/13.
                                                                                       AAZ49728 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY44649
                                                                                                                                                                                                                                                                                                                                                                WO200000613-A1
                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1999;
                                                                                                                                          18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1998;
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                                                                                                                                                                                                                                                                                                              mat_peptide
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                                                                                                                 AAZ49728;
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                                                                            AA249728/
ID AA24
                                                                RESULT
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278 accgigcgcigitccggggcgggacggcaccgciggiggcgitccicgaccggacggaca 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 tgcgtgcgctgccccaggtaagcgaggccgcgctgctgccacctgcaaccgtaccgagt 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ88151 encodes AAR74619 Xanthomonas campestris L-glutamyl tRNA reductase. The DNA as part of an expression vector can be used to transform a host cell, for the recombinant prodn. of the protein. The protein can be used in the prodn. of vitamin B12, glutamic acid-1-semialdehyde, 5-aminolevulinate, haem, chlorophyll and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 tcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggtcggcgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 agctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctggaggacg
                                                                                                                                                                                                                               Xanthomonas campestris; L-glutamyl tRNA reductase; vitamin B12;
glutamic acid-1-semialdehyde; 5-aminolevulinate (ALA); haem;
chlorophyll; phycobilin; recombinat production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragment encoding L-glutamyl tRNA reductase - derived from Xanthomonas sp., useful for production of 5-amino:levulinate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1549 BP; 291 A; 516 C; 514 G; 228 T; 0 other;
                                                             239 cctggtgatgaacaccggtggatgaacgtcgacgaggtgctg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54.4; DB 16;
Pred. No. 0.046;
0; Mismatches 101;
                                       ctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                                                                                                                                        Xanthomonas L-glutamyl tRNA reductase.
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
212..1492
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Pages 7-8; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KK.
                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas sp., useful for pro
vitamin=B12, chlorophyll, etc.
                                                                                                                           AAQ88151 standard; DNA; 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOGO KENKYUSHO
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53.2%;
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                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR74619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COSM-) COSMO
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                                                                                                                                                                                                                                                                                                                                                               JP07031480-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-1993;
                                                                                                                                                                                                                                                                                   Xanthomonas
                                                                                                                                                                              02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phycobilin.
                                                                                                                                                      AAQ88151;
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          179
                                    349
                                                                                                                                                                                                                                                                                                              Key
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA redduces branchling and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; blomass; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggtggagctecgatacgaggteggegatecgtatgeeateeggatgaegtteeaeettee 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GGTCGAGGAACGCCACCAGCGGTGCCGTCCCCGCCGGAACAGCGCACGGTCCGCGCGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
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NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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/label- SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luiten RGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           griseus ssgA gene-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 5; 60pp; English.
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299; CTGCTGCTGCTGGCGCGCGCAGACGACGAGCCCCGATGGCGGGGGGGCGTGCTGGACGGT
                                                                                                                                                                                                                                                                                                                         319 tteetegaeeggaeggaeaagetegtgeegeteggeeaggageaeaegetgggtgaette
                                                                                      199 ggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatc
                                                                                                                                              359 GCCGACGCGCGGGAGCTGCTGCACGCCGCAGACGACGAAGACGCCGACGCGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 GACGCTGACGCGCGCGGAGCTGCTGCTGGACGGCGCCAGACGACGAGACGCCG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas; maltopentaose; alpha-amylase; enzyme; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas alpha-amylase variant encoding DNA (FERM BP-6116).
                                                                                                                                                                                                                                                                                                                                                                                                                                               379, gacggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaacgccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX37293 standard; DNA; 1981
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nes 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY17904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas sp.
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                                                                                ceccerceccercescereirasecceserecaseasecreseseseseses 119
                                                                                                                                                                                                                                                           cggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacag 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 gcagaggtcatgatgagcttcctcgtctccgaggagctctcgttccgtattccggtggag 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human phosphoglycan protein and its coded sequence
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Pred. No. 0.073;
); Mismatches 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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Similarity 45.5%;
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P-PSDB; AAB74609.
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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylase variants (AAY17904-Y17909). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, O. et al., Biosci. Biochen. Vol. 56, 76-80, 1992 ). The variants have a replacement of the 57th or the 130th amino acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose in a high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gacctggggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacgg 206
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                                                                  Claim 4; Page 6-8; 23pp; Japanese.
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Search completed: July 18, 2002, 11:35:47 Job time: 11212 sec

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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46268
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Patent No. 5212296
Patent No. 5212296
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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5-08-363-255-1
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                                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-WAR-1998
CLASSIFICATION: 435
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US-08-804-198-1

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US-08-920-827-13

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US-08-920-828-13

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APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Ger
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09036987A Patent No. 6143526
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NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                          TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND TITLE OF INVENTION: TRANSFORMANT FILE REFERENCE: 8361-6003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER PLING DATE: 1998-10-21
NUMBER OF SEO ID NOS: 14
SOFTWARE: PATENTIN VOS: 14
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APPLICATE ITO, YOSHIFUMI
APPLICATE TO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
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INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
239 cctggtgatgaacaccggtggatgaacgtcgacgaggtgctg 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MUTATED GENOMIC DNA
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US-09-017-706-3
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                                                                                                                    ; Sequence 3, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
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Best Local Similarity 51.0%;
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: (85)..(1848)
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Best Local Similarity
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APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Crawford, Kathryn P
APPLICANT: Crawford, Kathryn P
APPLICANT: Traedway, Patti J
APPLICANT: Traedway, Patti J
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
CURRENT APPLICATION UNMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
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Pred. No. 0.0059;
0; Mismatches 132;
     ed. No. 0.0059;
Mismatches 132;
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EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SCFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 80161
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; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1
     Pred.
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Best Local Similarity 52.1%;
Matches 147; Conservative
       52.1%;
                            Matches 147; Conservative
     Best Local Similarity
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US-09-370-700-1
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APPLICANT: ITO, YOSHIEWI

TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: UNMBER: US/09/017,706A
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT APPLICATION NUMBER: JP 305071/1997
EARLIER PILING DATE: 1997-10-21
NUMBER OF SEO ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
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                        OTHER: INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: FEATURE:
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US-09-017-706-6
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OTHER INFORMATION: MUTATED GENOMIC DNA
FEATURE:
                                                                   OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                            ; OTHER INFORMATION: PLASMID pOS34100L57
US-09-017-706-5
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LOCATION: (85)..(1848)
      .(1848)
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Best Local $
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Sequence 5, Application US/09017706A

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Sequence 5, Application US/09017706A

Sequence 5, Application US/09017706A

Sequence 5, Application

Sequence 5, Application

Sequence 6087147

TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING

TITLE OF INVENTION: MALPOPENTAOSE, VECTOR CONTAINING SAID GENE AND

TITLE OF INVENTION: TRANSFORMANT

FILE REFERENCE: 8361-0003-0

CURRENT FILING DATE: 1936-02-05

SEALIER APPLICATION NUMBER: JP 305071/1997

SERLIER FILING DATE: 1997-10-21

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 5

SEQ ID NO 5
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FERTURE:
LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
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                                                                                                                                                   TYPE: DNA ORGANISM: Pseudomonas sp., Strain KO-8940
                        305071/1997
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US-09-017-706-4
CURRENT FILING DATE: 1998-02-05
FARLIER APPLICATION NUMBER: JP 305
FARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1981
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LOCATION: (7)..(1848)
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NAME/KEY: CDS
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US-08-034-650-9
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                                                                      642 ggccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac 701
                                                                                                             326
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APPLICANT: 1TO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER FILING DATE: 1997-10-21
NUMBER: OF SEQ ID NOS: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582 gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgtcgatgc 641
 gatetecegaetacetggtegaeetggtecagatgggegteaagggettgegegtegatge 641
                                                                                                                                                                                                                        762 geceagecagtaettegggeteggeggeggeaggteaeggtgaeegagttegeetaegg 821
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                                      cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca
                                                                                                                                                   702 cggtgccgcacggccattctggttcctggaggtgatcggcgcgcggggcgaggcggtgca
                                                                                                                                                                                        ccggacggacaagctcgtccgccaggagcacacgctgggtgacttcgacggcaa
                                                                                                               ggtcggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat_peptide
LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 53.4; DB 3; 51.0%; Pred. No. 0.011; tive 0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: PLASMID: pos3410H139
US-09-017-706-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09017706A Patent No. 6087147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 51.03
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (7)..(1848)
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                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: ITO, YOSHIFUMI
APPLICANT: ITO, YOSHIFUMI
APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPERANDE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: 05/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: J99-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53.4; DB 3; Length 1
Pred. No. 0.011;
0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: PLASMID: POS3410L139
US-09-017-706-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MUTATED GENOMIC DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VERRIPS, COLNELIS T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION O
                                                                                                                 Sequence 8, Application US/09017706A Patent No. 6087147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08034650
Patent No. 5641671
GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 51.0%;
Matches 126; Conservative
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LOCATION: (85)..(1848)
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LOCATION: (7)..(1848)
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822-caaggag 828
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822 caaggag 828
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2201 ATCCGGATCGCCAACGACACCACGCTGAGCCCTGAGCAGAGGCCGCGCGCTTGCCGCC 2260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 gacggcgatgtgcacatcggcccgaccgagcccgagggcttcggagatgtccacatccgg 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2261 crcaaceceaecrcaceceaacesaceaecececaecaecaeceecececere 2312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49.6; DB 1; Length 2
Pred. No. 0.06;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNK/5970/91731
                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-UUL-1991
ATYORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-387-942C-7; Sequence 7, Application US/08387942C; Patent No. 2939289 GENERAL INFORMATION: APPLICANT: ERTESVAG, HELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.9%;
Matches 118; Conservative
                                                                                                                                                                                           COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KOKULIS, Paul N. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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LOCATION:
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US-08-449-015-9
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TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 ctcgaccggacgacaagctcgtgccgctcggccaggagcacacgctgggtg 373
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Pred. No. 0.06;
0; Mismatches 114; Indels 0
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELCOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELERAX: (202) 822-0944
TELERX: (214627 CUSH
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PBUL N.
REGISTRATION NUMBER: 16,773
                                                              ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-449-015-9
; Sequence 9, Application US/08449015
Patent No. 5804409
; GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VERRIPS, Cornelis T.
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illarity 50.9%;
Conservative (
                                                                                                                                                 COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                    NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
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1559..2617
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483..1556
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                                                                                                               Washington
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Best Local Similarity
Matches 118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                 STATE: D
COUNTRY:
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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  Katz, L
Donadio, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 ggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgctggg 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 cggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacag 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 CGAGATGTCCGGCTACGGTTTCGATCCGCACGAGCAGACCATCAACCTGACGATCCGCGA 491
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Best Local Similarity 50.2%; Pred. No. 0.08;
Matches 152; Conservative 0; Mismatches 145; Indels
                                                    TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NOTE:
APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGIGSTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-07-642-734C-1/C
'Sequence 1, Application US/07642734C
'Patent No. 5824513
'GENERAL INFORMATION:
VALLA, SVEIN
SKJAK-BRAEK, GUDMUND
LARSEN, BJORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-7
                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                        22042
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                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                             CITY: 1
STATE:
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LOCATION: 744..11219
OTHER INFORMATION: /function= "gene="eryA""
OTHER INFORMATION: /product=""ORf! encoding modules 1 & 2 for OTHER INFORMATION: /Geoxyerythronolide B""
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LOCATION: 2250..3550
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 744..1868
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
APPLICANT: MCalpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SCUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Abbott Park
                                                                                                                                                                                                                                                    STATE: ___
COUNTRY: US

COUNTRY: US

ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DANCKETS, ANGRESS M
REGISTRATION NUMBER: 32652
REFERENCE/POCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFPAX: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /function- "approximate span of OTHER INFORMATION: acyl carrier domain 1 of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function= "APPROXIMATE SPAN OF MODULE 1"
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LOCATION: 3831..4811
OTHER INFORMATION: /function= "approximate span of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 744..6659
OTHER INFORMATION: ^function= "APPROTHER INFORMATION: MODULE 1"
OTHER INFORMATION: /label= FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 11219 base pairs TYPE: nucleic acid STRANDEDNESS: double
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INVENTION: Specific Polyketides SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 11219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 744..6659
OTHER INFORMATION: /func
OTHER INFORMATION: /labe
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                         NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                  STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5964 CGGTCAGGTCCAGCTCACCTCACCTCAGGTTGCGCGCCCCAAGCATTGGCGC 5905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 tgtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggt 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccctgtgac 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 ctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 cggcgcggaccgtgcgctgttccgggcggggggacggcaccgctggtggcgttcctcgaccg 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 gacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacg 382
                                               NAME/KEY: misc_feature
COGATION: 5574..6125
OTHER INFORMATION: /Lunction= "approximate span of
OTHER INFORMATION: /beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 9906.110454
OTHER INFORMATION: /tunction= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.2%; Score 49; DB 1; Length 11219; Best Local Similarity 50.2%; Pred. No. 0.078; Matches 147; Conservative 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678.8066
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacyl ACPsynthase of module;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 8262.9305
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
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Patent No. 6004787
GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
                                                                                                                                                                                         LOCATION: 6369..6626
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain 2 of module 1"
                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..11219
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

: LOCATION: 10707..10964

: OTHER INFORMATION: /function= "approximate span of

: OTHER INFORMATION: acyl carrier domain of module 2"

US-07-642-734C-1
                                                                                                                                                                     NAME/KEY: misc_feature
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NAME/KEY: CDS
LOCATION: 744..11219
COTHER INFORMATION: /function= "gene= "eryA""
OTHER INFORMATION: /froduct= ""ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
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NAME/KET:

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LOCATION: 744..1868
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 3831..4811
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase 2 domain of module 1"
ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= "APPROXIMATE SPAN OF MODULE 1"
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    NAME/KEY: misc_feature
    LOCATION: 5574..6125
    OTHER INFORMATION: /function= "approximate span of
                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 60064-3500
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORIVEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
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1251 Avenue of the Americas
                                                            USA
                    CITY: Ner
STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 ctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 tgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggt 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cggcgggaccgtgcgctgttccgggggggggacggcaccgctggtggcgttcctcgaccg 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 6678..8066
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACPsynthase of module 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 8262..9305
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 9906..10454
OTHER INFORMATION: _function= "approximate span of
OTHER INFORMATION: _beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 3; Length 11219;
Pred. No. 0.078;
0; Mismatches 145; Indels
                                    NAME/KEY: misc_feature
LOCATION: 6369..6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..11219
COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James F. Haley, Jr., Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nakamura, Etsuo
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Kitadokoro, Kongo
APPLICANT: Shin, Nasaru
APPLICANT: Tsraoka, Hiroshi
TITLE OF INVENTION: No. 566586el Protease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jamee 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08343428
Patent No. 5665586
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.2%;
Best Local Similarity 50.2%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-343-428-1
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                                                                                              COMPUTER REALBLE FORCE.

COMPUTER: IBM Compatible
CONTRIBUTION WINGER: US/08/343,428
FILING DATE: 18-NOV-1994
CLASSIFICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
APPLICATION NUMBER: JAPAN 4-126511
FILING DATE: 19-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
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E: Genomic DNA
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LOCATION: 359.364
IDENTIFICATION METHOD:
NAME/KEY: -10 signal
LOCATION: 378.383
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NAME/KEY: sig peptide
LOCATION: 435.944
DENTIFICATION METHOD:
US-08-343-428-1
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STRANDEDNESS: double
                                                                                  COMPUTER READABLE FORM:
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Best Local Similarity
                      New York
                                                          10020-1104
New York
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                                                                                                     APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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Pred. No. 0.25;
0; Mismatches 146; Indels 3
                                                                                                                                                                                                                                                            ADDREESER JACORSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRELIAR PRELAGES #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APFLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS PITICE
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECHONE: (202 638-6666
TELECHONE: (202 638-6666
TELEFAX: (202) 39305350
TELEFAX: RCA 248593 IDEA UR
: INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
THEAT OF THE CHARACTERISTICS:
                  Sequence 16, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
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Best Local Similarity 49.7%;
Matches 147; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-09-385-028-16
US-09-385-028-16
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Search completed: July 18, 2002, 11:24:25 Job time: 10855 sec

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Sequence:

Run on:

Searched:

Database

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Result

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Direct Submission

Direct Submission

B Direct Submission

Submitted (10-210)-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland bow to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                    AQ852043 LMAJFVI_
BB635178 BB633178
BB1730817 603351815
BH019916 L5873b.d_
BM658211 AGENCOURT
BI529148 1024065E0
BG859785 102406411
AG057280 Pan trog1
ALS88142 AL588142
AL395670 AJ395670
AL395670 AJ395670
AL064280 Drosophil
AL066742 Drosophil
AG043477 Pan trog1
AW911065 UFRZCOG.Y
BED440853 OFRIZOGO
AL287096 TELTAGOGON
AL066051 Drosophil
AG152796 Pan trog1
AG152796 Pan trog1
                AQ852321 LMAJFV1_1
AL108460 Drosophi1
AQ846145 LMAJFV1_1
BH018404 L14841.d_1
AQ846152 LMAJFV1_1
BH020269 L7165c.d_
BH019836 L5336c.d_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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BBG35178
BBG35178
BH019916
BH52918
BGB59785
AGB4055
AGB4055
AGB4055
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AGB1405
AGB1405
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BH020269
BH019836
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CNS006XK
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                                                    AQ846145
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Drosophila melanogaster
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CNS0091P/C
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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   RESULT
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AQ85496 nbeb0003C
AL066051 Drosophil
AQ851215 LMAJFV1_1
AQ851019 LMAJFV1_1
AQ851019 LMAJFV1_1
AQ851316 LMAJFV1_1
AQ851316 LMAJFV1_1
AQ851316 LMAJFV1_1
AQ851316 LMAJFV1_1
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1225.988 Million cell updates/sec
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L11211.d
Pan trog1
SCL074.G1
L24591.d
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Drosophil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                        438
1 atgcgcgagtcggttcaagc.....aggagcagaacgccggctga 438
                                                                                                                   July 18, 2002, 07:26:40 ; Search time 4821.96 Seconds
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BE418762
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              13736207 segs, 6748477542 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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AQ851336
CNS02DOV
C97336
AQ849196
CNS010EW
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AG032885
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Maximum DB seq length: 2000000000
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em_gss_hum:*
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Match Length DB
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928 bp DNA linear GSS 03-NOV-1999 nDeb0003C14f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0003C14f, DNA sequence. AQ856496 AQ856496.1 GI:6206953
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Ehrhartoldeae; Oryzeae; Oryza.

I (bases I to 928)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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                                                                                                                                                                                                                                                                                   gecatecggatgaegttecacetteceggegatgeeetgtgaeetgggegtteggeege 165
                                                                                                                                                                                                                                                                                                                         535 SMCGKKCGSTTBGSTTTTTTSSGSGYGKGCSSGSBSCSCCSSCSSSSSCSCCBCCCC 594
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/cultivar="Wipponbare"
/db_xref="taxon:4530"
/clone="nbeb0003c14f"
/clone=lib="CUGI Rice BAC Library (EcoRI)"
                                                                                               511 others
                                                                                                                                                                                                                                   Mismatches 124;
                                                                                                                                                                                        Score 57.8; DB 12;
Pred. No. 0.75;
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
Clemson University
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Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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High quality sequence stop: 194.
Location/Qualifiers
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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61 g
                                                                                                                                                                                        13.2%; Sco
llarity 14.3%; Pre
Conservative 152;
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- Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: n bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit AL053013)
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                       511 others
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                                                                                                                                             Query Match 13.4%; Score 58.8; DB 12;
Best Local Similarity 13.8%; Pred. No. 0.51;
Matches 49; Conservative 175; Mismatches 128;
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                                                       172
       /clone="BACR19D16"
/note="end : TET3"
61 c 61 9
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SOURCE ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

DEFINITION

CNS0091P

RESULT LOCUS ACCESSION VERSION KEYWORDS source

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FEATURES

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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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LMAJFV1_Im44f10.x1 Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_lm44f10 3' similar to
contains element V1-ch1_type_II.2 leishmania repetitive element;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases 1 to 556)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                  /lab_nost="c. coll billow site_l: EcoRI; Site_2: EcoRI; Alote="Vector: pBACIndigo: Site_l: EcoRI; Site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents: The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit

    Web : www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of a

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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gacctggggcgttcggccggcgagctgctgctggacgggctcaacagcccgagcggcgacgg 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 GAGCGAGGTGAAGGCCATGGCGCGCATCGACAGCCCTCGTCCGCTTCTACGGCTA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 GAGCTCGGTGTTCTCCATGGAGGAGATCCTGCGCGCCACCAACAACTTCTCGCCGCGGCGCT 332
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Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 4.9;
0; Mismatches 140; Indels
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:

If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
Seq primer: -400P from Gibco
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Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Willams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                           shotgun sequencing: a resource for DNA microarrays and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 cggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttccaccttc 130
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                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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46.6%; Pred. No. 5.6;
tive 0; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Leishmania major"
/strain="Friedlin strain V1"
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High quality sequence stop: 418.
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Contact: Akopyants, NS /
WashU Leishmania Project
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    AUTHORS
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Library construction: Natalia S. Akopyants, Ph.D.

Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing

If using this information please cite:

N.S. Akopyants and S.M. Beverley' A survey of the Leishmania major

Friedlin strain V1 genome by shotgun sequencing' and the Washington

University Genome Sequencing Center For Information on obtaining

clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wastl.edu)

Seq primer: -40UP from Gibco

Class: shotgun
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/clone_lib="Leishmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
                                                                                                                                                                                                                                                                                                                                                                                             AQ847989
LMAJFVL_IMS3NO1.x1 Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_IMS3NO1 3' similar to
contains element 212bp.2 leishmania repetitive element ;, DNA
                                                               62
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
371 gigacticgacggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaacg
                                                           121 ACGAAGACGCCGACGCGCGGGAGCTGCTGGACGCGCGCAGACGACGAGGACGCCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Contact: Akopyants, NS / Beverley, SM
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/strain="Friedlin strain Vl"
/db_xref="taxon:5664"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ847989.1 GI:6052637
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Fax: 314 286 1810
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Leishmania major.
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  and/or Stephen M. Beverley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 51.2; DB 12;
.larity 47.0%; Pred. No. 9.7;
Conservative 0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                                          major"
                                                                                                                                                              /strain="Friedlin strain V1"
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                                                                                                                         1. .555
/organism="Leishmania
                                                                                                                                                                                     /db_xref="taxon:5664"
(natalia@borcim.wustl.edu) ar
(beverley@borcim.wustl.edu)
Seq primer: -400P from Gibco
                                                                                 High quality sequence stop: ...
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
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                                                                                                                                                                  CAACGAAGACGCCGACGCCGAGGCTACTGCTGCTGGACGCCGCAAGAGGC 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gggtgacttcgacggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaa 428
                                                             tccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttccacct 128
                     Gaps
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                                                                                                  TGCGGAGCTGCTGGACGGCGCACGACGACGACGCCGACGCGGGGGGGCTGCTGCT 91
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Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
WashIngton University School of Medicine
WashIngton Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leishmania major.
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                     Indels
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                   198;
ed. No. 6.5;
Mismatches
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1 (bases 1 to 555)
Best Local Similarity 46.3 Matches 171; Conservative
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Fax: 314 286 1810
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LMAJFVI_lm29c04.yl Leishmania major FVI random genomic library Leishmania major genomic clone LMAJFVI_lm29c04 5' similar to contains element V1-ch1_type_II.2 V1-ch1_type_I leishmania repetitive element ;, DNA sequence.
/uncarter_readours.
/clone=linaJFVI_ind3e03"
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/lab_host="TOPIO (invitrogen)"
/note="Vector: peeco-2" (invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pzero-2 vector's EcoRV site."
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/strain="Friedlin strain V1"
/db_ref="Lexon:5664"
/clone="Luka_FFV1_lab_2004"
/clone="Luka_FFV1_lab_2004"
/clone="Luka_FFV1_lab_2004"
/lab_host="ToPI0 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: ECORV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECORV site."
84 a 140 c 204 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
Seq primer: -40RP from Gibco
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               1 (bases 1 to 474)

Akopyants, M.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., K.

Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A.,

Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, T., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M.,

I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M.,

Barvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y.,

Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M.

A survey of the Leishmania major Friedlin strain v1 genome by shotyun sequencing: a resource for DNA microarrays and expression
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                                                                                                                                                                                                                                                                                                                                    Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 1
Tel: 314 286 1800
Fax: 314 286 1810
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21192569
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Pred. No. 12;
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Location/Qualifiers
1. .474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: shotgun
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                    REFERENCE
                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                         TITLE
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CNSO2DOV 755 bp DNA linear GSS 13-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 260D06 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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1 (bases 1 to 755)

10 (bases 1 to 755)

11 (bases 1 to 755)

12 (bases 1 to 755)

13 (bases 1 to 765)

14 (bases 1 to 765)

15 (bases 1 to 765)

16 (bases 1 to 765)

17 (bases 1 to 765)

18 (bases 1 to 765)

19 (bases 1 to 765)

10 (bases 1 to 765)

11 (bases 1 to 765)

12 (bases 1 to 765)

13 (bases 1 to 765)

14 (bases 1 to 765)

15 (bases 1 to 765)

16 (bases 1 to 765)

17 (bases 1 to 765)

18 (bases 1 to 765)

18 (bases 1 to 765)

19 (bases 1 to 765)

10 (bases 1 to 765)
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Roest-Crollius, L. Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence ID : COAG260DB03LP1-end : T7" g 111 t 3 others
                                  404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 TTCCTCCGCCTGCCCGGGGACAAGGTCCAGGAGCTGATCCTCAGGGAGGAGGTGGAGGTG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 GAGGACGAGAGCCTGGTGTACGAGGCCGTGATCGACTGGGTCAAGGCCGACACGGAGCGC 396
345 gccgctcggccaggagcacacgctgggtgacttcgacggcaacctggaggacgcactggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="260D06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
16;
                                                                                                                                   437
                                                                                                                                                                         Score 50;
Pred. No.
                                                                                                                                   405 ccgcatcctcgccgaggagcagaacgccggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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/note="Genoscope
1 238 c 266
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us-09-749-185-1.rst

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/_clone="LMAJFV1_lmd3e09"
/clone="Liba"Leishmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: ECORV;
/note="Vector: pZero-2 (Invitrogen); Site_1: ECORV;
denomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECORV site."

136 c 195 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
                                                                                                                AQ849196 LMAJFVI_Im43e09.yl Leishmania major FVI random genomic library Leishmania major genomic clone LMAJFVI_LM43e09 5' similar to contains element V1-chl_type_II.2 leishmania repetitive element;
                                                                                                                                                                                                                                                                                                                                                                                  Leishhania.

1 (bases 1 to 442)

1 (bases 1 to 442)

1 (kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishhania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 gcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgatgtg 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                          Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
346 CCTGATGGGCGAGTTCGTGCCGTGCGACGAGGTGCGCGACCTG 388
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Pred. No. 18;
0; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Leishmania major"
/strain="Friedlin strain Vl"
/db_xref="taxon:5664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Akopyants, NS / Beverley, SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 302.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (beverley@borcim.wustl.edu)
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU Leishmania Project
                                                                                                                                                                                                                                           AQ849196
AQ849196.1 GI:6053844
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48.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                   Leishmania major.
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                                                                                                                                                                                                                       DNA sequence.
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Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    profiling
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                                                                      11
                                                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE AUTHORS
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COMMENT
                                                                                                                                                                                                                                           ACCESSION
VERSION
                                                                      RESULT 1
AQ849196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                          KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:6300"
/clone="t6000211A"
/clone=lib="Raice callus"
/clone="vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1994)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgatgtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctcca 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggtcggcgcggaccgtgcgctgttccggggcggggacggcaccgctggtggcgttcctcga 326
                                               301 acggcaccgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggag 360
                                                                        457 TACCTGCTGAAGACGGTGCCTCCGAGGAGCTGGTCATGTGCCACAAGCTGGGCGGGAG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgaggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgt 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 cgaccreecesesesesesesesesesesesesesesesesererreraceseseaacesesa 171
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172 GCCGGGGTTCTTCGCGGCCGACGCCATGAGGGACAGCCTCGCCAGGGCGCTCGTGGCGTT
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Fax: 81-298-38-7468
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- O	RESULT CNSO2A LOCUS	DEFINI	ACCESS VERSIC KEYWOR SOURCE ORGA	REFERE	TITI	JOUR REFERE AUTH	TIL	JOUR REFERE AUTH	TITL JOUR	FEATUR	-	BASE C	Quer Best Matc	δλ	QQ	ò á	λo	O Qy
214 cacatoggcccgaccgagccccgaggcctcggagatgtccacatccggctccaggtcggc 273 	274 gcggaccgtgcgctgttccgggcggggacgcaccgctggtggcgttcctcgaccggacg 33		394 gacgcactgggccgcatcctcgccgaggagcagaacgccg 433 	RESULT 12 CNSO10EW/C LOCUS CNSO10EW CNSO10EW CNSO10EW LOCUS LOCUS DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BARCN3P19 of DrossBAC library from Drosophila melanogaster (fruit	ACCESSION AL098882 VERSION AL098882.1 GI:5610493	Σ	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. T (bases 1 to 1009) AITHHORS Genescope		 - Web: www.genoscope.cns.fr) - Obtermination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebl.ac.uk - This Drosophila melanogaster BAC 	Library (Dros HAC) was made by Alain Biliaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genewieve Payan. It has been constructed in the vector	FEATURES FORTING 11 1009	BAC BAC	178 9 64	Query Match 11.3%; Score 49.6; DB 12; Length 1009; Best Local Similarity 32.8%; Pred. No. 19; Matches 77. Concervative F. Mismaches 103. Indale 0. Care 0.	cetteceggegatgecetgtgacetgggegtteggeegegagetgetgetggaeggget 185	919	186 caacagcccgagcggcgacggcgatgtgcacatcggcccgaccga	246 agatgtccacatccggctccaggtcggcggaccgtgcgctgttccgggggggg
oy Op	Oy Db	g 5	O. D.	# 5 X B	AC VE	N N	RE		ម		F		B. OF		δý	g	9	oy B

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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at Location/Qualifiers

Location/Qualifiers

1. 1129

/organism="Tetracdon nigroviridis"
/db_xref="taxon:99883"
/clone="151L09"
/clone="251L09"
/clone="251L09"
/clone="1b="G"
/note="Genoscope sequence ID : COAG251CF05SP1-end :
                                                                                                                        CNS02AGC 1129 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 251L09 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetler, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished
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306 accgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggag 360
                    739 CCSGSTGCGGSCCCCCCCCCCCCCCCCCCGGCCRSKCSCVGCCGGGGGGG 685
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0; Mismatches 179; Indels
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us-09-749-185-1.rst

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AG032885.1 GI:16559758
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-007M05.F.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chases 1 to 1313)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:i81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RsD process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                         AG032885 1313 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-007M05.F, genomic survey sequence.
AG032885
                              107 ccatccggatgacgttccaccttcccggcgatgccctgtgacctgggcgttcggccgcg 166
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                                                                                                                                     gatgtccacatccggctccaggtcggcgcggaccgtgcgttccgggggggacggca
                                                                             477 NAGGACGAAGACGCCGACGCGCGCGCAGCTGCTGGACGCCCCANAGGACGAAGACGCC
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/clone_lib="PTB Chimpanzee Male BAC Library"
389 c 502 g 132 t 225 others
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Pred. No. 20;
0; Mismatches
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Fullyama,A., Watanabe,H. and Sakaki,Y.
Tocoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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/db_xref="taxon:9598"
/clone="PTB-007M05.F"
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Location/Qualifiers
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Matches 158; Conservative
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R.Site 2
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/clone_lib="Leishmania major Friedlin Cosmid Genomic
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/strain="Friedlin"
/db_xref="taon:5664"
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Sequence Streptomy

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AK00722 Sequence
AK195770 Streptomy
AK007220 Sequence
AK195771 Streptomy
AK195771 Streptomy
AL036852 Streptomy
AL13778 Streptomy
AL13778 Streptomy
AL03833 S-ablus bet
AL049587 Streptomy
AK089419 Sequence
AL049863 Streptomy
AL159139 Streptomy
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AL031702 Streptomy
AL035640 Streptomy
AL035640 Streptomy
AL03564 Saccharop
AR165018 Sequence
AL646084 Rasistonia
D15673 Xanthomonas
E08655 DNA encodin
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AP004006 Oryza sat
Continuation (8 of
D87846 Streptomyce
X72787 S.griseus n
AC092558 Oryza sat
AX007216 Sequence
D50051 Streptomyce
AR103043 Sequence
AR103045 Sequence
AR103047 Sequence
AR103047 Sequence
AR103047 Sequence
E24180 Alpha-amyla
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Actinomycetales; Streptomycineae; Streptomyces.
Actinomycetales; Streptomycineae; Streptomyces.
Actinomycetales; Streptomycineae; Streptomyces.
I (basea 1 to 40)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: Wo 0000613-A 3 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARI.
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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Sequence 3 from Patent W00000613.
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AE004767
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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_htg_other:*
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Maximum DB seq length: 200000000
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Post-processing:

Database

Total number of

Searched:

Scoring table:

Perfect score:

Title:

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Score

Result No.

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BLVARELDRTDKLVMGGGPTLGGDFGAUEDALGR"
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Streptomyces griseus
Bacteria; Firmlcutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Cloning and characterization of a gene involved in regulation
sportulation and call division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
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Isolation of mutants of Streptomyces griseus that sporulate
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Pred. No. 9.7e-43;
; Mismatches 0;
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D50051, GI:1772323
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Actinomycetol. 9, 124-135 (1995)
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Best Local Similarity 100.0%;
Matches 407; Conservative 0
                                                             /gene="ssgA"
                    /gene="ssgA"
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                                                                                                      /codon_start=1
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/translation="WSFLVSEELSFRIPVERRY
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 1 06-JAN-2000; DUITEN RUDOLE GIJSBERTUS MARIA (NL); KRAL BARRND (NL); LUITEN RUDOLE GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/gene="ssgA"
/note="strain ATTC of Streptomyces griseus"
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Pred. No. 9.9e-43;
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Matches 407;
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Best Local Similarity
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                                                    Shinichi, K. and Ensign, J.

Shinichi, K. and Ensign, J.

Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus

L. Unpublished (1995)

E. Shases I to 1513)

Shinichi, K.

Direct Submission

L. Submitted (06-APR-1995) Kawamoto Shinichi, National Food Research
Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)

L. 1513

Irce

L. 1513
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DKLVPLGQEHTLGDFFDGNLEDALGRILAEEQNAG"
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Pred. No. 7e-43;
0; Mismatches 0;
                                                                                                                                                                                                 /organism="Streptomyces griseus"
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385. 389
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Best Local Similarity 100.
Matches 407; Conservative
                                  97286526
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BASE COUNT
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AUTHORS
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RESULT AF195772

AX007224

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
PAT 06-SEP-2000
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                                                                                                                                                                                                                             Streptomyces netropsis.
Streptomyces netropsis
Streptomyces netropsis
Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gigeacaicggeocgaccgagecegaggecteggagaigtecacaiceggetecaggie 240
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DNA
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                       AX007222
Sequence 7 from
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                       LOCUS
DEFINITION
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158 c 142 g 68 t
   BCT 01-NOV-2000
                                                                                                                                                                                                                                                                                 /note="similar to Streptomyces griseus SsgA; possible cell division protein"
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                                                                                       Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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Direct Submission
Submitted (18-OCT-1999) Biochemistry, University of Leiden, 9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
                                                                                            (bases 1 to 438)

van Wezel, G. P., Rousseau, C. and Kraal, B.

Cloning and sequencing of the Streptomyces netropsis ssgA (unbulished)

2 (bases 1 to 438)
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                                                                  Streptomyces netropsis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   DNA linear BC
gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 438;
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1. .438
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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Pred. No. 4.9e-29;
0; Mismatches 68;
Streptomyces netropsis SsgA (ssgA)
AF195772
AF195772.1 GI:11066162
                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                        netropsis.
                                                                                                                                                                                                                                                /gene="ssgA"
                                                                                                                                                                                                                                                                       /gene="ssgA"
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Best Local Similarity 83.3%;
Matches 339; Conservative
                                                       Streptomyces
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                                VERSION
KEYWORDS
SOURCE
ORGANISM
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             DEFINITION
                                                                                               REFERENCE
AUTHORS
TITLE
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145 q 71 t
                                                                                                                                                                                                                            Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms
Patent: WO 0000613-A 7 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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PAT 06-SEP-2000
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Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
Actinomycetales: Streptomycineae: Streptomyces.
1 (bases 1 to 407)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Streptomyces goldeniensis'
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/db_xref="taxon:121022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.8%; Score 259.8; DB 6; Best Local Similarity 77.4%; Pred. No. 3.4e-24; Matches 315; Conservative 0; Mismatches 92;
  DNA
407 bp
Patent WO0000613
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="strain ATCC
                                                                                                                  Streptomyces goldeniensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/trans1_table=11
                                                                     GI:9995088
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BCT 08-JUL-1999

linear

361 GACGAGGCGCTGGACCGCATCCTGGCCGAGGAGCAGAACGCCGGCTG 407

g

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Jun/Ggi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13pb before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the cannot be identified we choose the most upstream initiation codon. If we have not be entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the AseI-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Substitution of significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Blibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                            AL096823.1 GI:5457267
abaB; bldA regulation; cysA; cystathionine/methionine
gamma-synthase/lyase; gntR-family; integrated element; korSA;
lysR-family; membrane protein; phosphotyrosine protein phosphatase;
pra; pSAM2; ptpA; ssgA; thiamine biosynthesis; thiC;
transcriptional regulator; traSA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycesces. 1 (bases 1 to 15441)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-UUL-1999) Streptomyces coelicolor sequencing proje Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1878 E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seeger, K. and Harris, D. Unpublished
3 (bases 1 to 15441)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                     Streptomyces coelicolor cosmid Q11. AL096823
                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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RELLIDGGPRECGDGTVHIAPADPEFFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KVPLGGGESLADFPALDFALDRILAEEQNAG"
135 c 171 t 171 t 771 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to Streptomyces griseus SsgA; possible cell division protein"
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                                                 BCT 01-NOV-2000
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                                                                                                                                                                                                                                                                     1 (bases 1 to 408) van Wezel, G.P., Rousseau, C. and Kraal, B. Cloning and sequencing of the Streptomyces goldeniensis ssgA gene
                                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submission Submitted (18-021-1999) Biochemistry, University of Leiden, 9502, Leiden 2300 RA, Netherlands Location/Qualifiers
                                               F195770 408 bp DNA linear BCT 0 treptomyces goldeniensis SsgA (ssgA) gene, complete cds.
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                                                                                                                                                                       Streptomyces goldeniensis.
Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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    408
    forganism="Streptomyces goldeniensis"
/db_xref="ATCC:21386"
/db_xref="taxon:121022"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAG28481.1"
/db_xref="GI:11066159"
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/product="SsgA"
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0
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1. .408
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77.4%;
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van Wezel, G.P.
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project,

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SW.CYSA_STRCO (EMBL.037580), cysA, S. COCIICOLO PUTGITIVE
Cystathionine gamma-lyase (392 aa). Similar to many e.g.
SW.MEGL_PSEPU (EMBL.018854), mdeA, Pseudomonas putida
methionine gamma-lyase (398 aa), fasta scores; opt: 608
z-score: 653 6 E(): 4.5e-29, 36,9% identity in 404 aa
overlap. Highly similar to TR:053668 (EMBL.39139)
Streptomyces antibloticus hypothetical protein found
upstream of the abaB gene (232 aa) (87.1% identity in 232
aa overlap). Contains Pfam match to PF01653
aa overlap. Cys/Met metabolism PLP-dependent enzyme
and PS00868 Cys/Met metabolism enzymes pyridoxal-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-tyrosine-phosphatase, len: 164 aa; previously sequenced as SW:PTPA_STRCO (EMB:U3/580), ptpA, scoelicolor low molecular weight. protein-tyrosine-phosphatase (164 aa). Contains Pfam match to PF01451 LMWPC, Low molecular weight phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTYRVCFVCTGNICRSPWAEAVFRARVEDAGLGHLVVEADSGTG GWHEGEGADPRTEAVLADHGYGLDHAARQFQQSWFSRLDLVVALDAGHLRALBRLAPT ERDAAKVRLLRSYDPAVAGGDLDVPDPYYGGRDGFEECLEMVEAASTGLLAAVREQVEGRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGGETLVFASGMAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKVAEALRTRPEITGLRYPGLPDDPSHKVASQQMLRYGCVVSFTLPSRARADRFLDA
LRLVEGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IETPSNPGLDVCDVRRLVEAAHAGGALVAVDNTLATPLGQRPLELGADFSVASGTKQL
len: 392 aa; previously sequenced as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGHGDVLLGYVAGRDAGAMAAVRRWRKIVGAIPGPMEAWLAHRSIATLQLRVDRQDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 tggggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1533. .2624)
/gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
complement(2031. .2075)
/gene="SCQ11.03c"
/note="PSO0868 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
/gene="SCQ11.04c"
/gene="SCQ11.04c"
/gene="SCQ11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 groggogatccgtatgccatccggatgacgttccaccttcccggcgatgccctgtgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5535 ACCCGGGATCCCTATGCCGTACGCCTGACCTTTCATCTGCCCGGAGACGCGCGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 256.6; DB 1; Length 15441; Pred. No. 3.3e-24; 0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2693. .3187)
/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"putative cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="low molecular weight
protein-tyrosine-phosphatase"
/protein_id="CAB46959.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma-synthase/lyase"
/protein_id="CAB46958.1"
/db_xref="G1:5457270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:545727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.08;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"ptpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=cysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-ptpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 76.9
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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complement(360. .1265)

/gene="SCQ11.02c" abaB, probable lysR-family
/note="SCQ11.02c, abaB, probable lysR-family
transcriptional regulator, len: 301 aa; previously
sequenced as TR:Q53869 (EMBL:U37580) s.coelicolor
lysR-like procein (301 aa). Highly similar to
SW:ARAB_STRAT (EMBL:W31939), araB, Streptomyces
antibioticus transcriptional regulatory protein (301 aa),
fasta scores; opt: 1581 z-score: 1813.2 E(;; 0, 80.3%
identity in 300 aa overlap. Similar to many other
transcriptional regulators. Conteains probable
helix-turn-helix motif at aa 17-38 (Score 1659, +4.84 SD).
Contains Pfam match to PF00126 HTH., Bacterial regulatory
helix-turn-helix protein, lysR family and PS00044
Bacterial regulatory proteins, lysR family signature"
                                                                                                                                                      complement(<1...289)
/gene="SCO11.01c"
/gene="SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDLALLRTEVTVHRAGSFTRAAALLGLSOPAVTSOIRTLERQLG
RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAETGLEDDSTLRTLHLAGPPEFTA
ERALPALGELTGEDGQAFALRASFGNAEETLEGLAAGHHDLAIGTTRPRGALHTATPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTVRPVVKRTARAVLLDGDHLILIKRTKPGVDPYMVTPGGGVEP
DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDEVHVLVATPHWAERAGVEDVRDTDASALKHVPVVEVHESLPFVGRYMASVFDARPA
SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
RTGTLAMPHIARAHEWLLRAAADWN"
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/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="GI:5457269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00044 Bacterial regulatory proteins, lysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (172 aa), fasta scores; opt: 158 z-score: 206.4
E(): 0.00036, 46.2% identity in 65 aa overlap. Continues
as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1. .4279)
/note="sequence corresponding to EMBL:U37580 from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .98
/note="overlap with Streptomyces coelicolor cosmid H24
(EMBE.AL049826) from 41528 to 41625"
complement(360. .1265)
/gene="SCOII.02c"
/note="abaB"
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/gene="SCQ11.02c"
/note="March to PF00126 HTH_1, Bacterial regulatory
holix-turn-helix protein, lysR family Score 145.96"
/gene="SCQ11.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
/protein_id="CAB46956.1"
/db_xref="G1:5457268"
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                                                                                 complement(1. .289)
/gene="SCQ11.01c"
                                          /clone="cosmid Q11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/label=abaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/label=SCQ11.01c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/translation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
RELLVEGVLDAAGDGDVRVCPVGQTATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
QCISLGSERAHADFDSHLDDALNRSLAEEQSAG"
1219 c 192 g 80 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces griseus SsgA; possible cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomycineae; Streptomycetaceae; Streptomyces
61 gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgacc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 ATGAGCTTCCTCGTCTCCGAGGAGCTCGCCTTCCGCATCGGTGGAGCTGCGGTGAGG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Strept 1 (bases 1 to 566) van Wezel, G.P., Rousseau, C. and Kraal, B. Cloning and sequencing of the Streptomyces albus ssgA gene Unpublished
                                                                   241 ggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgg
                                                                                                                                                    241 GGCTCCGAGCAGGCGCTCTTCCGCGTCGGCAAGGCGCCCGCTGCTCGCCTTCCTCGACCGC
                                                                                                                                                                                      301 acggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgagetteetegteteegaggagetetegtteegtatteeggtggageteegataegag
                                                   gtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 566;
                                                                                                                                                                                                                                                                                                                                                                      Streptomyces albus SsgA (ssgA) gene, complete cds. AF195771
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.7%; Score 239; DB 1; 74.2%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-OCT-1999) Biochemistry, Un
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
1. .566
/organism="Streptomyces albus"
//db_rref="taxon:1888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAG28482.1"
/db_xref="G1:11066161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to
division protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="SsgA"
                                                                                                                                                                                                                                                                                                                                                                                                                           AF195771.1 GI:11066160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ssgA"
26. .433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ssgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ssgA"
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                                                                                                                                                                                                                                                                                                                                                                            PAT 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
RELLVEGVEDAAGDGDVRVCPVGQTATREVH1TLQVGSEQALFRVGKAPLLAFLDRTD
QGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
1 150 c 1139 g t 1
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
                                                                                 5714
240
                                                                                                                  241 ggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgg 300
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                                                                   5715 GGCAGCGAGCGCTGTTCCGTTCCTCCGCCGCCCTGGTGGCCTTCCTCGACCGC
                                                                                                                                                                                       acggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/note="strain ATCC of Streptomyces albus
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Pred. No. 1.4e-21;
0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces albus/db_xref="taxon:1962"
                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              filamentous microorganisms
Patent: WO 0000613-A 5 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL);
VAL); NL ORGANISATIE VOOR WETENSCHAP
VAN (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAC07386.1"
/db_xref="GI:9995087"
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 from Patent W00000613.
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/product="SsgA"
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74.28;
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1. .>405
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Correct initiation codon. Where possible we choose an initiation codon (att) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the AseI-E genomic restriction fragment.
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TGYTFARENLEKAHALAEATCLPAVADOSGLCVDUKNAPAGTESARWACRHGDDQANL
DLILAGOLADIADERGAHFACAAALALPDGTERVUEGOLKGTLRHAFAGTGGFGYDPI
LOPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCE19A.01"
/note="SCE19A.01, hypothetical protein, partial CDS, len:
/note="SCE19A.01, hypothetical protein, partial CDS, len:
/note="SCE19A.01, hypothetical protein members of the alkyl
hydroperoxide reductase C/thiol-specific antioxidant
family e.g. TR:051226 (EMBL.AL021185), bcp, Mycobacterium
tuberculosis bacterioferritin comigratory protein (157
aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06,
63.3% identity in 30 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 aa; unknown function, similar to many e.g.
SW:Y03Q_MYCTU (EMBL:273902) Mycobacterium tuberculosis
hypothetical protein (204 aa), fasts acores; opt: 633
r-score: 743.6 E(): 0, 52.0% identity in 200 aa overlap.
Similar to SW:YGGY_ECOLI (EMB:JU28377), yggV, Escherichia
coli hypothetical protein (197 aa) (49.5% identity in 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SCE19A.03c, possible secreted protein, len: 134 aa
unknown function, probable CDS suggested by GC frameplot,
                            Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                     predicted the
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/gene="SCE19A.02c"
/note="SCE19A.02c, conserved hypothetical protein, len:
   where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="tRNA Leu anticodon TAG, Cove score 69.78"
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140. .226
                                                                                                                                                                                  may not have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
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/protein_id="CAB50982.1"
/db_xref="G1:5531350"
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/protein_id="CAB50983.1"
/db_xref="GI:5531351"
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                                                                                                                                                      http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
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complement(892. .1296)
/gene="SCE19A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="tRNA-Leu"
complement(243, .845)
/gene="SCE19A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="cosmid E19A"
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/transl_table=11
/label=SCE19A.02c
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/transl_table=11
/label=SCE19A.01
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James K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Direct Submission
Submitted (16-JuL-1999) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. [ bases 1 to 35284]
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                  325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCGTCGATCCGTACGCGGTGCGGCTGAGCTTCCACCTCCCCGGAGACGCCCCGGTCACC
                                                                                                                                                                                                                                                                                                                                        ggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgg
                                                                                                                                                                                                                                                                                                                                                                     tgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgat
                                                                                                                                                                                                               gtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggtc
                                                                                                                                                                                                                                                                        GTCCGGGTCTGCCCGGTGGGCAGACGGCCACCAGGGAGGTGCACATCACCCTCCAGGTC
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Seeger, K. and Harris, D.
Unpublished
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/gene="SCE19A.04c"
/forto="SCE19A.04c"
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/protein_id="CAB50984.1"
/protein_id="CAB50984.1"
/boxere="fg1:5531352"
/translation="WASRHRERETVTAVATVATIALTAGLTTGCDAVDKALDCVRT ADAIADSVTELQQAVENADDFTQWEESLNSIDKNLDRIGDQTDNTDVNKAVDDLGKAV DOWNTSVENDEDFLSPPLSPPLSPPLSPPLSPACTVRTFTV
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positional base preference and amino acid composition. Contains probable N-terminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1201. .1233)
/gene="SCE19A.03c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
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phosphotransferase system, EIIB, score 43.00, E-value
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/gene="SCE19A.05c"
/note="SCE19A.05c, hypothetical protein, len: 77 aa;
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/protein_id="CAB50985.1"
/db_xref="G1:5531353"
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/label=SCE19A.05c
/product="hypothetical protein"
/protein.id="CAB50986.1"
/db_xref="GI:5531354"
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/gene="SCE19A.04c"
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/gene="SCE19A.05c"
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/label=SCE19A.03c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 29-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane protein; membrane transferase; protein-export membrane protein; regulator; secreted protein; sugar transferase; threonine-tRNA synthetase; transport system inner membrane protein. Streptomyces coelicolor $3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomýces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 38640)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8. Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetyltransferase; acyltransferase; adenine
phosphoribosiltransferase; DNA helicase; DNA polymerase III;
elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase;
                                                                                                             (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20202 CGGACGATCCCTACGCCGTGCACATCACCTTCCACATCGACTCCGGCCACCCGGTGCACT 20261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          possible PTS transmembrane component,
                                                                                                                                                                                                                                                                                                                                       20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGGCATTCCGGTGCCGGCCCGGCTCGGCTACCACA 20201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctgg 361
                                                                                                                                                                                                                                                                               2 tgagcttcctcgtctccgaggagctctcgttccgtattccggtggagctccgatacgagg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacgatg
                                                                                                                                                                                                                                                                                                                                                                                               62 teggegateegtatgeeateeggatgaegtteeacetteeeggegatgeeetgtgaeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcacateggecegacegagecegagggeeteggagatgtecacateeggeteeggteg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 gogoggaccgtgcgctgttccgggcggggacggcaccgctggtggcgttcctcgaccgga
                                                                                                                                                                  Length 35284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                               Score 110.4; DB 1;
Pred. No. 7e-06;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                  len: 431 aa; similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38640 bp
Streptomyces coelicolor cosmid L2.
AL137778
2660. .3955
/gene="SCE19A.06"
/note="SCE19A.06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seeger, K.J. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL137778.1 GI:6822206
                                                                                                                                                                        27.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 38640)
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                                                                                                                                                                                            55.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 aggacgcactgggccg 377
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                               Best Local Similarity
Matches 210; Conserv
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COMMENT

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identical to previously sequenced SW.RELA_STRCO (RMEL:X87267) Streptomyces coellicolor GTP pyrophosphokinase (Ec 27.6.5) RelA, 847 aa and highly similar to SW.RELA_STRAT (EMBL:AR072829) Streptomyces antibioticus RelA protein, 841 aa; fasta scores: opt: 4969 z-score: 4966.2 E(): 0; 90.8 identity in 848 aa overlap and to SW.RELA_CORGL (EMBL:AR038651) Corynebacterium glutamicum GTP pyrophosphokinase (Ec 2.7.6.5) RelA, 760 aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.78 identity in 774 aa overlap. Contains Pfam match to entry PRO1842 ACT, ACT domain and match to prosite entry PS00017 APP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /yorde="SCL2.04c, apt, adenine phosphoribosiltransferase, /yorde="SCL2.04c, apt, adenine phosphoribosiltransferase, len: 182 as; identical to previously sequenced SW:APT_STRCO (EMBL:X87267) Streptomyces coelicolor adenine phosphoribosyltransferase (EC 2.4.2.7) Apt, 182 as and highly smilar to SW:APT_ECOLI (EMBL:M14040) Escherichia coll adenine phosphoribosyltransferase (EC 2.4.2.7) Apt, 183 as, fasta scores: opt: 600 z-score: 682.8 E(): 1.2e-30; 54.8% identity in 168 as overlap. Contains Pfam match to entry PF00156 Pribosyltran, phosphoribosyl transferase domain and match to Prosite entry PS00103 Purine_Pyrimidine phosphoribosyl transferases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3273...7460)

Complement(3273...7460)

S.coelicolor secD, secF & apt genes"

complement(378...3781)

complement(3904...4568)

Complement(3904...4568)

EMBL: x87267 S.coelicolor apt & relA genes"

complement(3956...4453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPDEAQPLTAAKPESASAAKPAPSAPQAKNDTHGPIQHAPAA
PVDKPAEQQPRPKPLPAERPQNAPVVRAPAGQPARSGSSNRVRARLARLGVQRANPYN
PVLEPLLRIVRGNDPKIETSTLRQIERAYQVAERWHRGQKRKSGDPYITHPLAVTTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AELGMDPATLMAGLLHDTVEDTEYGLEDLRRDFGDVYTLLVDGYTKLDKVKFGEAAQA
ETVRKMVVAMAKDPRVLVIKLADRLHNMRTMRYLKREKQEKKARETLEIYAPLAHRLG
MNTIKWELEDLAFAILYPKMYDEIVRLVAERAPKRDEYLAVVTDEVQQDLRAARIKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTGRPKHYZSVYOKNIVRGRDFAETYDLVGIRVLVOTVRDCYAALGTYHARWNPYGR
FKDY TAMPKFNWYQSLHTTVIGPGGKPVELQIRTFDMHRRAEYGIAAHWKYKQEAVAG
ASKVRTDAPKSSGKSKDDHLNDMAWLRQLLDWQKETEDPGEFLESLRFDLSRNEVFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPKGDVIALPAGATPVDFAYAVHTEVGHRTIGARVNGRLVPLESTLDNGDLVEVFTSK
AGAGGPSROMULGFVKSPRARNKIRAMFSKERRDBATBGGRAAVTRAMRKONLPTQRIL
TGDSLVTLAHEMRYSDISALY FAAGGGGHVSAPNIYORLUQALGGEBAATEGIDSSVPP
SRGRCRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIIGFVTRGSGVSVHRSDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVDSLSREPERILEVEWAPTQSSVFLVAIQVEALDRSRLLSDVTRVLSDOHVNILSAA
VQTSRDRVATSRFTFEWGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
                                                                                                                                                                                                                                                                                                     len: 847 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15" complement(2378. .2401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note-"PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                             /note="previously sequenced region SW:SCAPTRELA
EMBL:X87267 S.coelicolor apt & relA genes"
complement(1229. .3772)
                                                                                                                                                                                                                                                                                                     /note="SCL2.03c, relA, GTP pyrophosphokinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="adenine phosphoribosiltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="GTP pyrophosphokinase"
/protein_id="CAB70915.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1256. .1474)
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                                                                                                                                                                                                                                complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:6822209'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                      /gene-"relA"
                                                                                                                                                                                                 /gene="relA'
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                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                          The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest socring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):478-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

hutp://www.nih.go.jp/
iun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most important initiation codon). If this cannot be identified we choose the most important initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCL2.01, hypothetical protein, len: >328 aa;
similar to TR:033236 (EMB:298209) Mycobacterium
tuberculosis hypothetical 49.8 kD protein mTCY17.11, len:
450 aa; fasta scores: opt: 843 z-score: 874.7 E(): 0;
45.9% identity in 296 aa overlap. Contains possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="SWQAGSPEEALAYERRYEGLVVEIGLLEKRVKTTDLSAKDAQT
AVBHLREDVODHHAVGDLEALBARLDOLVALVPTRREEKRAQPRAKQSPBARGSREALVA
ARABELARSDQWRAAGERLRSLVDTWKGLPRLDKSDDELWHRFSHRRSGREKRKQH
FAQLDAQREERARIKERLVSEAEALSNSTDWGPTAARYRDLMSEWKAAGRAQREHEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"hypothetical protein SCL2.02"
/protein_id="CaB70914.1"
/db_xref="G1:6822208"
/translation="MDKLRSQVEQARAQGNDAKADKLARELEGRQALLDQALKGLHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LWNRFRGAQDVFFAARSSVFAERDAEQSENLKLKEELVTEAEKLVPVTDLKSARAAFR
SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGPTPRHARVPRA"
                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRR and Beowulf Genomics
Details of S. Coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                              (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 38640
/organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein SCL2.01"
/protein_id="CAB70913.1"
/db_xref="G1:6822207"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1010. .1150
/gene="SCL2.02"
/note="SCL2.02, unknown, len: 46 aa"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coiled-coils region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cosmid L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=3
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SCL2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCL2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1010. .1150
/gene="SCL2.02"
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/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686.
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                                                                                                                                                                                                                                                                                                                                                                               strand)
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FEATURES

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32704 bp Di
Streptomyces coelicolor cosmid 8All.
AL391041
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beta-lactamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
87275916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="inverted repeat"
540 c 496 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="inverted repeat"
                                                                                                                                                               /gene="beta-lactamase"
243. .1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="beta-lactamase"
                                                                                                                                                                                                              /gene="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1204. .1216
/gene="beta-lactamase"
                                                                                                                                 /db_xref="taxon:1888"
                                                        Location/Qualifiers
                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%;
64.0%;
                                                                                                                 /strain="G"
                                                                                                                                                     243. .1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 64.0
Matches 137; Conservative
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ORIGIN
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MEDLINE
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KEYWORDS
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                /db_xref="G1:6822210"
/translation="MADYPEPGYVFKDITPLIADPGAFAALTDALAEAAGRTGATKVVGLEARASFILAOPALRAGLGEIPVRKAGKLPGATLSQAYDLEYGSAEIEVHAEDLTAGDRVLVVDDVLATGGTABASLELIRRAGAEVAGLAVLMEGFLGGRARLEPALAGAFLAG
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Bebottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J., Erpicum, T., Frere, J.-M. and Ghuysen, J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                                                                                                 /note="Pfam match to entry PF00156 Pribosyltran,
Phosphoribosyl transferase domain, score 150.30, E-value
                                                                                                                                                                                                                                                                                                                                                                                    /note="SCL2.05c, secF, protein-export membrane protein, len: 373 aa; identical to previously sequence SW.SECF_STRCO (EMBL:X8599) Streptomyces coelicolor protein-export membrane protein SecF, 373 aa and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15030 TGGCCTCGTTGTGTCGAGCGAGTCCTCCCTGCCTGTCCCCGAGGCCTGCGGTACGACA 35089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35090 CGCCCGACCCTACGCCGTGCACCCTTCCACACCGGAGCCGAGGAGACCGTCGAGT 35149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35150 GGGTCTTCGCCCGCGACCTGCTCGCCGAAGGTCTCCACCGTCCCACCGGCACCGGGAGG 35209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35210 rccerercrescerecescastcacesceaeceaeceaecerescerescerecereces 35269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 toggogatocgtatgccatccggatgacgttccaccttcccggcgatgccctgtgacct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgcacateggcccgaccgagcccgagggcctcggagatgtccacatecggctccaggtcg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 gcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgga 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctgg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                /gene="apt"
/note="PS00103 Purine/pyrimidine phosphoribosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.2%; Score 106.8; DB 1; Length 38640;
54.6%; Pred. No. 1.9e-05;
iive 0; Mismatches 177; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-lactamase.
Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
Bacteria: Firmicutes; Actinobacteriae, Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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'protein_id="CAB70916.1"
                                                                                                                                                                                                                                                                                                                           /gene="secr"
complement(4501. .5622)
/gene="secr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 aggacgcactgggccgcatcctcgccgagg 391
                                                                                                                                                                                                              complement(4103. .4141)
                                                                                                                                                                                                                                                                   transferases signature" complement(4468. 4503) complement(4501. 5622)
                                                                                                               complement(3980. .4429)
                                                                                                                                     /gene="apt'
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M28303.1 GI:153338
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                                                                                                               misc_feature
                                                                                                                                                                                                              misc_feature
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SOURCE
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SVSDAERRLAGLERASGARLGYYAYDTGSGRTVAYRADELFPMCSVEKTLSSAAVLRD
LDRNCEFLSRRILYTQDDVEQADGAGFETGRPQNLANAQLTVEELCFVSITASDNCAA
LUMLRELGGRAVYTRFVRSLGDRVTRLDRWEPELNSAEBGRVTDTTSPRAITRTYGRL
VLGDALNPRRRLLISWLLANTTSGRRFRAGLPDDWTLGDKTGGGRYGTNNDAGVTWP
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Amino acid transport integral membran protein; branched amino acid binding secreted protein; branched amino acid transport system binding protein; branched amino acid transport system permease; integral membrane protein; ion transport integral membrane protein; polysaccharide biosynthesis protein; requiator; requiatory protein; secreted amidase; secreted peptidase; secreted protein; sigma factor; transcriptional regulator; transcriptional regulatory
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Streptomyces coelicolor A3(2)
Satebicmyces coelicolor A3(2)
Satebicmyces frimiopacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 32704)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CGGCTGACGTTCCACCTCCCCGGAGACGCCCCGGTCACCTGGGTCTTCGGGCGTGAACTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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/organism="Streptomyces albus"
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/ CLEARS 1 & LION = "IGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA VRARILORAAGNPLALVELPLSPSAAAELLDADAPGLADA VRARILORAAGNPLALVELPRAAQGISPPLDDLPLTQRLETAFASRTDSLTRECRTFL LVLAABEPAPLNGULDVASRLAGSEVTYVALQEAVDAGLVVLTGRTPERHPLARSAI LYTAATVADRLSTHRALAETLEGSPGRRLVHLAAATLGPDDELAGGLERFADDAQKRGQ LAAAVPALROAGELVHDPRROTGLLVRAAATCPDDELAGGLERFADDAQKRGQ LAAAVPALROAGELHNBROTGLLVYRAATEPPREDAGSINDRVQAQILLNRAAARTEFDDEPRROTGLLVYRAYTEPPREDAGSSINDRVQAQILLNRAAARTEFDDEPRROTGLLYRAAGSAGSSINDRAAGAGSTLHYL GSGSWAIGDVGRATRKLADAAACAGSORGRICLHYLGGLAGAREESAE GSGSWAIGDVGRATRKLAAGAASALVRAGGREGAAGSWAYAGSWAQQQSWADAAAAGREBABE GIALAFDSRAYBYAYATVATVARGERAAARSVRELRAHSLFPVWPFASVWAQQQSSWAIGNDRARSEFORTDHYHISTSRALLVPDLVDAAAAGRENBGARE LLVELPELADDSRAVENYDAAAAGRENGARE LLVELPELADSRAYBAYAATVASTAVLAPDDTAGCCYDSALSALPDTWPLARARHLH GHERRQRRNVDARKPLRARREDENGAQBWADWAREGLSALPDTWPLARARHLH GHERRQRRNVDARKPLRARREDENGAQPWADWAREGLSALPDTWFLARARHLH GHERRQRRNVDARKPLRARREDENGAQPWADWAREGLSALPTWRYGERGAAAAA
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complement(3297..7058)

/gene="SC8A11.04c, probable secreted peptidase, len: 1253
/gene="SC8A11.04c, probable secreted peptidase, len: 1253
aa; similar to TR:09RL54 (EMBL.AL12196) Streptomyces
coelicolor probable secreted peptidase SCF5IA.10, 1245 aa;
faste scores: opt: 1827 z-score: 1848.3 E(): 0; 37.28
identity in 1300 aa overlap, to TR:P95684 (EMBL:083672)
Streptomyces albogriseolus subtilisin-like protease, 1102
aa; fasta scores: opt: 1365 z-score: 1380.6 E(): 0; 33.48
identity in 1268 aa overlap and to Streptomyces coelicolor probable secreted peptidase SCBAII.16c, 1239 aa; fasta scores: opt: 1835 z-score: 147.4 E(): 0; 46.98 identity in 1279 aa overlap. Contains Pfam matches to entries PF00082 Peptidase_S8, Subtilase family and PF02225 PA, PA
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PDHPLLVTIRFAPEGAPPVTWHVGRDLLHEGLRTTSGLGDVQVWADTPTDRETAWLQV
MAGGDIATSELVPPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
complement (3297, 7058)
/gene-"SC8A11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein SC8A11.02c"
/protein_id-"CAC015'4.1"
/d_xref-"GI:9716213
/translation-"MASAAATAGTAGALPVMSGQAHADTRGLPSLWDVDRSVVNPENA
YTVTVDQVRAEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
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/gene="SCBA11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                   //transl_table=11
/product="putative transcriptional regulator (fragment)"
/protein_id="CAC01573.1"
/db_xref="G1:9716212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 49.10, E-value
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/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
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/product="putative regulator"
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/db_xref="GI:9716214"
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2787. .3257
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/gene="SCBA11.01"
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/gene="SC8A11.03"
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/transl_table=11
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//octe="SCBA11.01"
//octe="SCBA11.01, possible transcriptional regulator
//octe="SCBA11.01, possible transcriptional regulator
(fragment), len: >>70 as; similar to TR:095124
(EMBL:AL109747) Streptomyces coelicolor probable
transcriptional regulator SCJ21.13, 919 as; fasta scores:
opt: 818 z -score: 913.7 E(): 0; 32.6% identity in 775 as
overlap. Contains Pfam match to entry PF00196 GerE,
Bacterial regulatory proteins, luxR family and match to
Prosite entry PS000622 bacterial regulatory proteins, luxR
family signature. Also contains a possible
helix-turn-helix motif at residues 699. .720 (+3.25 SD)"
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jun/Gqi-lan/frameplot.pl. CAUTION: We may not have predicted the jun/Gqi-lan/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If cannot be the entire insert of the IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot Program of Blbb et al., Gene 30:157-66(1984) as implemented at
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A. A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                     Unpublished 5.2704)
3 (bases I to 32704)
Cerdeno.A M., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
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ABC transporter; amino acid permease; BCCT family;
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Oliver, K. and Harris, D.
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GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSGGRAVEYRQDISLLGQ
PLGIVPTQVRAQGELTSWYTADDDVRWVSFASRPDLGQRGVARSYEPRSTTRETWFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGEDVNERIVWVGGLSPGPKPYRLVLEGSRNLPDRPYSTRTWWDFTSATTDPTRL
TPLPLVQLDYAVAVDLSGRAHRRTELTVTASHLEGAAGAGAIRTATVEVSYDDGATWH
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                                                                                                                                                                                                       /translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPTAPA
domain and matches to Prosite entries PS00136 Serine proteases, subtilase family, aspartic acid active site, PS00137 Serine proteases, subtilase family, histidine active site and PS00138 Serine proteases, subtilase family, serine active site. Also contains possible N-terminal region signal peptide sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 ttcccggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctca 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 cgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgc 337
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                                                                                                                                               /product="putative secreted peptidase"
/protein_id="CAC01576.1"
/db_xreff="GI:9716215"
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/gene="SC8A11.04c"
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/transl_table=11
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correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
carboxypeptidase; D-amino acid oxidase; ddah, dimethylarginine dimethylaminohydrolase; dehydrogenase; efflux protain; endonuclease; enoyi CoA hydratase; IPP isomerase; metallopeptidase; oxidoreductase; racemase; regulator; thiolase; transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk RR4 70H, UK
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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                           Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria: Firmicutes; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
I (bases 1 to 37245)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
MOL. Microbiol. 21 (1), 77-96 (1996)
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence coverlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 37245)
Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Streptomyces coelicolor A3(2)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 105
/note="Nominal overlap with cosmid 4C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cosmid 5F2A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(83. .859
/gene="SC5F2A.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(83. .85 /gene="SC5F2A.01c"
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/AFTLSGGERFRAALAALMAEPAPOLLMADPFNNLDMASVRQLTGALEAYEGALLV
/GONDLEMENT(3290) .3787)
/GONDLEMENT(3290) .3787)
/GONDLEMENT(3743 .3766)
/GONDLEMENT(3743 .3766)
/GONDLEMENT(3743 .3766)
/GONDLEMENT(3743 .3766)
/GONDLEMENT(3743 .3766)
/GONDLEMENT(374 ATP/GTP-binding site motif A (P-loop)."
complement(3245. .4879)
/gene="SC5F2A.03c"
/dete="SC5F2A.03c, probable ABC transporter, len: 544aa;
/note="SC5F2A.03c, probable ABC transporter, len: 544aa;
similar to many involved in antibiotic resistance egs.
TR:054381 (EMBL:X79146) from the lincomycin-production
gene cluster of Streptomyces lincolnensis 78-11 (578 aa)
fasta scores: opt: 1624, z-score: 1696.3, E(): 0, (50.3%
identity in 541 aa overlap). Contains two Pfam matches to
entry PP00005 ABC_tran, ABC_transporter, two Prosite
matches to PS00017 ATP/GTP-binding site motif A (P-loop)
and Prosite match to PS00211 ABC transporters family
signature. Also contains a possible coiled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4739. .4762)
/gene="SCSF2A.03c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6117 CGGCGACGTCCGGGTGCGCCGTACGCGTACGACCGCACCG-----TCCTGGAGTT 6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 cggcgatccgtatgccatccggatgacgttccaccttcccggc-----gatgcccc 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 tgtgacctgggcgttcggccgcgagctgctggacgggctcaacagcccgagcggcga 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 gagottoctcogtctccgaggagctctcgttccgtattccggtggagctccgatacgaggt 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"PS00211 ABC transporters family signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6237 CGCCGACCCGTTCGCCGTCCGCATGACCTTCCCGGCCCCGGCCACCCTCGAGGGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 cggcgatgtgcacatcggcccgaccgagcccgagggcctcggaggtgtccacatccggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pfam match to entry PF00005 ABC_tran, ABC transporter, score 143.80, E-value 3.1e-39" complement(4403. 4447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79.2; DB 1;
Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ABC tra
/protein_id="CAB40670.1"
/db_xref="G1:4584467"
/db_xref="SPTREMBL:Q9X7M6"
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/gene="SC5F2A.03c"
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/gene="SC5F2A.04"
4942. .5850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label-SC5F2A.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     around 250aa
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54.6%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(976. 3234)
/gene="SC5F2A.02c"
complement(976. 3234)
/gene="SC5F2A.02c"
/gene="Sc5P2A.02c"
/gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MPSKKAIVRPSPRIABEGIVTHVEREKVDHGLALEGWDAYVEAL GAHGWETLEVDPADDCPDSVFVEDAVVFRNVALITRPGAESRRAETAGVEEAVARLG GAHGWETLEVDPADDCPDSVFVEDAVVFRNVALITRPGAESRRAETAGVEGARVANFUSK SOSNWWWEDSGTLDGGDVLKIGDTIYVGRGGRTNAAGVQQLRAAFEPLGARVYANPVSK VLHIKSAVTALPDGTVIGHTPLTDVPSLFPRFLPVPEESGAHVVLLGGSRLLMAASAP KTAELLADLGHEBVLVDIGEFRLEGCVTCLSVRLRELXD"
complement(976...3234)
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/db_xref="G1:4884466"
/db_xref="SPTREMBL:09x7M5"
/db_xref-"SPTREMBL:09x7M5"
/db_xref-"SPTREMBL:19x7M5"
/db_xref-"SPTREMBL:TIGARENILQDVTLRIPKGRLTVFTGVSGSGKSSVVFD
/ITANESRROLNBTFFWFVRRILPKTERPHADALEGILPAIVVDORPVGGHSRSTVGTM
TDIHSVLRVLFSRHGTPGAGGATAYSFNDPSGMCPGCDGLGRRVQPDMDRILDPARSL
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GTWGTEYEGLADRFERLYLKRDLSGMSERTRDLVRGFLVEARCPDGGGARLNAAALAS
RIDGHSIADCSRWQTYDLIAVLRGIDDPVALPYAGAAVAALERVEAGLGCYLSLDRET
ATLSGGEGGRLKTVRHLGSSLTGWTYTFDEPSVGLHPRDVGRLGDLLLRLRDKGUTVL
VYEHDPDVIALADHYVDMGFRAGADGGRVVFEGTPAGLAASDTLTGRCLGRRTAVKDT
VREHDPDVIALADHYVDMGFRAGADGGRVVFGTPAGLAASDTLTGRCLGRRTAVKDT
VRAPTGELWVKGAERHNLREVTVAFPTGVLTAVTGVAGSGKSTLVAELTGAHPDAVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQSAIGISARSTPATYLGIMDTVRKVFARETGAEPGFFSFNSAGACGTCEGRGIIHTD
LAFMDPVTTTCHDCEGRRFREEVLRLTVDGRSVADVLAMTAGQALGFFSDPGVRRRLR
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ALLDRLVDAGNTVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
        /note="SC5F2A.01c, ddah, dimethylarginine dimethylaminohydrolase, len: 258 aa; hydrolyses asymmetrically methylated arginine with preference for dimethylated arginine over monomethylated arginine (experimental). Similar to TR:D1038106 (EMBL:AB001915) NG.NG-dimethylarginine dimethylaminohydrolase from Homo sapiens (285 aa) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 aa overlap)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00005 ABC_tran, ABC
transporter, score 35.60, E-value 4e-08."
complement(3118 .3141)
/gene="SC5F2A.02c"
/note="P500017 ATP/GTP-binding site motif A (P-loop)."
/gene="SC5F2A.03c"
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//gene="SC5F2A.02c"
//note="Psfam match to entry PF00005 ABC_tran, ABC transporter, score 101.40, E-value 1.7e-26."
/gene="R505A.02c"
//oce="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="dimethylarginine dimethylaminohydrolase"
/protein_id="CAB40668.1"
/db_xref="GI:4584465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS-PROT:Q9X7M4"
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/gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrophobic regions."/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=SC5F2A.02c
                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/label=ddah
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DB	21	21	21	21	22	22	20	9
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Location/Qualifiers

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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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           Streptomyces griseus.
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, runinant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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Best Local Similarity
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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, erryme inhibitors, antimigraine agents, herbicides, antiparaslic agents, runniant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                             gtgcacatcggcccgaccgagcccgagggctcggagatgtccacatccggctccaggtc
                                                              181 gtccacatcgccccgaccgaccccgagggcctgtcggacgtctccatccggctccaggtg
                                                                                              acggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ssgA; liquid culture; filamentous bacteria; secondary metabolite;
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                                                                                                                                                                                                                           gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 407
                                                                                                                                                                                                                                            (NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces goldeniensis ssgA gene.
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a DNA (ATCC 23940) encoding S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, eryme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antimisarisic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agent; antagonist; biomass; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 1..405
                                                                                                                                                           Streptomyces netropsis ssgA gene.
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                                                              BP.
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83.3%;
                                                            AAZ49731 standard; DNA; 407
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                                                                                                                                                                                                                                                                                         Streptomyces netropsis.
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AAF88315/c
ID AAF88315 standard;
                                           Disclosure; Fig 5;
                branching
P-PSDB; AAY44650.
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                                                                                                                                 tgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgat 180
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 3004; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                      1 atgagetteetegteteegaggagetetegtteegtatteeggtggageteegataegag
                                                                                                                                                  tgggcgttcgggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacggggac
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                          Length 407;
                                           Indels
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                          DB 21;
                                   1.3e-40;
thes 92;
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                                          0; Mismatches
                         Score 259.8;
Pred. No. 1.3
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/label= SsgA_protein
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1..405
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                                                                                                                                                                                                                                                                                                                                    BP.
                         63.88;
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                                          Conservative
                                                                                                                                                                                                                                                                                                                                    DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces albus G.
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                                                                                                                                                                                                                                                                                                                                    standard;
                                   Similarity
BP;
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Sequence 407
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mat_peptide
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                                          Matches 315;
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                         Query Match
Best Local
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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour antimigraine agents, hebblicides, antiparaslit agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccttgtgacc 120
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transgenic plant; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 tgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgat
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 407 BP; 57 A; 150 C; 139 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 239; DB 21
Pred. No. 1.1e-36
                                                                              60pp; English.
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macrolide; insecticidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.78;
74.28;
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Best Local Similarity 74.29
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polyketide synthase; biosynthesis; transgenic plant; insect resistance;

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S. spinosa DNA fragment SEQ ID 1.
                                                                                                       spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
                                                                                   Forosamine; trimethylrhamnose;
      28-AUG-2001 (first entry)
                                                                                                                                                               Saccharopolyspora spinosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-267102/28.
                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG.
                                                                                                                                                                                                     DE19957268-A1.
                                                                                                                                                                                                                                                                                   29-NOV-1999;
                                                                                                                                                                                                                                                                                                                           27-AUG-1999;
                                                                                                                                                                                                                                            08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                        Eberz G,
      This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide carpynes, which are used for recombinant production of the corresponding enzymes, which are used for production of the corresponding enzymes, which are used for production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raise specific antibodies, useful for identifying corpusations in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of expression clones in a gene bank. Cells transformed with (I) may produce (II). This sequence represents a genomic DNA fragment of the S. Spinosa of formation and trianthylly and produce for contains the coding regions for proteins involved in
                                                                                                                                                                                                     New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                        Salas JA;
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                                                                                                                        Velten R,
                                                                                                                                                                                                                                                                                 Claim 7; Page 58-74; 354pp; German.
                                                                                                                      Froede R,
    99DE-1057268
                                           99DE-1040596
                                                                                                                      Moehrle V,
                                                                                                                                                             WPI; 2001-267102/28.
                                                                                (FARB ) BAYER AG.
29-NOV-1999;
                                                                                                                        Eberz G,
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enzymes for spinosyn blosynthesis, useful for insecticidal spinosyns and their derivatives

Salas JA;

Velten R,

Froede R,

Moehrle V,

99DE-1057268 99DE-1040596

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Query Match 18.5%;
Best Local Similarity 53.4%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 20911 GAGGCAGGCGAAGGCGATGTGCGGATCGGCC---CTCGACGGGGTTTTCCGGGGTTGGTC 20855
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                                                                                                                                                                                      43 giggagciccgatacgaggicggcgatccgtatgccatccggatgacgitccaccitccc 102
                                                                                                                                     Gaps
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                                                                                 Length 45624;
                                                                                                                                     3;
Sequence 45624 BP; 7933 A; 14913 C; 14940 G; 7838 T; 0 other;
                                                                                                                                0; Mismatches 156; Indels
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                                                                               DB 22;
                                                                               Score 75.4; DB 22
Pred. No. 5.5e-06;
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                                                                               18.5%;
53.4%;
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AAF88312;

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Query Match

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to dentify, inactivate or modulate genes involved in the biosynthesis of [II]; (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of the corresponding enzymes, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as an arkers for sequencing of the Saccharopolyspora spinosa genome. (II) are marchides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying also be used to raise specific antibodies, useful for identifying cyprocension clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of concerning the contains the coding regions for protein sinvolved in the contains the coding regions for proteins involved in the contains and contains and contains involved in the contains and contains and contains involved in the contains and contai
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0; Mismatches 156;
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Pred. No. 5.5e-06;
Claim 7; Page 14-31; 354pp; German.
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/lansl_except= r
/*tag= r
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linitiator module"
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extender module 1"
38916..35374
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extender module 1"
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/note= "Acyl transferase domain (AT1): part of
initiator module"
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/note= "Enoyl reductase domain (ER2): part of
extender module 2"
34082..34621
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extender module 1"
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24102..25349
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27582..28121
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/note= "Spinosyn biosynthesis
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  Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode: insect; polyketide; polyketide synthase; PKS; extender module; initiator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase;
DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes
                                                                                                                                                                                                                                                                                                                                                                 "Protein involved in transcription control"
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complement (11530..12492)
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complement (3416.4165)
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2024..2791
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139 62 ctcggccaggagcacacgctgggtgacttcgacggcaacctg 360

319 239 BP.

(first entry)

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Xanthomonas campestris; L-glutamyl tRNA reductase; vitamin B12; glutamic acid-1-semialdehyde; 5-aminolevulinate (ALA); haem; chlorophyll; phycobilin; recombinat production; ds.
                                                                                                                                                                                                             Xanthomonas L-glutamyl tRNA reductase.
                                                                                                                                                                                                                                                                                                                                                                                   (COSM-) COSMO SOGO KENKYUSHO KK
                                                                                                                                                            AAQ88151 standard; DNA; 1549
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                                       /note= "Acyl carrier protein domain (ACP2): part of extender module 2"
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extender module 5"
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/note= "Beta-ketoreductase domain (KR2): part
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module 5"
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15077..46348
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35518..36786
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Location/Qualifiers 212..1492

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93JP-0184709 93JP-0184709.

toggcccgaccgaggcctcggagatgtccacatccggctccaggtcggcgcgg 247 Gaps AAQ88151 encodes AAR74619 Xanthomonas campestris L-glutamyl tRNA reductase. The DNA as part of an expression vector can be used to transform a host cell, for the recombinant prodn. of the protein. The protein can be used in the prodn. of vitamin B12, glutamic acid-1-semialdehyde, 5-aminolevulinate, haem, chlorophyll and DNA fragment encoding L-glutamyl tRNA reductase - derived from Xanthomonas sp., useful for production of 5-amino:levulinate, vitamin-B12, chlorophyll, etc. ö Length 1549; Indels Sequence 1549 BP; 291 A; 516 C; 514 G; 228 T; 0 other; Score 54.4; DB 16; Pred. No. 0.057;); Mismatches 101; Claim 3; Pages 7-8; 9pp; Japanese. ; 0 13.4%; 53.2%; Conservative Similarity Matches 115; phycobilin Query Match Best Local S 188 g ò

ij

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Length 80161;

DB 20;

13.5%; Score 54.8; DB 20; 52.1%; Pred. No. 0.04; tive 0; Mismatches 132;

Conservative

Local Similarity les 147; Conserv

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Query Match Best Loca Matches 79 atccggatgacgttccaccttcccggcgatgccctgtgacctgggcgttcggcgcgag 138

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Gaps 62

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Indels

Mismatches 189;

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Conservative

182

242

89

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243 cgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccggac 302
                                                                                                  cggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccctgtgacctg 122
                                                                                                                                                                                                                                                                 187 TGAGCCCGTCCAGCAGCAGCTCGCGGCCGAACGCCCAGGTCACAGGGGCATCGCCGGGAA
                                 gagetteetegtetecgaggagetetegtteegtatteeggtggageteegataegaggt
                                                                                                                                                                      ggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgatgt
                                                                                                                                                                                                                                         gcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggtcgg
                                                                                                                                   307 GTGCCGTCCCCGCCCGGAACAGCGCACGGTCCGCGCCGACCTGGAGCCGGATGTGGACAT
                                                                                                                                                                                                                                                                                                                                       127 GGTGGAACGTCATCCGGATGGCATACGGATCGCCGACCTCGTATCGGAGCTCCACCGGAA
                                                                                                                                                                                                    247 CICCGAGGCCCTCGGGCTCGGCCGATGTGCACATCGCCGTCGCCGCTCGGGCTGT
                                                                                                                                                                                                                                                                                                                                                                          303 ggacaagetegtgeegeteggeeaggageacaegetgggtgaettegaeggeaace 358
                                                                                                                                                                                                                                                                                                                                                                                                        67 TACGGAACGAGGCTCCTCGGAGACGAGGAAGCTCATCATGACCTCTGCTTGAACC 12
167;
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                                                                                                                                                                                                                                                                                                                                                                                                     ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; biomass; ds.
                                                                                    367
                                                                                                                 315 tgcgtgcgctgccccaggtaagcgaggccgcgctgctgccacctgcaaccgtaccgagt
               agctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctggaggacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 A; 145 C; 153 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                  435 ctctgagcggttatctgtaccagcaccaggaagccg 470
                                                                                                                                                   368 cactgggccgcatcctcgccgaggagcagaacgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "SsgA protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 31..438
                                                                                                                                                                                                                                                                                                                                                                            griseus ssgA gene-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 27; 60pp; English.
                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                          Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1998;
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ID AAZ497
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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylase variants (AAY17904-Y179069). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, O. et al., Blosci. Blotech, Blochem. Vol. 56, 76-80, 1992 ). The variants have a replacement of the 57th or the 130th amino acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6119, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared from the alpha-amylase variants produce maltopentaose
                                                                                                                                                                                                                                                                                                                                                                                                                      production of malto-pentaose
                                                                                               Pseudomonas alpha-amylase variant encoding DNA (FERM BP-6116).
                                                                                                                             Pseudomonas; maltopentaose; alpha-amylase; enzyme; variant; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1981 BP; 342 A; 678 C; 678 G; 283 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        SOGO.
                                                                                                                                                                                                                                                                                                                                                                                                                      New alpha-amylase gene - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 6-8; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                       (NORQ ) NORINSUISANSHO SHOKUHIN
 BP
AAX37293 standard; DNA; 1981
                                                                                                                                                                                                                                                                          97JP-0305071
                                                                                                                                                                                                                                                                                                         97JP-0305071
                                                                 (first entry)
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                                                               27-JUL-1999
                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                         11-MAY-1999
                                                                                                                                                                              Synthetic.
                                 AAX37293;
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Length 438;

21;

53.6; DB No. 0.085;

Score Pred.

13.2%;

Query Match Best Local Similarity

Gaps

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Indels

Mismatches 121;

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Conservative

126;

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence as compared to the wild-type. The sequences are deposited under the accession numbers FRRM BP-6116, 6119, 6115, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose
                                                          gacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacgg 176
                                                                                                                 177 cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca 236
                                                                                                                                                                                                       761
                                                                                                                                                                                                                                  coggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa 356
                                                                                     582 gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgtcgatgc 641
                               Gaps
                                                                                                                                               ggccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac
                                                                                                                                                                                               ggtcggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New alpha-amylase gene - useful for production of malto-pentaose
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0
Length 1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas alpha-amylase variant encoding DNA (FERM BP-6119).
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1981 BP; 343 A; 679 C; 678 G; 281 T; 0 other;
                            121;
 DB 20;
Score 53.4; DB Pred. No. 0.087; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Page 9-11; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                           AAX37294 standard; DNA; 1981 BP.
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13.1%;
51.0%;
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                              Conservative
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P-PSDB; AAX17905.
                Similarity
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                            Matches 126;
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   Query Match
                  Best Local
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Length 1981;

53.4; DB 20; No. 0.087;

Score Pred.

13.1%; 51.0%;

Query Match Best Local Similarity

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gacctggggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgg 176
                                                 641
                                                                                                                                            642 ggccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac 701
                                                                                                                                                                                                                                                                                                 coggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa 356
                                                                                                                                                                                                                                                                                                                           Gaps
                                                 gatctccgactacctggtcgacctggtccagatgggcgtcaaggggcttgcggcgtcgatgc
                                                                                                     cyatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca
                                                                                                                                                                                                                                                  702 eggtgeegeacggeeattetggtteetggaggtgateggegeegeegggegaggeggtgea
                                                                                                                                                                                                      ggtcggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (FERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 53.4; DB 20; 51.0%; Pred. No. 0.087; ive 0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas alpha-amylase variant encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX37295 standard; DNA; 1981 BP
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Best Local Similarity 51.0
Matches 126; Conservative
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P-PSDB; AAY17906.
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582 gatetecgaetacetggtegaeetggtecagatgggegteaagggettgegegegtegatge 641

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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylase variants (AAY17904-Y17909). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, O. et al., Biosci. Biotech, Biochem. Vol. 56, 76-80, 1992 ). The variants have a replacement of the 5th or the 130th amino acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose in a high yield.
                                                                                                                                                                                           ccggacgacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa 356
 gacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcgacgg 176
                                                                                                                                                                                                                      762 geceagecagtaettegggeteggeggegggeaggteaeggtgaeegagttegeetaegg 821
                                                                                gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgtcgatgc
                                                            cgatgtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas; maltopentaose; alpha-amylase; enzyme; variant; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-amylase variant encoding DNA (FERM BP-6117).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 14-16; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                    caaggag 828
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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylase variants (AAY17904-Y17909). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, O. et al., Blosci. Biochem. Vol. 56, 76-80, 1992 ). The variants have a replacement of the 57th or the 130th amino acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose
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                            ggccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac 701
 cgatgtgcacatcggcccgaccgagcccgagggcctcggaagatgtccacatccggctcca
                                                                ggtcggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcga
                                                                                             702 cggtgccgcacggccattctggttcctggaggtgatcggcgcgcgggcgaggcggtgca
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                                                                                                                                                                                                                                                                                                      AAX37297 standard; DNA; 1981 BP.
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Best Local Similarity
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Search completed: July 18, 2002, 11:36:11 Job time: 11236 sec

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                         Compugen Ltd
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Copyright (c) 1993 - 2000 Comp
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Sequence 3, Appli
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Patent No. 5215881
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APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTR.

2.IP: 46268
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
                              5215881-1
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0S-07-945-283-1
0S-08-920-812-13
0S-08-921-177-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECHONE: (317)337-4816
TELECHONE: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09036987A Patent No. 6143526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
1683
1683
1831
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1831
8438
9515
9515
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71989
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71984
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74377
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Length 80161;

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Score 54.8;

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RESULT. 3
US-09-017-706-3
US-09-017-706-3
US-09-017-706-3
Sequence 3, Application US/09017706A
Fatent No. 6087147
GENERAL INFORMATION
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT FAPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1997-10-21
FARLIER APPLICATION NUMBER: JP 305071/1997
SEARLIER REPLICE FILING DATE: 1997-10-21
SOFTWARE: PATENTION OF: 2.0
SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.0
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Pred. No. 0.014;
0; Mismatches 121; Indels
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LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09017706A
Patent No. 6087147
GENERAL INFORMATION:
APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABI
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE REPRENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pseudomonas sp., Strain KO-8940
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; OTHER INFORMATION: PLASMID POS3410F57
US-09-017-706-3
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Best Local Similarity 51.0%;
Matches 126; Conservative (
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                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
TILLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE REFERENCE: 50489 DIVI
CURRENT APPLICANTON NUMBER: US/09/370,700
EARLIER APPLICATION NUMBER: US/09/370,700
EARLIER PILLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 39
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Pred. No. 0.0067;
0; Mismatches 132;
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13.5%; Score 54.8; DB 4;
Best Local Similarity 52.1%; Pred. No. 0.0067;
Matches 147; Conservative 0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Saccharopolyspora spinosa US-09-370-700-1
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Best Local Similarity 52.1
Matches 147; Conservative
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APPLICANT: ITO, YOSHIFUMI
APPLICANT: TTO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
FILE REPERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT PILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: J9 305071/1997
SARLIER PILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
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                                                                                                                                                                                                                    13.1%; Score 53.4; DB 3; Length 1 llarity 51.0%; Pred. No. 0.014; Conservative 0; Mismatches 121; Indels
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                          OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); OTHER INFORMATION: PLASMID: pos3410F139
US-09-017-706-6
                                                                    OTHER INFORMATION: MUTATED GENOMIC DNA PEATURE:
                                                                                                                  ; OTHER INFORMATION: PLASMID POS34100L57
US-09-017-706-5
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US-09-017-706-6; Sequence 6, Application US/09017706A... Patent No. 6087147...
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LOCATION: (85)..(1848)
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Matches 126; Conserva
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APPLICANT: ITO, YOSHIEDMI

TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: TRANSFORMANT
FILE REPERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
BARLIER FILING DATE: 1997-10-21
NUMBER: OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (7)..(1848)
FEATURE:
LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
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CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: JP 305071/1997
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1981
                                                                                                                                                                                              ORGANISM: Pseudomonas sp., Strain KO-8940
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US-09-017-706-4
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US-09-017-706-5
; Sequence 5, Application US/09017706A
; Patent No. 608/147
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Query Match 13.1%;
Best Local Similarity 51.0%;
Matches 126; Conservative
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LOCATION: (85)..(1848)
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357 cctggag 363
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Sequence 7, Application US/09017706A

GENERAL INFORMATION:
TOO YOSHITUMI

TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: TRANSFORMANT

TITLE OF INVENTION: TRANSFORMANT

TITLE OF INVENTION: TRANSFORMANT

TITLE OF INVENTION: TRANSFORMANT

CURRENT APPLICATION NUMBER: US/09/017,706A

CURRENT APPLICATION NUMBER: US/09/017,706A

CURRENT FILING DATE: 1998-02-05

EARLIER PLICATION NUMBER: JP 305071/1997

EARLIER FILING DATE: 1997-10-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PALENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582 gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgtcgatgc 641
                                                                          642 goccaagcacatcagcccgacggacttgggtgccatcatcgacagcgtcaacgcgcgcac 701
                                                                                                                ggtcggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcga 296
                                                                                                                                                      761
                                                                                                                                                                                                                                762 geceagecagtaettegggeteggeggegggeaggteaeggtgaeegagttegeetaegg 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca 236
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                                                                                                                                                                                            ccggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (83):.(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: PLASMID: poS3410H139
US-09-017-706-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MUTATED GENOMIC DNA
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LOCATION: (85)..(1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (7)..(1848)
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177 cgatgtgcacatcggcccgaccgaggcccgagggcctcggagatgtccacatccggctcca 236
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Sequence 9, Application US/08034650
Sequence 9, Application US/08034650
Sequence 9, Application US/08034650
Sequence 9, Application US-08034650
SPELICANT: BOS, Jannetje W.
APPLICANT: FREMKEN, Leon G.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: PROBUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53.4; DB 3; Length 1 Pred. No. 0.014; 0; Mismatches 121; Indels
SQUENCE 8, Application US/09017706A
Fatent No. 6087147
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABI
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CON
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: PLASMID: pos3410L139
US-09-017-706-8
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2081 CCGGCCGCCATGCAGCTCGGCTCGATCAGCGCGCGGGGCGTGGCCGACCGCACGCTCGGC 2140
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LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 0.071;
0; Mismatches 114; Indels
                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: APACHINE Release #1.0, Version #1.25
SURRENT APPLICATION NUMBER: US/08/449,015
FILING DATE: 34-MAY-1995
CLASSIFICATION NUMBER: US 07/727,235
PRIOR APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-7UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL NIMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNK/5970/91731
                                                                     NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08387942C Patent No. 5939289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PNK,
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISICS:
LENGTH: 2900 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.2%;
Best Local Similarity 50.9%;
Matches 118; Conservative (
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LIFE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
                        TITLE OF INVENTION:
                                                                                                                                                                    Washington
                                                                                                                                                                      CITY: Wash
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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US-08-449-015-9
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US-08-387-942C-7
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TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2261 CTCGACGCGCAGCTGACCCGGACGAGCGCGCCAGCAGCGCGCTGCATG 2312
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                                                                                                                                                               COUNTRY: USA

ZIP: 20036-5601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRICOR APPLICATION 1433
PRICOR APPLICATION DATA
PPLICATION NUMBER: US 07/727,235
FILING DATE: 03-2016-1991
FILING DATE: 03-2016-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/COCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 861-3000
TELEFAX: (302) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49.6; DB Pred. No. 0.071; 0; Mismatches 1
                                                                     ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-449-015-9
; Sequence 9, Application US/08449015
; Sequence 9, Application US/08449015
; Patent No. 5804409
; GENERAL INFORMATION:
; APPLICANT: BOS, Jannetje W.
APPLICANT: FERNERN, Leon G.
; APPLICANT: VERRIPS, Cornelis T.
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ilarity 50.9%;
Conservative 0
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1559..2617
                      NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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Best Local Similarity
Matches 118; Conserv
                                                                                                                                           STATE: D.C
COUNTRY: U
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NAME/KEY: misc_feature LOCATION: 1998..2198
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  Katz, L
Donadio, S
                                                                                                                                                                      CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                    ns
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 ggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgctggg 341
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9
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          APPLICANT: STATK BRABK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O.BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSILICATION: 433
ATORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION UNDHABER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEFONE: 703-205-8000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANBENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-642-734C-1/c
; Sequence 1, Application US/07642734C
; Patent No. 5824513
v, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-7
VALLA, SVEIN
                                                                                                                                                                                                                                                    22042
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| 546 CGG 548
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APPLICANT:
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APPLICANT: Donald, S
APPLICANT: Mothline, S
APPLICANT: Wathline, S
APPLICANT: Wathline, S
TITLE OF INVENTION: Recombinant DNA Method for Producting
TITLE OF INVENTION: Recombinant DNA Method for Producting
TITLE OF INVENTION: Recombinant DNA Method for Droducting
TITLE OF INVENTION: Packed H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 one Abbott
STREET: Abbott Babott Laboratories
COMPITER: IN COMPITER: I
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FEATURE:

NAME/KEY: CDS

LOCATION: 744.11219

OTHER INFORMATION: /function= "gene= "eryA""

OTHER INFORMATION: /product= "'ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 2250..3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 744.1868
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
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OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1998..2198
COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain 1 of module FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 744..6559
OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
OTHER INFORMATION: /label= FUNCTION
                       NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F. Weinstock
STREET: Abbort Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 5574..6125
OTHER INFORMATION: /function= "approximate span of
                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,009A

FILING DATE: 11-MA'-1995

CLASSIFICATION: 435

ATTORREY/AGENT INFORMATION:

NAME: Casuto, Dianne

REGESTRATION NUMBER: 40,943

REFERENCE/DOCKET NUMBER: 4952.US.DI

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENOTH: 11219 base pairs

TYPE: unknown.

TYPE: unknown.
TITLE OF INVENTION: Specific Polyketides NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ONGINAL SOURCE:
ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 3831..4811
                                                                                                                                                      CITY: Abbc
STATE: IL
                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 ctgggcgttcggccgcgagctgctgctgacgggctcaacagcccgagcggcgacggcga 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 tgtgcacatcggcccgaccgagcccgagggcttcggagatgtccacatccggctccaggt 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 eggeggacegtgegetgttcegggegggggaeggeacegetggtggegtteetegaeeg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgac 119
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                                               NAME/KEY: misc_feature
LOCATION: 5574..6125
OTHER INFORMATION: _function= "approximate span of
OTHER INFORMATION: _bcta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 9906.110454
OTHER INFORMATION: /Lunction= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.0%; Score 49; DB 1; Length 11219; Best Local Similarity 50.2%; Pred. No. 0.088; Matches 147; Conservative 0; Mismatches 145; Indels
  OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 6678..8066
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACPsynthase of module:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Kat. L
APPLICANT: Mat. L
APPLICANT: Mat. J B
TILE OF INVENTION: Method of Directing Biosynthesis of
                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 3369..6526
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature;
CCATION: 10707..10964
OTHER INFORMATION: /function= "approximate span of;
OTHER INFORMATION: acyl carrier domain of module 2"
                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..11219
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 2"
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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1759 GGGCGCGCCCACCGCGTCGGGTACGTGGAGGCCGTGGGCGTACGGGCGGACCGCCGCCGC 1818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 ggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggtcggcgggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.8%; Score 48; DB 1; Length 2064;
Best Local Similarity 53.1%; Pred. No. 0.14;
Matches 102; Conservative 0; Mismatches 90; Indels
                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: VAID COMPATIBLE TO CASSIFICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
APPLICATION NUMBER: JAPAN 4-126511
FILING DATE: 19-MAY-1992
ATTONNEY/AGENT INFORMATION:
NAME: HALEY, Jr., James F.
REGISTRATION NUMBER: 27794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by experiment
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SHGN-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces fradiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -35 signal
LOCATION: 359.364
IDENTIFICATION METHOD:
NAME/KEY: -10 signal
LOCATION: 378.383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IDENTIFICATION METHOD:
; NAME/KEX: sig peptide
LOCATION: 435.944
; IDENTIFICATION METHOD:
US-08-343-428-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1879 Trceccecerc 1890
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                                                  New York
                                                                                             10020-1104
                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CORIGINAL SOURCE:
                                                                         USA
                                                                      COUNTRY:
ZIP: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcga 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggcgcaccgtgcgctgttccgggcggggacggcaccgctggtggcgttcctcgaccg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgac 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 tgtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 gacggacaagctcgtgccgctcggccaggacacacgctgggtgacttcgacg 352
                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678.8066
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
FEATURE:
OTHER INFORMATION: beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= "approximate span of beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 3; Length 11219;
Pred. No. 0.088;
0; Mismatches 145; Indels
                                          NAME/KEY: misc_feature
LOCATION: 6369..6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module
                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..11219
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 10707 .10964
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James F. Haley, Jr., Fish & Neave
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APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Kitadokoro, Kengo
APPLICANT: Tradokoro, Hiroshi
TITLE OF INVENTION: No. 5665586el Protease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr Fire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08343428
Patent No. 5665586
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.0%;
Best Local Similarity 50.2%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 9906..10454
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CAGGGGAGCGCTCGCTCGCGCGACCCTGGTGCACGCCCCTCGGTCGCGCCCGACCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 cregrecrececerecresaacecrareacerecarecerrecescresares 357
                                                                     APPLICANT: Susan E. Jensen
APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo

TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: ALS ADDRESS:
COUNTRY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PAtentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.29;
0; Mismatches 146; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-7M-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEFAN: (202) 3930550
TELEFAN: (202) 3930550
TELEFAN: (202) 3930550
TELERAN: RABATTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                 Sequence 16, Application US/09385028 Patent No. 6232106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: DNA (genomic) US-09-385-028-16
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Best Local Similarity 49.73
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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US-09-385-028-16
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Search completed: July 18, 2002, 11:24:51 Job time: 10881 sec

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AQ851019 LMAJFV1_1 BH020269 L7165c.d_ BH019193 L24591.d_ BH019836 L5336c.d_

A0852043 LMAJUVL BB6535178 BB6535178 BB65351815 BR019916 L588730.4 BM458211 ACENCOURT B1529148 102409651 BC859785 102409651 ACOF 2007280 Part A1588142 AL588142 AL588

AL287096 Tetraodon AG152796 Pan trog1 AG032939 Pan trog1 BE597437 PI1_69_E0 BH018881 L2031k.d_ AQ849292 LMAJFV1_1

L3651.d_

BH018881 L AQ849292 I BH019456 I AZ131579 C BI956687 H

Perfect score: Sequence: Scoring table:

Searched:

OM nucleic

Run on:

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A Genoscope.

A Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

B Sibmitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and bow to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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AG152796
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BM458211
BG859785
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BB635178
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AL053013
AL053013.1 GI:4934461
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RESULT 1
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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AL055013 Drosophil
AQ856496 nbeb0003C
AL066051 Drosophil
AQ847989 LMAJFV1_1
AQ851336 LMAJFV1_1
AQ851315 LMAJFV1_1
AL192712 Tetracodon
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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928 bp DNA linear GSS 03-NOV-1999 clone nbeb0003C14f CUGI Rice BAC Library (ECORI) Oryza sativa genomic AQB56496 GI:6206953 GSSS.
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                                                                                                                                                                    511 others
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Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                14.0%; Score 57; DB 1
ilarity 14.3%; Pred. No. 1.2;
Conservative 161; Mismatches
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Class: BAC ends
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/db_xref="taxon:4530"
/clone="nbeb0003C14f"
/db_xref-"taxon:7227"
/clone_lib-"RPCI-98"
/clone-"BACR19D16"
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- Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                655 KSSSSGSSSSSSTITSKSTSASGSGSWSAGGGSGSTGSTSSSSSSSSSSSSSSSSST 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 accgagcccgagggcctcggagatgtccacatccggctccaggtcggcgggaccgtgcg
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Pred. No. 0.87;
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                                  /note="end : TET3"
61 c 61 g
/clone="BACR19D16"
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AQ851215/c
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                                                                                       on fice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 411 Mbp (Arumuqanathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55.296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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/note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely
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Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRx cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 ggtoggogoggacogtgogctgttccgggogggacggcaccgctggtggcgttcctcga 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CGTCGCCGTCAAGCGCGCCAAGCTCCGGAACCCGCACGTGGAGTTCCG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 coggacgacaagetegtgeegeteggeeaggageacaegetgggtgaettegaeggeaa 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 GAGCGAGGTGAAGGCCATGGCGCGCATCGAGCACCAGAGCCTCGTCCGCTTCTACGGCTA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 CAAGGTCGCCCAGGGCGGCTTCGGCGCCGTCTACAGGGGCGTTCTCCCCGACGGCACGCT 392
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 5.5;
0; Mismatches 140; Indels
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. Por further information please see http://www.fruitfy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosst in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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contains element V1-ch1_type_II.2 leishmania repetitive element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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28.0%; Pred. No. 5.5;
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/clone="BACR14N09"
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1 (bases 1 to 556)
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DNA Sequencing by: Washington University Genome Sequencing Center

If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major

Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining

clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.

Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pzero-2 (Invitrogen); Site_1: EcoRV; decomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephospharted with Shrimp Alkaline Phosphatase and ligated into pZero-2 vector's EcoRV site."
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Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, J., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S. M. A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="LMAJFV1_Im44f10"
/clone_lib="Leishmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                 Other GSSs: lm44f10.y1
Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
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/organism="Leishmania major"
/strain="Friedlin strain Vl"
/db_xref="taxon:5664"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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      AUTHORS
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DNA Sequencing by: Washington University Genome Sequencing Center If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Eriedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. Seq primer: -400P from Gibco
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/clone_lib-"Leishmania major FV1 random genomic library"
/lab_host-"TOP10 (Invitrogen)"
/note-"Vector: pZero-2 (Invitrogen); Site_l: ECORV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECORV site."
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1 (Dases I to 414)

1 (Dases I to 414)

Kissinger, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenss, M., Gibbons, M., Bowers, Y., McCann, R., Tsagareishvill, R., Wilson, R. and Beverley, S.W. A survey of the Leishmania major Friedlin strain vi genome by shotgun sequencing: a resource for DNA microarrays and expression
341 gigacticgacggcaacciggaggacgcacigggccgcatccicgccgaggagcagaacg 400
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
                                                                          Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Location/Qualifiers
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AQ847989.1 GI:6052637
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Length 414;

DB 12;

Score 52.2;

12.8%;

us-09-749-185-2.rst

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Beverley Ph.D.

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Tetraodon nigroviridis genome survey sequence T7 end of clone 260D06 of library G from Tetraodon nigroviridis, genomic survey sequence
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Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygi: Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 755)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catecggatgaegttecacetteeeggegatgeeeetgtgaeetgggegtteggeegga 137
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(natalia@borcim.wustl.edu) and/or Stephen M. (beværley@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: shorgun
High quality sequence stop: 399.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                    /strain="Friedlin strain Vl"
/db_xref="taxon:5664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.6; DB
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 ccgcatcctcgccgaggagcagaacgccggctg 407
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Tetraodon nigroviridis.
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llarity 47.3%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
186; Conserv
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
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LMAJFVI_Lm29C04.yl Leishmania major FV1 random genomic library Leishmania major element clone LMAJFVI_lm29c04 5' similar to contains element V1-ch1_LYPe_II.2 V1-ch1_LYPe_II leishmania repetitive element ; DNA sequence.
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                                                                                                                                                 teceggegatgeceetgtgaeetgggegtteggeegegagetgetgetggaegggeteaa 158
                                                                                                                                                                                                                                                                                                                     tgtccacatccggctccaggtcggcgcggaccgtgcgctgttccggggcggggacggcacc 278
                                                                                                                                                                                                                                                                                                                                                                                                     getggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgct 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gggtgacttcgacggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaa 398
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                        Gaps
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                                                                 tccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttccacct
                                                                                                     GCTGGACGCCCAGGACGACGCCCGACGCCGCGGAGCTGCTGCTGGACGCCCAGA
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                                                                                                                                                                                                                                                                                                                                                           Washington Universitý School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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                     Mismatches 198; Indels
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21192569
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Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
    Š.
  Pred.
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Similarity 46.3
1; Conservative
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314 286 1810
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Leishmania major
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Best Local
Matches 17
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                  159
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COMMENT
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254 273

ä

Length 474; Indels

93 11

REFERENCE AUTHORS

JOURNAL

TITLE JOURNAL

COMMENT

FEATURES

AUTHORS

JOURNAL REFERENCE

TITLE

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AQ849196 1442 bp DNA 11near GSS 25-MAY-2001
LMAJFV1_lnd3e09.yl Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_lnd3e09 5' similar to
contains element V1-chl_type_II.2 leishmania repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="cutitivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4330"
/clone="C60023_11A"
/clone="C60023_11A"
/clone="Nector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid.
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Leishmania major.
Leishmania major.
Leishmania major.
Leishmania major.
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Leishmania .
Li, Enter, Chinte, T., Chintalla, A.,
Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko
J., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M.,
Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y.,
Rowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M.
A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA microarrays and expression
              National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7446
Email: tsasak'eabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 CTGCACCGGCGAGGCGTGTTCGCCACGGCGAGTCCGGGCACTACGCGCTCGACGA 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 ceaectreecececececececereacececeaegererrerreraceceaeaacecea 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.8; DB 10;
Pred. No. 19;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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    Takuji Sasaki
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51.2%;
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This sequence is a single read and was generated as part of a large
scale clone-and sequencing project of the Terracodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracodon.
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                                                                                                                                                                                                                            2 (bases 1 to 755)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                   Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 acggeaccgetggtggcgtteetegaccggacgacaagetegtgeegeteggeeaggag 330
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Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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/db_xref="taxon:99883"
/clone="260D06"
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18;
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238 c 266 g 111
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Pred. No.
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Best Local Similarity 49.2%;
Matches 131; Conservative
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                                                 Weissenbach, J.
Charaterization and
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSO2AGC 1129 bp DNA linear GSS 12-MAY-200C Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 251LO9 of library G from Tetraodon nigroviridis, genomic survey
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1 (bases 1 to 1129)
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 CCSGSTGCGGGSCCCCCCCMCCSCCCCCGGCCCRSKCSCVGCCGGGGGGG 685
                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachygera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1009)
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freshwater pufferfish Tetraodon nigroviridis
Unpublished
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/plasmid="pBeloBAC11"
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32.8%; Pred. No. 21;
tive 55; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="DrosBAC"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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377 c 178
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AL188517
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Matches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="reledin strain VI"
/db_xref="taxon:564"
/db_xref="taxon:564"
/clone="taxon:564"
/clone=lib="Ledishmania major FVI random genomic library"
/lab_host="ToPl0 (Invitrogen)"
/lab_host="ToPl0 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's EcoRV site."
31 a 13 c 195 g 30 t
                                                                                                                                                                                                     Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
If using this information please cite:
If S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.

(hatalia@borcim.wustl.edu)
Actalia Seq primer: -40RP from Gibco
Class: shotgun
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37919 of Drossback library from Drosophila melanogaster (fruit
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                                              Washu Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                           Contact: Akopyants, NS / Beverley, SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Leishmania major"
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Pred. No. 20;
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                                                                                                                                                         Fax: 314 286 1810
Email: est@watson.wustl.edu
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ilarity 48.6%;
Conservative
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Fax: 314 286 1810
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                                                                                                                                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracdon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
1. il29
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-007M05.F.
Pan troglodytes
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                                               Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                 Bouneau, L., Fisher, C.,
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           Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="251L09"
/clone_11b="6"
/note="Genoscope sequence ID : COAG251CF05SP1~end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttc
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Pred. No. 21;
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Best Local Similarity 46.7%;
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AWB001.G03F000328 ITEC AWB Wheat Melotic Stage Library Triticum aestivum cDNA clone AWB001.G03, mRNA sequence.
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2 (bases 1 to 1313)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tortodi,Y., Watanabe,H. and Sakaki,Y.
Tortodi,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
T-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 agctgctgctggacgggctcaacagcccgagcggcgacggcgatgtgcacatcggcccga 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 ccatccggatgacgttccaccttcccggcgatgccctgtgacctgggcgttcggccgcg
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 389 c 502 g 132 t 225 others
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Pred. No. 22;
0; Mismatches 214;
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-007M05.F"
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SacI
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Search completed: July 18, 2002, 10:12:46 Job time: 9966 sec
                         fruit fly.
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/clone="AWBOOI.603"
/clone_lib="ITEC AWB Wheat Meiotic Stage Library"
/tissue_type="excised florets"
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/dev_stage="meiotic stage no later than metaphase I"
/note="Wector: pSport 1 (Life Technologies cat. no.
18248-013); Site_1: Sall; Library constructed in pSport 1
Directionally cloned using the Superscript Plasmid System for cDNA synthesis and plasmid cloning. M13 Reverse sequencing primer used to obtain 5' sequence data. 1.4
Kbp average insert size."
Special Research Centre, Basic and Applied Plant Molecular Biology Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA Tel: 61 8 8303 7368 Fex: 61 8 8303 7102
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                       Email: plangridge@waite.adelaide.edu.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
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Pred. No. 27;
0; Mismatches
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AL108460
AL108460.1 GI:5628764
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49.2%;
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Best Local Similarity 49.2
Matches 128; Conservative
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Geneyieve Payan. It has been constructed in the vector
                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1101)
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN37L08"
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July 18, 2002, 11:22:50 ; Search time 130.38 Seconds (without alignments) 115.010 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                           The present sequence is S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                              VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                             1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibictic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antihigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
           microorganisms used to improve their liquid culturing properties
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Reducing branching and enhancing fragmentation in filamentous
                                                                                                                                                                                                                                         Length 135;
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                                                                                                                                                                                                                                        100.0%; Score 704; DB 21;
100.0%; Pred. No. 5.7e-72;
tive 0; Mismatches 0;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces netropsis SsgA protein.
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                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY44652 standard; Protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-NL00395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 135; Conservative
                                      Fig 5; 60pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Kraal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces netropsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147269/13.
                                                                                                                                                                                                  135 AA;
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                                      Disclosure;
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mycelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                           VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                                                                                                                                                                                                     Gaps
The present sequence is S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycel in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, berbicides, antiparastic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                               1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhancing fragmentation in filamentous improve their liquid culturing properties
                                                                                                                                                                                                                                                              86.1%; Score 606; DB 21; Length 135; 85.9%; Pred. No. 7.5e-61;
                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                   7; Mismatches
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us-09-749-185-3.rag

ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.

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                                                                                                                                                                                                                                                                                                                  VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                   1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, ronzyme inhibitors, antimigraine agents, herbicides, antiparastic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                     SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellun; antiblotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                 Score 556; DB 21;
Pred. No. 3.5e-55;
                                                                                                                                                                                                 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44650 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces albus G SsgA protein.
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                                                                                                                                                                 79.0%;
78.5%;
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                                                                                                                                                                                                                                                                                                                                                                                       Van Wezel GP, Kraal B,
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N-PSDB; AAZ49729.
                                                                                                                                                                               Local Similarity
                                                                                                                 Sequence 135 AA;
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                                                                                                                                                                                                  Matches 106;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                           VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                            Gaps
                                                                                                                                                                            1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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9.7e-45;
                                                                                                                            18; Mismatches
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                                                                                             Score 464;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #24735.
                                                                                                                                                                                                                                                                                                                                                                                                           ABG24744 standard; Protein; 321 AA.
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                                                                                             65.9%;
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23-AUG-2000; 2000US-0649167
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                                                                                      Query Match
Best Local Similarity 65.99
Matches 89; Conservative
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N-PSDB; AAS88931.
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                                               AA;
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990S - 0.13884.
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990S - 0.13884.
990S - 0.13945.
990S - 0.13945.
           990S-0134256.
990S-0134218.
990S-0134221.
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990S-0134768.
990S-0134941.
990S-0135353.
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99US-0145085.
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99US-0145089.
           11 - MAY - 1999;
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14 - MAY - 1999;
16 - MAY - 1999;
19 - MAY - 1999;
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21 - MAY - 1999;
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08-JUN-1999;
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23-JUN-1999;
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08-JUL-1999;
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          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                         ---REL-LLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGA----DRALFRAGTAPLVA 96
 polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                    42;
                                                                                                                                                            22; Length 321;
                                                                                                                                                                                    52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 12181.
                                                                                                                                                                                                         1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG
                                                                                                                                                                                                                                                                                                         97 FLDRIDKLVPLGQEHTLGDF----DGNLEDAL-GRILAE 130
                                                                                                                                                                                                                                                                                                                     11.9%; Score 84; DB 22
27.7%; Pred. No. 0.39;
ive 21; Mismatches
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99US-0125748.
99US-0125784.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
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990S-0130510.
990S-0130891.
990S-0131449.
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990S-0132484.
990S-0132485.
990S-0132486.
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                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                         Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                       321 AA;
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
08-APR-1999;
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23-APR-1999;
23-APR-1999;
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06-MAY-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                             58 DGDVHIGP----TEPEGLGDVHIRLQVGADRALFRAGTAPL----VAFLDRTDKLVPLG 108
                                                                                                                                   Gaps
                                                                                                                                                 4 LVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGR-----ELLLDGLNSPSG 57
                                                                                                                                                                                             31;
                                                                                                                 11.9%; Score 83.5; DB 21; Length 456; 25.0%; Pred. No. 0.7; ive 22; Mismatches 52; Indels 31.
                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 32224.
                                                                                                                                                                                                                                                                           AAG27402 standard; Protein; 456 AA
                                                                                                                                                                                                                   109 QEHTLGDFDGN--LEDALGR 126
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990S-0126785.
990S-0126785.
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990S-0130445.
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                                                                                                                                   35; Conservative
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                                                                                                                           Local Similarity
         22-0CT-1999;
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905-0145192 905-0145145 905-0145218 905-0145224 905-0145276 905-0145918 905-0145918 905-0145918 905-0146388 905-0146388 905-0146388 905-0146388	9905-014726 9905-0147303 9905-01474303 9905-0147431 9905-0147431 9905-0148171 9905-0148171 9905-0148565 9905-0148664 9905-0149765 9905-0149723 9905-0149929 9905-0149929 9905-0149930 9905-0149930 9905-0149930 9905-0149930	905-0151303 908-0151303 908-0151303 908-015303 908-015303 908-015403 908-015403 908-0155139 908-0156486 908-0156486 908-0156486 908-0156486 908-0156486	90S-0158029 90S-0158029 90S-0158289 90S-0159294 90S-0159295 90S-0159289 90S-0159331 90S-0159638 90S-0159638 90S-0160741 90S-0160769
2.7UL-1999 3.7UL-1999 3.7UL-1999 6.7UL-1999 6.7UL-1999 7.7UL-1999 7.7UL-1999 7.7UL-1999 7.7UL-1999 7.7UL-1999 7.7UL-1999 7.7UL-1999 7.7UL-1999 8.7UL-1999 8.7UL-1999 8.7UL-1999 8.7UL-1999 8.7UL-1999	05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 09-AUG-1999; 110-AUG-1999; 112-AUG-1999; 113-AUG-1999; 113-AUG-1999; 123-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 21-AUG-1999; 23-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999;	11-AUG 11-AUG	7 - 0 C C T - 1999 9
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Gaps

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carcinoma, bile duct, bladder or colorectal cancer. Crohn's disease, carcinoma, bile duct, bladder or colorectal cancer. Crohn's disease, colitis-associated neoplasia or chronic ulcerative colitis. These conditions, where associated with a homozygous deletion, can be treated by administering an agent that: (a) modulates DPC4 expression, specifically a sense DPC4 sequence (particularly in the form of a vector, i.e. by gene therapy), but also an antisense sequence where DPC4 protein is over expressed or (b) mimics the activity of DPC4 nucleic acid is also used as hybridisation probes for detecting nucleic acid is also used as hybridisation probes for detecting concleic acid is also used as hybridisation probes for detecting a homozygous deletion is detected in this region, an agent can be administered that accumulates within, or kills, only cells which contain such a deletion. This agent exploits the absence of an enzyme (or other protein) encoded by a neighbouring gene and lost by the
                                                                                                                                                                                                                                                                                                                                       304 vhnelafqppisnhpapeywcsiayfemdvqvge-----tfkvpsscpi-----vtv 350
                                                                                                                                                                                                                                                                                                                                                                               -----ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                 50 DGLNSPSGDGD------VHIG---PTEPEGLGDVHIRLQVGADRAL
                                                                                                                                                                                                                                                        Ouery Match 11.5%; Score 81; DB 18; Length 552; Best Local Similarity 25.7%; Pred. No. 1.7; Matches 38; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                408 fvqsyyldreagrap----gdavhkiyp 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70071 standard; Protein; 552 AA.
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                                                                                                                                                                                                                                                                           DGDVHIGP----TEPEGLGDVHIRLQVGADRALFRAGTAPL----VAFLDRTDKLVPLG 108
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                         LVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGR-----ELLLDGLNSPSG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;
tumour suppressor gene; proliferative disease; bile duct; bladder;
colorectal; cancer; Crohn's disease; colitis.
                                                                                                                                                                                                                                                                                                                               Human deleted in pancreatic cancer locus 4 - DPC4 - polypeptide.
                                                                                                                                                                                                                               31;
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                                                                                                                                                                                                     Length 456;
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                                                                                                                                                                                                                                52;
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                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                     11.9%; Score 83.5; DE 25.0%; Pred. No. 0.7; ive 22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
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29-OCT-1999
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Treatment of a cell proliferative disorder by administration of tumor suppressor polypeptide Dpc4 (Smad4) coupled to a nuclear localization
                                                                                   Cell proliferative disorder; nuclear localisation factor; neoplasm; Dpc4; Delted in Pancreatic Carcinoma; locus 4; Smad-binding element; SBE; tumour suppressor; transforming growth factor-beta; TGF beta; anti-cancer drug; treatment; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Human tumour suppressor protein, Dpc4.
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                      using a chimeric Doc4 (Deleted in Pencratic Carcinoma, locus 4) polypeptide coupled to a nuclear localisation factor. Upon localisation to the nucleus and binding to Smad-binding element (SBE), Dpc4 shows tumour suppressor action. This method can also be used for identifying transforming growth factor-beta (TGF beta) inducible genes, modulators of Dpc4 nuclear localisation and in screening for anti-cancer drugs. Dpc4 can be used in the treatment of neoplasms and in gene therapy. The present sequence is that of human Dpc4 tumour suppressor protein. Note: It is indicated in the claims section that the present peptide sequence is sequence Id No: 1 and elsewhere in the specification as
             discloses a method of treating cell proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smad4; MADH4; DPC4; TGF-beta signalling pathway; transcription factor; expression inhibition; antisense therapy; tumour formation; inflammation.
                                                                                                                                                                                                                                                                                                       304 vhnelafqppisnhpapeywcsiayfemdvqvge-----tfkvpsscpi-----vtv 350
                                                                                                                                                                                                                                                                                                                                                 ------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                              5 VSEELSFRIPV-------ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense inhibition of the human Smad4 gene, useful for diagnosing, preventing and treating conditions associated with Smad4 expression e.g. inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents human Smad4. The Smad proteins are a family of cytosolic proteins which are involved in TGF-beta
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Pred. No. 1.7;
                                                                                                                                                                                                                                                    16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                        AAY69622 standard; Protein; 552 AA
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                                                                                                                                                                                                                                                                                                                                 50 DGLNSPSGDGD---
                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                    552 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                    Sequence
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                                                                                                       heterodimerisation partner for the pathway restricted members of the Smad family (Smadl-3, 5 and MADH6) and is known as the common mediator. The N-terminus of Smadd promotes the binding of the Smad complex to DNA, and the C-terminus provides an activation signal required for the complex to stimulate transcription. The invention relates to antisense oligonucleotides targetted to the human Smadd gene, which inhibit its expression. A series of oligonucleotides (AAZS9749-Z59788) were designed to target different regions of the human Smadd RNA, and were analysed for their effect on Smadd mRNA levels by quantitative real-time PCR. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with Smadd expression, such as tumour formation, inflammation and certain infections.
superfamily signal transduction. On ligand binding, TGF-beta superfamily
                       proteins (such as bone morphogenetic protein (BMP), activin and TGF-betas themselves) phosphorylate Smad proteins, which then homo- or heterodimerise and translocate to the nucleus to activate target gene transcription. Smad4 (also known as MADH4 and DPC4) is a shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VSEELSFRIPV------ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Smad4 gene; fusion protein; green fluorescent protein; GFP; intracellular signalling; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 81; DB 21; Length 552; 25.7%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smad4-green flourescent protein fusion product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW85025 standard; Protein; 798
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Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-DK00145.
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 DGLNSPSGDGD
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Tullin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW85025;
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WO9625424-A1
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                                                                                                                                          The present sequence represents a human Smad4-green flourescent protein fusion product. The fusion protein is used in an assay that exemplifies the invention. The specification describes how quantitative information about the influence of a molecule on a claim intact into the influence of a molecule on a claim intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light emission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in) directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and to identify new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 vhnelafqppisnhpapeywcsiayfemdvqvge-----tfkvpsscpi-----vtv 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 dgyvdpsg-gdrfclgqlsnvhrteaierarlhigkgvqleckgegdvwvrcl--sdhav 407
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particularly for identifying toxins and potential therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 81; DB
; Pred. No. 2.8;
16; Mismatches
                                                                               Example 17; Pages 176-178; 326pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F-----RAGTAPLVAFLDRTDKLVP 106
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Chimeric - Homo sapiens.
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25.7%;
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Best Local Similarity
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Tullin S;
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                                            The present sequence represents a human Smad4-green flourescent that exemplifies the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light emission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Periplasmic chitodextrinase; periplasmic Beta-N-acetylglucosaminidase; Beta-N-acetylglucosamidase; chitin; oligosaccharide; catabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 DGLNSPSGDGD-------VHIG---PTEPEGLGDVHIRLQVGADRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 81; DB 19; Length 806; 25.7%; Pred. No. 2.8; ive 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ပ်
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keyhani N, Roseman S,
Example 17; Pages 108-109; 326pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            662 fvqsyyldreagrap----gdavhkiyp 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW02156 standard; Protein; 1046 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 68-71; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    to identify new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Periplasmic chitodextrinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.7
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-393335/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 806 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VSEELSFRIPV --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio furnissii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT36387
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                       AAU56775;
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                               RESULT. 15
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                                                                                                                                                                                                                                                                                                                                                            Chitodextrinase; periplasmic; endI; Endo-I; chitin; chitosan; endoenzyme;
                                                                                                                                                                                                                                                                                                                                                                    beta 1-4 N-acetylglucosamine; GloNc; degradation; catabolism;
oligosaccharide; agriculture; medicine; nitrogen fixing nodules;
disease resistance; induction; fungicide; antimetastatic;
Lewis lung carcinoma; immune system, macrophage; activation; production;
       Periplasmic chitodextrinase (AAW02156), periplasmic Beta-N-acetylglucosaminidase (AAW02157) and aryl Beta-N-acetylglucosaminidase (AAW02158) can be used to produce chitin Oligosaccharides with the structure (GICNAc)n where n is 2 or higher, by contacting them with soluble chitin. The enzymes are encoded by the genes end!, exoI and exoII respectively. They are all genes involved in the catabolic pathway of chitin.
                                                                                                                                                                                  920 vafslpawktlpagdtyeldmvyylpisgpanysvningvdyafkfeqpdlpladlssgn 979
                                                                                                                                           19; Gaps
                                                                                                                                                              LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Periplasmic localisation signal peptide"
                                                                                                                       Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31..1046
/note= "Mature periplasmic chitodextrinase"
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keyhani NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding periplasmic chitodextrinase endoenzyme
                                                                                                                       DB 17;
                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                        Vibrio furnissii periplasmic chitodextrinase.
                                                                                                                      Score 75.5; DB
Pred. No. 17;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roseman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Columns 33-40; 37pp; English.
                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                           AAY52304 standard; Protein; 1046
                                                                                                                                                                                                                74
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                                                                                                                       10.7%;
30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0600452.
                                                                                                                                                                                                       53 NSPSGDGDVHIGPTEPEGLGDV
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                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                Query Match
Best Local Similarity 30.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitlaru E,
                                                                                                                                                                                                                                                                                                                                                                                                             recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-022280/02
                                                                                          1046 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio furnissii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ38240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bassler B,
                                                                                                                                                                                                                                                                                                AAY52304;
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                   AAY52304
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in contrast to other organisms, which only require two enzymes to degrade chitin to GLONAc. Endo-I is an endoenzyme, cleaving internal glycosidic bonds in soluble chitin-derived oligosaccharides to produce GLONAc dimers and/or trimers. Chitin oligosaccharides have been recently shown to be physiologically active and are useful in agriculture and medicine. Derivatised oligosaccharides are generated by Rhizoblum species as signals for the formation of nitrogen fixing nodules by leguminous plants and also induce disease resistance in certain plants. They also inhibit antimetastatic agent against Lewis lung carcinoma, and GloNAc polymers of varying lengths activate macrophages and the immune system. Prior art methods of production of such oligosaccharides are prohibitively methods of production of such oligosaccharides are prohibitively compounds. Use of recombinant V. furnissi chitin catabolic enzymes may help to reduce or eliminate these problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes immunogenic protein #17671
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Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 75.5; DB
Pred. No. 17;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%;
30.5%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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les 25; Conservative
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N-PSDB; AAS59578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1046 AA;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (Synovitis, acne, constitutosis, hypertosis and osteomypaltis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central criving system, however it is particularly involved in the inflammatory consence or absence of P. acnes in a patient comprises contacting a presence or absence of P. acnes in a patient comprises contacting a comple with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigons in the production of antibodies of specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and crivity of P. acnes polypeptides and diagnostic agents for determining P. acnes presence, for example, by contact in the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO XXX
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124 LGRI 127

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173 ldrv 176

Search completed: July 18, 2002, 14:15:01 Job time: 10331 sec

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Sequence 9,
Sequence 10
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Sequence 12
Sequence 12
Sequence 10
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Sequence 10
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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5-09-096-776B-9
5-08-984-618-10
5-08-386-727-2
5-08-600-452A-2
5-09-413-814-93
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5-08-857-076-114
5-09-012-710-12
5-09-556-273-12
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                                                                                                                                                                                                                                                                                                                                                              231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 MSFLVSEELSFRIPVELRYE.
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                   Sequence 7, 1
Sequence 2, 1
Sequence 41,
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Sequence 7
Sequence 7
Sequence 8
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                                                                                                                                                                                                                                                                                            APPLICANT: Kern, Scott E.
APPLICANT: Hahn, Stephan A.
TITLE OF INTENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,821
FILING DATE: 19-JAN-1996
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
RECISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/079001
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
COMPUTER ALICATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                           US-08-836-943-2
US-08-836-943-2
US-09-413-814-70
US-09-335-409-7
US-09-568-102-7
US-09-568-480-7
US-09-568-486-7
US-09-568-472-7
                                                                                                                                                        US-08-455-543A-41
3-09-500-358-3
3-09-498-809-3
3-08-984-618-9
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US-09-355-115-7
                                                                                                                                              US-09-082-059-2
                                                                                                                                                                                                            ALIGNMENTS
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Patent No. 5712097
                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 552 amino acids
amino acid
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Best Local Similarity 25.7
Matches 38; Conservative
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                    5 VSEELSFRIPV---
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 MEDIUM TYPE:
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US-09-460-145-4 US-08-827-208-3

68 67.5 67.5 67.5

Sequence Sequence Sequence

.08-448-164-6

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RESULT 4
US-08-701-582D-14
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STATE: CA
COUNTRY:
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28; Indels 66; Gaps
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                                                                                                                                                                             Sequence 2, Application US/08915214
Patent No. 5814457
GENERAL INFORMATION:
GENERAL INFORMATION:
TYLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
CORRESPONDENCES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: The PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,214
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-AN-1996
ATORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 93,347
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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25.7%; Pred. No. 0.27;
tive 16; Mismatches
                                                    87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                               87 F-----RAGTAPLVAFLDRIDKLVP 106
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Patent No. 5955292
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TELEFAX: 619/678-5099
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amino acid
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Best Local Similarity 25.7'
Matches 38; Conservative
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US-08-915-214-2
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-----VHIG---PTEPEGLGDVHIRLQVGADRAL 86
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GENERAL INFORMATION:
APPLICANT: Kern, Scott E.
APPLICANT: Hahn, Stephan A.
TITLECANT: Hahn, Stephan A.
TITLECANT: BOUGHOUS: 91
CORRESPONDENCE ADDRESS: 91
CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WRANN, Jeffrey
APPLICANT: ATISANO, Lilian
APPLICANT: SCHERER, Stephen W.
TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STRIE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                      ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38,347
SER: 07265/079001
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APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-7AN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A. 8,347
REGISTRATION NUMBER: 36EGISTRATION NUMBER: 07265/0790C
TELECHONINICATION INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 F-----RAGTAPLVAFLDRTDKLVP 106
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; Patent No. 6017755
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.7'
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-005-532-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                 USA
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APPLICANT: de Lencastre, Herminia
APPLICANT: TOMASZ, Alexander
TITLE OF INVENTION: AUXILLIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
                                304 VHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGE-----TFKVPSSCPI-----VTV 350
                                                                                                  191.YLYQSGKGHTIQEVRIVKGLNNP--DLDAAVGEDLAQQLRD-ELELVKGASNEFDKELFL 247
  -- ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------REL-LLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGA----DRALFR 88
                                                                              -----VHIG---PTEPEGLGDVHIRLQVGADRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600-1-213 CIP
                                                                                                                                                          ,87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                 408 FVQSYYLDREAGRAP ---- GDAVHKIYP 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,618
                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08984618 Patent No. 6251647 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07bul
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 529 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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Matches 41; Conservative
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
    5. VSEELSFRIPV-
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                                                                              50 DGLNSPSGDGD-
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US-08-984-618-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 81; DB 3; Length 552;
; Pred. No. 0.27;
16; Mismatches 28; Indels
                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CURRENT APPLICATION NUMBER: US/09/096,776B
CURRENT FILING DATE: 1998-06-12
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: REA, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 024916-004
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
                                                                                                               APPLICATION NUMBER: US/08/701,582D
FILING DATE: 22-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 FVQSYYLDREAGRAP----GDAVHKIYP 431
                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09096776B Patent No. 6270994
                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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APPLICANT: Miyazono, Kohei
APPLICANT: Kawabata, Masahiro
TITLE OF INVENTION: SMAG6 AND
                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.7%;
                                                                                                                                                                                                                                                                                                                                                       552 amino acids
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Best Local Similarity 25.7%
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VSEELSFRIPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-701-582D-14
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-096-776B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                amino acid
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LENGTH: 552
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APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
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Patent No. 6225064
GREEAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Indels
APPLICANT: CHITLARU, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHRIES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75.5; DB 2;
Pred. No. 2.7;
                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4125 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT TREORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07662/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1046 amino acids
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APPLICANT: Dougherty, Brian A
PAPLICANT: Goldberg, Steven L
APPLICANT: HOFIE, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
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Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-600-452A-2
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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STRANDEDNESS: si
                                                                                                                                                                                                                 USA
                                                                                                                                                                                                              COUNTRY: US
ZIP: 92037
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                                                                                                                                                                                                                       APPLICANT: KEYHANI, NEMAT O.
APPLICANT: CHTTLARU, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,727
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Pred. No. 2.7;
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89 AGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOBBS, ANN S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130/206916
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-861-3000
TELEFAX: 202-822-0944
TELEFAX: 201-822-0944
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                         248 AGEITPVFF---GTALGNFGVDHML---DGLVE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                               Sequence 2, Application US/08386727
Patent No. 5792647
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30.5%;
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BASSLER, BONNIE
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Best Local Similarity 30.59
Matches 25; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                           GENERAL INFORMATION:
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TOPOLOGY:
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APPLICANT: Bloecker, Helmut
APPLICANT: Cloo, Paul M
APPLICANT: Cloo, Paul M
APPLICANT: Cloo, Paul M
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mealler, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
                                                                                                                                                                                                                                                                                                                                                                      869 MQVLGRIESSLGIRTTLRTLFEHPTLAQLASHLSSGAASTSAAAATALERGLTRPDGPSS 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     875 MQVLGRIESSLGIRTTLRTLFEHPTLAQLASHLSSGAASTSAAAATALERGLTRPDGPSS 934
                                                                                                                                                                                                                                                                                                                           1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 3079;
                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHIG-PTEP----EGLGDVHIRLQVGADRALFRAG-TAPLVAFLD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VHIG-PTEP----EGLGDVHIRLQVGADRALFRAG-TAPLVAFLD 99
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                                                                                                                                                                                                                                         Score 73; DB Pred. No. 22; 7; Mismatches
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EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
LENGTH: 3072
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EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
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Pred. No. 2
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1S-08-348-353-17
Sequence 17, Application US/08348353
Patent No. 5932217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80, Application US/09413814
Patent No. 6225064
                                                                                                                                                   ; ORGANISM: Sorangium cellulosum US-09-413-814-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Sorangium cellulosum US-09-413-814-80
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.4%;
Matches 33; Conservative
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Best Local Similarity 31.4%;
Matches 33; Conservative
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                                                                                                                                 TYPE: PRT
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53 LALDGGAGVALQSAKASGTLHVQGGEHLDLGTLAAVGAVDVNGTGDVRVAKLVSDAGADL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TILLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 RAGTAPLVAFLDRTDKLVPLGQEH-TLGDF--DGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600-1-097CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08465965
Patent No. 5968512
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                    STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 LLLDG-----LNSPSGDGDVH-----
                                                                                    NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.2%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-348-353-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                   STATE: New Jersey COUNTRY: U.S.A. ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New Jersey COUNTRY: U.S.A. ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 29; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 LLLDG-----LNSPSGDGDVH------IGPTEPEGLGDVHIRLQVGADRALF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08465966
Patent No. 6015560
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 RAGTAPLVAFLDRTDKLVPLGQEH-TLGDF--DGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 72; DB
27.6%; Pred. No. 8.7;
tive 11; Mismatches
                                                                                      PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION 1424
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION ATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson, David
REGISTATION UNDBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEFAN: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 29; Conserva
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                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE:
US-08-465-965-17
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APPLICANT: Paradis, Suzanne
APPLICANT: Pissenbaum, Heidi
APPLICANT: Tissenbaum, Heidi
APPLICANT: Koweek, Allison
TITLE OF INVENTION: THERAPECTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351001
CURRENT APPLICATION NUMBER: US/08/857,076C
CURRENT FILLING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 RAGTAPLVAFLDRTDKLVPLGQEH-TLGDF--DGNLEDALGRILA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                     FILING DATE: 30.NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION NUMBER: 08/247,572
FILING DATE: 04-MAY-1992
CLASSIFICATION DATA: MAPLICATION DATA: PRIOR APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: JACKBOIN, DAVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 72;
27.6%; Pred. No. 8
FILING DATE: 06-JUN LOSSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
APPLICATION NUMBER: 08/348,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 114, Application US/08857076C
; Patent No. 6225120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 LLLDG-----LNSPSGDGDVH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1248 amino acids
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GENERAL INFORMATION:
APPLICANT: Kimura, Koutarou
APPLICANT: Patterson, Garth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 27.69
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-966-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-08-857-076-114
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LENGTH: 212
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                                                                                                                                                                                                        51 IERARLHIGKGVQLECKGEGDVWVRCL--SDHAVFVQSYYLDREAGRAP----GDAVHKI 104
                                                 Gaps
                                                                                                                    |: :||: || || || 5 EMDVQVGE-----TFKVPSSCPI------VTVDGYVDPSG-GDRFCLGQLSNVHRTEA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EELSFRIPV-ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLD-GLNSPSGDGDVHIG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Vinkemeier, Uwe
APPLICANT: Wasneil. Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Wasneil, Jr., James E.
APPLICANT: Wasneil, Jr., James E.
APPLICANT: Wasneil, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
WUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
Ouery Match 10.2%; Score 71.5; DB 4; Length 212; Best Local Similarity 27.0%; Pred. No. 0.98; Matches 33; Conservative 13; Mismatches 25; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.1%; Score 71; DB 3; Length 837;
Best Local Similarity 28.2%; Pred. No. 6.7;
Matches 37; Conservative 18; Mismatches 54; Indels
                                                                                        16 ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNET/AGENT INFORMATION:
NAME: Jackson Esq., David A.
RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-012-710-12; Sequence 12, Application US/09012710; Patent No. 6087478; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 837 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hackensack
: New Jersey
RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New COUNTRY: US ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                        105 VP 106
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Search completed: July 18, 2002, 14:16:06 Job time: 9696 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2002, 11:38:30 ; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec Run on:

Perfect score:

US-09-749-185-3 704 1 MSFLVSEELSFRIPVELRYE......FDGNLEDALGRILAEEQNAG 135 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 3: :

SUMMARIES

Description	probable regulator			probable regulator	type II secretion	hypothetical prote	carbonate dehydrat	2-keto-3-deoxygluc	probable transcrip	conserved hypothet	carbonate dehydrat	endoglucanase C (E	peptide chain rele	translation releas	peptide chain rele	v-type ATP synthas	carbonate dehydrat	hypothetical prote	endopeptidase La (receptor-like prot	endopeptidase La (penicillin-binding	penicillin binding	probable ClpA/B-ty	chitinase (EC 3.2.	conserved hypothet	hypothetical prote	probable alcohol d	hexokinase (EC 2.7
QI	T37179	T36147	T35247	T35319	E84182	T19428	A22612	A69648	S71811	AD3237	152551	S15271	E91295	159305	G86136	D75487	A43641	T35718	A70322	T45690	A36895			G83635	_		_	^	S68694
% Query Match Length DB	•	142 2	•	142 2	•	•	259 2	324 2	552 2	408 2	260 2	1101 2	529 2	529 2	529 2	690 2	•	•	795 1	•		•	•			760 2	•	346 1	484 2
% Query Match I	77.6	31.1	27.0	19.9	12.0	٠	•	11.5	11.5		11.2	11.2	11.1	11.1	11.1	11.1	11.0	11.0	10.9	10.9	10.9	10.9	10.9	10.7	10.7	10.7	10.4	10.4	10.4
Score	546	219	190	140	84.5	84	83.5	81	81	79.5	78.5	78.5	78	78	78	78	77.5	77.5	77	77	77	76.5	76.5	75.5	75.5	75	73.5	ω.	m.
Result No.	-	7	33	4	Ŋ	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	. 26	27	28	53

translation releas probable acetylorn	hypothetical cytos peptide chain rele	probable 9-cis-epo tRNA-intron endonu	2-oxoacidferredo endopeptidase La-l	peroxisome biogene probable ATP-depen	filamentous hemagg aminonucleoside an	Clp ATPase [import CDA peptide synthe	hypothetical prote DNA-Binding Protei
D75381 D95388	AE3254 AD1072	A86425 T44993	G69170 T01765	S71090 G70951	S21010 S68981	AE0358 T36180	H70678 I57557
77	77	~ ~		0 0	7	~ ~	0.0
538	389	589 339	512 1096	980 1101	3591 558	891	291
10.4 10.4	10.4	10.4	10.3	10.2	10.2	10.2	10.1
	73						
30 31.	335	3.4 3.5	36 37	38 36	40 41	4 4 2 8	44

ALIGNMENTS

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C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T3/179
R; Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A; Reference number: 22159
A; Accession: T37179
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-136 CSEE>
A; Cross references: EMBL; AL096823; PIDN: CAB46964.1; GSPDB:GN00070; SCOEDB:SCO11.09
A; Experimental source: strain A3(2)
C; Genetics:
A; Genetics:
probable regulator - Streptomyces coelicolor
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Gaps ; Length 136; Indels Ouery Match 77.6%; Score 546; DB 2; L. Best Local Similarity 77.8%; Pred. No. 6.3e-47; Matches 105; Conservative 12; Mismatches 18;

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2 MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGD 61 1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60 ô g

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EDALGRILAEEQNAG 135 121 δ

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probable regulator - Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C; Accession: T3647
R; Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A; Reference number: 221598
A; Reference number: 221598
A; Accession: T36147
A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-142 <SEE>

A;Cross-references: EMBL:AL096852; PIDN:CAB51005.1; GSPDB:GN00070; SCOEDB:SCE19A.24 A;Experimental source: strain A3(2) C;Genetics:

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Similarity 26.6
                                                                                                                                                                                                                                                         122 DALGRILAE 130
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Best Local S
Matches 41
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    C; Genetics
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                                                                                                                                                                                                                                                                                                                                           probable regulator - Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C; Accession: T35247
R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
aubmitted to the EMBL Data Library, April 1999
A; Reference number: 221573
A; Accession: T35247
A; Steulminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAB40672.1; GSPDB:GN00070; SCOEDB:SC5F2A.05c
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A;Residues: 1-142 <OLI>
A;Cross-references: EMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
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                                                                                                                                                                               VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHT-LGDFDGN 119
                                                                                                                                                                                                -----SGELRRF 107
                                                                                           Gaps
                                                                                                                      1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
                                                                                                                                     36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 LLDGLNSPSGDGDVHIGP-----TEPEGLGDVHIRLQVGADRALFRAGTAPLVAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSFLVSEELSFR------IPVELRYEVGDPYAIRMTFHLPG---DAPVTWAFGREL 47
                                                                                           .
9
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C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                           Length 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                           31.1%; Score 219; DB 2; 37.7%; Pred. No. 1.6e-14; live 22; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.0%; Score 190; DB 2; ilarity 31.3%; Pred. No. 1.1e-11; Conservative 19; Mismatches 46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|||:| || | : : : LQAAGELVPVGLEHLQLDLDHDLAELM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 LDRTDKLVPLGQEHTLGDFDGNLEDAL 124
                                                         Query Match
Best Local Similarity 37.7%
Matches 49; Conservative
                                                                                                                                                                                                                                         120 LEDALGRILA 129
                                                                                                                                                                                                                                                          ::| | :||
132 IDDGLAELLA 141
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Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C24H11.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19428
R;Lloyd, C.
                                                                                                                                                                                                                                                                                    63 IGPTEPEGLGDVHIRLQVGADRA---LFRAGTAPLV-------AFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 GLGDVHIRLQVGAD-----RALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 FDVPVRIYRTPGDDADAFTTTYAVREPDRLPGDDARIAACKDRIWTNGVATGDSDAGDDH 243
                                                                                                                             Gaps
                                                                                                                                                                                                   12 RIPV--ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 FRIPVELRYEVGD------PYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGD-GDVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein [imported] - Halobacterium sp. NRC-1 sp. NRC-1
                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 548;
                                                                                   Length 142;
                                                                                Query Match 19.9%; Score 140; DB 2; Length 142
Best Local Similarity 31.0%; Pred. No. 1e-06;
Matches 40; Conservative 20; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted to the EMBL Data Library, November 1996 A; Reference number: 219123 A; Accession: T19428 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 84.5; DE 26.6%; Pred. No. 1.7; iive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 .LGQEHT------LGDF-----DGNLED 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 VGDDHVADLAYYVVRDLVGDAELTIPIRDPNLED 322
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A, Atutora: Yoshikawa, H.; Danchin, A.
A, Attutors: Yoshikawa, H.; Danchin, A.
A, Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Reference number: A69580; MUID:98044033
A, Accession: A69548
A, Status type: Dan
A; Molecule type: DnA
A; Residues: 1.324 < KUN>
A; Residues: 1.324 < KUN>
A; Residues: 1.324 < KUN>
A; Cross-references: GB:299115; GB:AL009126; NID:92634478; PIDN:CAB14128.1; PID:926346
A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein Atu6078 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the TGF-beta
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Sylear

Sylear

Sylear tenance names: tumor supressor DPC4

C, Specials: Homo sapiens (man)

C, Specials: Homo sapiens (man)

C, Specials: Homo sapiens

C, Accession: S71811

R; Zhang, Y; Feng, X.H.; Wu, R.Y.; Derynck, R.

Nature 383, 168-172, 1996

A; Title: Receptor associated Mad homologues synergize as effectors of the TGF-be

A; Reference number: S71811

A; Status: not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-552 czMA>

C; Superfamily: human transcription regulator MAD-4

C; Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 ADWFFPGIAEGELLTGEKTPEGIADYYLKKGASFVAIKLGKEGAYFKTGTSE--GFLEGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --VHIG---PTEPEGLGDVHIRLQVGADRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DGDVHIGPTEPEGLGDVHIR-----LQVGADRALFRAGTAPLVAFLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 IPVELRYEVGDPYAIRMTFHL-------PGDAPVTWAFGRELLLDGLNSPSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 81; DB 22.8%; Pred. No. 2; iive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 RVDRVV----DTVGAGDGFAVGVISGIL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-----RAGTAPLVAFLDRTDKLVP 106
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                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: kdgK
C;Superfamily: ribokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 38; Conserv
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CiSpecies: Bacil
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                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                               A;Cross-references: EMBL:Z81475; PIDN:CAB03913.1; GSPDB:GN00021; CESP:C24H11.6
A;Experimental source: clone C24H11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbonate dehydratase (EC 4.2.1.1) III - horse
N'Alternate names: carbonate dehydratase III
C;Species: Equus caballus (domestic horse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 25-Apr-1997
C;Accession: A22612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GDP----VTSHLLPSGRVPIGHVF----LRGDNGPVSTDSRHFGPV-PEALVQIRLSLR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 PYRLRO-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTYGGALKQPDG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDPYAIRMTFHL--PGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP-----TEPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-259 <WEN>
Cs. Superfamily: carbonic anhydrase homology .
Cs. Superfamily: carbonic dehydratase; carbonic anhydrase homology .
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; zinc
F;4-258/Domain: carbonic anhydrase homology <CAH>
F;1/Modified site: acetylated amino end (Ala) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 VGADRALFRAGTAPLVAFLDRTDKLVPLGQEHT ----LGDFDGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                                                                                            Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Wendorff, K.M.; Nishita, T.; Jabusch, J.R.; Deutsch, H.F.
J. Biol. Chem. 260, 6129-6132, 1985
A;Title: The sequence of equine muscle carbonic anhydrase.
A;Reference number: A22612; MUID:85207593
                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
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                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 84; DB 2; 28.7%; Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 83.5; ilarity 27.1%; Pred. No. 0.8 Conservative 16; Mismatches
                                                                                                                                                                                 A;Gene: CESP:C24H11.6
A;Map position: 3
A;Introns: 25/1; 56/3; 126/1; 194/3
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-259 <WEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                              A; Residues: 1-261 <WIL>
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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A; Title: Identification of an abundant S-thiolated rat liver protein as carbonic anhy A; Reference number: $13896; MUD: 91112820
A; Accession: $13896
A; Status: preliminary
A; Molecule type: protein
A; Residues: 25, X', 27-34, 38, 'T', 40-42, 'XX', 45-46, 'S', 48-51, 'X', 53-56, 'RVV', 74, 'XXTFX'
C; Superfamily: carbonate dehydratase; carbonic anhydrase homology
C; Reywords: blocked amino end; carbon-oxygen lyase; hydro-lyase
F; 5-259/Domain: carbonic anhydrase homology <CAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
E91295
E91295
C) Species: Bscherichia coli (strain 0157:H7, subs C; Species: Escherichia coli (strain 0157:H7, subs C; Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Nucleotide sequence of the endoglucanase C gene (cenC) of Cellulomonas fimi, A;Reference number: S15271; MUID:92065819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1101 CCOUD
A; Cross-references: EMBL:X57858; NID:948847; PIDN:CAA40993.1; PID:9580980
A; Note: the authors translated the codon GAC for residues 361, 380, 400, 550, 670, e
R; Moser, B.; Gilkes, N.R.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Appl. Environ. Microbiol. 55, 2480-2487, 1989
A; Fitle: Purification and characterization of endoglucanase C of Cellulomonas fimi,
A; Reference number: A43636; MUID:90103465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endoglucanase C (EC 3.2.1.-) - Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 01-Dec-2000
C;Accession: 515271; A43636
R;Coutinho, J.B.; Moser, B.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Mol. Microbiol. 5, 1221-1233, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTSEEALKQPDG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 RMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQV----GAD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M29707; NID:g144417; PIDN:AAA23087.1; PID:g144420 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 RALFRAGTAPLVAFLDRTDKLVPLGQEHTL------GDFDGNLEDALGRILAEE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                     Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 LGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP----
                                                                                                                                                                                                                                                                                                                                                                                     11.2%; Score 78.5; DB 2; 27.1%; Pred. No. 2.6; tive 14; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Local Similarity 27.4%; Pred. No. 15;
Nes 32; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Start codon: GTG
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <WOS>
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A43636
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A; Status: Unidance Life Life Composition of CDNA Clones for muscle carbonic annydrase III.
A; Accession: 15251
A; MUID:89166882
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-260 <RES>
A; Cross-references: GB:M22413; NID:9203224; PIDN:AAA40846.1; PID:9203225
A; Cross-references: GB:M22413; NID:9203224; PIDN:AAA40846.1; PID:9203225
B; Lynch, C.J.; Brennan, W.A.J.; Vary, T.C.; Carter, N.; Dodgson, S.J.
Am. J. Physiol. 264, E621-E630, 1993
A; Title: Carbonic anhydrase III in obese Zucker rats.
A; Reference number: A48856; MUID:93236031
A; Reference number: A48856
A; Molecule type: protein
A; Residues: 19-45; L20-128, XFG', 132-142 <LXN>
A; Roperimental source: Zucker, adipocytes
A; Note: sequence extracted from NCBI backbone (NCBIP:129636, NCBIP:129637)
A; Note: sequence extracted from NCBI backbone (NCBIP:129636, NCBIP:129637)
A; Note: sequence extracted from NCBI backbone (NCBIP:129636, NCBIP:129637)
A; Title: Analyses of polypeptides in the liver of a novel mutant (LEC rats) to hereditar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein

A; Mesidues: 19-28, X', 30-33 < NAG>
A; Residues: 19-28, Z', 30-33 < NAG>
A; Experimental source: Long-Evans Cinnamon

B; Chai, Y. C.; Jung, C. H.; Lii, C. K.; Ashraf, S. S.; Hendrich, S.; Wolf, B.; Sies, H.; Thd

Arch. Blochem. Blophys. 284, 270-278, 1991
                                   R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell: Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                          ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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N;Alternate names: carbonic anhydrase III
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Nug-1996 #sequence_revision 12-Nug-1996 #text_change 11-May-2000
C;Accession: I52551; A48856; B61530; S13896
R;Kelly, C.D.; Carter, N.D.; Jeffery, S.; Edwards, Y.H.
Biosci. Rep. 8, 401-406, 1988
A;Title: Characterization of CDNA clones for rat muscle carbonic anhydrase III.
                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-408 <KUR
A;Cross-references: GB:AE008690; PIDN:AAL46314.1; PID:g17744099; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 PSG-----DGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 QIEHDQRYRLADEFVNALKALWRSDEPVTFSGKSPWRIKEGFITPKPRFGRPLISATGS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79.5; D
Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 RIPVELRYEVGDPYAIRMTFHLPGDAPVTWA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 QEHTLGDFDGNLEDALGRILA--EEQNAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 PIIVCRDTDQEAQEYYGAIVAAVEQRNVG 315
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A; Reference number: A61530; MUID:92070082
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24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.3%
Best Local Similarity 24.8%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
       C; Accession: AD3237
                                                                                                                                                                                                                                                                                                                     A; Accession: AD3237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: Atu6078
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A;Status: .nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-529 < RLAT>
A;Cross-references: GB:AE000508; GB:U00096; NID:Q2367382; PIDN:AAC77328.1; PID:g17908
A;Experimental source: strain K-12, substrain MG1655
A;Grentzmann, G; Brechemier-Baey, D; Heurque, V; Mora, L; Buckingham, R.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5848-5852, 1994
A;Title: Localization and characterization of the gene encoding release factor RF3 in
A;Reference number: IS9306; MUID:94286535
A;Reference number: IS9306
A;Reference number: IS9306
A;Reference number: LOS306
A;Reference number: LOS306
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-314, L'.316-529 < RE2>
A;Cross-references: EMBL:226313; NID:q435273; PIDN:CAA81223.1; PID:g435274
A;Genetics:
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: translation elongation factor Tu homology
C;Superfamily: translation elongation factor Tu homology
C;Superfamily: translation elongation factor Tu homology
C;Tequetics:
C;Superfamily: translation elongation factor Tu homology
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C;Superfamily: translation elongation factor Tu homology
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Atture 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G86136
peptide chain release factor RF-3 [imported] - Escherichia coli (strain 0157:H7, subs
C.Species: Escherichia coli
C.Species: Lereb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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Matches 41; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-529 <STO>
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-529 <RES>
A; Cross-references: GB:D1724; NID:g409376; PIDN:BAA04578.1; PID:g409377
B; Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A; Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A; Reference number: S56314; MUID:95334362
A; Accession: S56599
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Mortensen, R.K.; Hansen, H.F.; Grentzmann, G.; Buckingham, R.H.; Sperling-Petersen, H. Eur. J. Biochem. 234, 732-736, 1995
A;Title: Osmo-expression and fast two-step purification of Escherichia coli translation A;Reference number: S63518; MUID:96163454
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N.Alternate names: peptide chain release factor 3; translation termination factor RF-3
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: 159305; S56599; S63518; F65525; 159306; $33336
R;Mikuni, O.; Ito, K.; Moffat, J.; Matsumura, K.; McCaughan, K.; Nobukuni, T.; Tate, W. Proc. Natl. Acad. Sci. U.S.A. 91, 5798-5802, 1994
A;Title: Identification of the prfC gene, which encodes peptide-chain-release factor 3 and A;Reference number: 159305; MUD:94286525
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A; Residues: 2-19 <MOR>
A; Residues: 2-19 <MOR>
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: F65252
                                               R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DAN Res. 8, 11-22, 2001

A; Rtle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Status: preliminary
A; Molecule type: DNA
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A; Residues: 1-529 <HAY>
A; Cross-teferences: GB:BA000007; PIDN:BAB38756.1; PID:g13364811; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: ECS5333
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Pred. No. 7.1;
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A; Residues: 1-529 <BUR>
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01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
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Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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vibrio furn
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salmonella
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Q99kq9
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P14141
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P1
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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CYF_PHOLA
ENDA_HALVO
GSHB_SYNP7
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SMA4_PIG
SMA4_RAT
CAH3_RAT
GUNC_CELFI
VATI_DEIRA
CAH3_MOUSE
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HXK1_SCHPO
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STA6_MOUSE
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Maximum Match 100%
Listing first 45 summaries
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KDGK_BACSU
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DMWD_MOUSE
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                                                                    - protein search, using sw model
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1 MSFLVSEELSFRIPVELRYE.
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seq length: 200000000
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Match 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Akuell P., Lewis S., Matsuo Y., Nikaido I., Ring B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lowns P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw Bashi H., Rohtsuki S., Marshizaki Y., Rawaji H., Kohtsuki S., Masaki Y., Rawashi Z., Kawaji H., Kohtsuki S., Masaki Y., Kawashi Zaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYCOKING GTOWTH FACTOR REV. 11:49-58(2000).

-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA (TRANSPORTHING GROWTH FACTOR) SUPERFAMILY; SWAD4 IS THE COMMON AND (CO-SMAD) (BY SIMILARITY). REQUIRED FOR GASTRULATION. MAY ACT. AS A TUMOR SUPPRESSOR.

-!- SUBBUNT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).

-!- SUBCELLULAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND; MIGRATION. TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=A/J; IISSUE-Lung;
MEDLINE=97311184; PubMed=9166592;
Anna C.H., Devereux T.R.;
Anna C.H., Devereux T.R.;
"Sequence and chromosomal mapping of the mouse homolog (Madh4) of the
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against DPP homolog 4) (Deletion target in pancreatic carcinoma 4 homolog)
                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weinstein M., Yang X., Deng C.-X.;
"Functions of mammalian Smad genes as revealed by targeted gene
disruption in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: BELONGS TO THE DWARFIN/SMAD FAMILY.
-!- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
-!- SIMILARITY: CONTAINS 1 DWB/MH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20175825; PubMed-10708952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mamm. Genome 8:443-444(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 67-551 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human DPC4/MADH4 gene.
                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                MADH4 OR DPC4.
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EMBL; U79748; AAB57905.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the Bacillus subtilis chromosome region between the serA and Kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).

-!- CATALYTIC ACTIVITY: ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + beta-L-arabinose I-phosphate.
-!- PATHMAY: PECTIN DEGRADATION.
-!- BATHMAY: PECTIN DEGRADATION.
-!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 DGLNSPSGDGD-------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34; Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) (2-keto-3-deoxygluconokinase) (3-deoxy-2-0XO-D-gluconate kinase) (KDG kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                          :99
                                                                                                                                                                                                                                                                                                                  11.6%; Score 82; DB 1; Length 551; 26.4%; Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                       S -> A (IN REF. 2).
R -> P (IN REF. 2).
0835EF88D9C1C980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA.
                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                               Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                         POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVOSYYLDREAGRAP----GDAVHKIYP 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-168 / MARBURG;
MEDLINE-96349105; Pubmed-8760912;
           MGD; MGI:894293; Madh4.
InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin_A.
                                                                                                                                                                                                                                                            60417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L47838; AAB38479.1; -. EMBL; 299115; CAB14128.1; -.
                                                                    Pfam; PF00968; Dwarfin; 1.
                                                                                                                               Transcription regulation;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 26.49
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                      SMART; SM00523; DWA; 1
SMART; SM00524; DWB; 1
                                                                                                                                                                                 320
450
257
292
551 AA;
1DD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDGK_BACSU
P50845;
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                                                                                                                                                                                 DOMAIN
DOMAIN
CONFLICT
                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                DOMAIN
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
KDGK_BACSU
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Dev. 11:3157-3167(1997).
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                                                                                                                                                                                                                                                                                                                                                        Massague J.
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  Genes
  8
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                                                                                                                                                                                            137 IPPALSAEMKD----FTYHVMNDMRNAGKTISFDPNVRPSLWP-DQATMVHTINDLAGL 190
                                                                                                                  Gaps
                                                                                                                                      13 IPVELRYEVGDPYAIRMTFHL------PGDAPVTWAFGRELLLDGLNSPSG- 57
                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against DPP homolog 4) (Caletion target in pancreatic carcinoma 4) (hSMAD4).
MADH4 OR SMAD4 OR DPC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97253203; PubMed-9098646;
Moskaluk C.A., Hruban R.H., Schutte M., Lietman A.S., Smyrk T.,
Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fetal brain;
MEDLINE=96144684; PubMed=8553070;
MADLINE=96144684; PubMed=8553070;
MADLINE=96144684; PubMed=8553070;
Ada Costa L.T., Rozenblum E., Weinstein C.L., Fischer A., Yeo C.J.,
Hruban R.H., Kern S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98051189; PubMed-9389648;
Liu F., Pouponnot C., Massague J.;
"Dual role of the Smad4/DPC4 tumor suppressor in TGFbeta-inducible
transcriptional complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequencing of DPC4 in the analysis of familial pancreatic
                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DPC4, a candidate tumor suppressor gene at human chromosome
                                                                                              Length 324;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                  Indels
                                                              6345AAD7AEDA0759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT CARCINOMA HIS-493.
                                                                                                                 43;
                                                                                             DB 1;
                                                                                            Score 81; DB 1;
Pred. No. 0.64;
5; Mismatches
        InterPro; IPR002173; PĒKB.
Pfam: PF00294; pĒKB.1.
PROSITE: PS00583; PFKB_KINASES_1; FALSE_NEG.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                 552 AA
                                                   Transferase; Kinase; Complete proteome.
SEQUENCE 324 AA; 35035 MW; 6345AAD7
                                                                                                                                                                                                                                    249 RVDRVV----DIVGAGDGFAVGVISGIL 272
                                                                                                                                                                                                                        RTDKLVPLGQEHTLGDFDGNLEDALGRIL 128
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagn. Mol. Pathol. 6:85-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
MEDLINE=96371046; PubMed=8774881;
                                                                                                                26;
                                                                                            11.5%;
22.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 383:168-172(1996).
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                        Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta response
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Q13485;
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                 MEDINE-20102728; PubMed-10636916; de Caestecker M.P., Yahata T., Wang D., Parks W.T., Huang S., Hill C.S., Shioda T., Roberts A.B., Lechleider R.J.; "The Smad4 activation domain (SAD) is a proline-rich, p300-dependent transcriptional activation domain."; J. Biol. Chem. 275:2115-2122(2000).
                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 285-552.
MEDLINE-20113477; PubMed-10647180;
Oin B., Lam S.S., Lin K.;
"Crystal structure of a transcriptionally active Smad4 fragment.";
Structure 7:1493-1503(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The L3 loop and C-terminal phosphorylation jointly define Smad
                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 319-543.
MEDLINE-97351157; Pubmed-9214508;
Shi Y., Hata A., Lo R.S., Massague J., Pavletich N.P.;
"A structural basis for mutational inactivation of the tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verschueren K., Huylebroeck D.; "Remarkable versatility of Smad proteins in the nucleus of transforming growth factor-beta activated cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tokine Growth Factor Rev. 10:187-199(1999)
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Chacko B.M., Qin B., Correia J.J., Lam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Annu. Rev. Biochem. 67:753-791(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein trimerization.";
Nat. Struct. Biol. 8:248-253(2001)
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SAD DOMAIN
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Wrana J.L., Attisano L.;
"The Smad pathway.";
                                                                                                                                                                                                                                                                                                                                 suppressor Smad4.";
Nature 388:87-93(1997).
CHARACTERIZATION OF
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Rattus norvegicus (Rat).
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552 AA;
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                                                                                                  SIMILARITY).
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070437;
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      Usage by and for commercial
                      (See http://www.isb-sib.ch/announce/
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09GKO9;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence with a 
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA
(TRANSFORMING GROWTH FACTOR) SUPERFAMILY; SMAD4 IS THE COMMON
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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POLY-ALA.
POLY-ALA.
POLY-ALA.
/FIId-VA[IN PANCREATIC CARCINOMA).
/FIId-VAR.011380.
MW: 7EE3C4647712DA90 CRC64;
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SMART; SM00523; DWA; 1.
SWART; SM00524; DWB; 1.
Transcription regulation; Phosphorylation; Multigene family;
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modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@lsb-sib.ch).
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                                                                        EMBL, AF045447, AAC03051.1; --
EMBL, AF045438; AAC03051.1; JOINED.
EMBL, AF045449; AAC03051.1; JOINED.
EMBL, AF045441, AAC03051.1; JOINED.
EMBL, AF045441, AAC03051.1; JOINED.
EMBL, AF045441, AAC03051.1; JOINED.
EMBL, AF045444; AAC03051.1; JOINED.
EMBL, AF045445; AAC03051.1; JOINED.
EMBL, AF045445; AAC03051.1; JOINED.
EMBL, AF045445; AAC03051.1; JOINED.
EMBL, AF045446; AAC03051.1; JOINED.
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InterPro; IPR003619; Dwarfin_A.
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1YGS; 08-NOV-98.
1DD1; 24-NOV-99.
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MIM; 600993; -.
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Matches 38; Conserv
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Miyakita A., Okuno S., Watanabe T.K., Oga K., Tsuji A., Hishigaki H.,
Suto T., Nakagawa K., Nakahara Y., Higashi K.;
"Molecular cloning of rat Smad4 gene.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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SUBUNIT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SWAD (R-SMAD).
INTERACTS WITH C-SKI, MSGI AND ATF2 (BY SIMILARITY).
SUBGELLULAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against
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                                                                                                                                   MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 81; DB 1; Length 552; 25.7%; Pred. No. 1.2; ive 16; Mismatches 28; Indels
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SMART; SM0523; DWA; 1.
SMART; SM00524; DWB; I.
SMART; SM00524 bWB; I.
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MEDLINE-20134216; PubMed-10670756;
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SEQUENCE FROM N.A.
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INIT_MET
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                           and Smad4 and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osaki M., Tsukazaki T., Ono N., Yonekura A., Hirota Y., Miyazaki Y., Shindo H., Sonta S., Yamashita S.; "cobha clohing and chromosomal mapping of rat Smad2 and Smad4 and the expression in cultured rat articular chondrocytes."; Endocr. J. 46:655-701(1999).
-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA (TRANSPORMING GROWTH FACTOR) SUPERFAMILY; SMAD4 IS THE COMMON
                                                                               SMAD (CO-SMAD) (BY SIMILARITY).

-!- SUBUNIT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).

INTERACTS WITH C-SKI, MSGI AND AFF2 (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND;

MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
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01-JAN-1990 (Rel. 13, Created)
15-JUL-1999 (Rel. 38, Last aquence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
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25.7%; Pred. No. 1.2;
ive 16; Mismatches 28; Indels
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7AE0540AB4DF0E77 CRC64;
                                                                                                                                         SIMILARITY).
SIMILARITY: BELONGS TO THE DWARFIN/SWAD FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                             ranscription regulation; Multigene family.
                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE UMAREIN SHAFE.
-!- SIMILARITY: CONTAINS 1 DWA/M11 DOMAIN.
-!- SIMILARITY: CONTAINS 1 DWB/M42 DOMAIN.
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InterPro; IPR003619; Dwarfin_A.
Pfam; PF00968; Dwarfin; 1.
SMART; SM00523; DWA; 1.
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                                                                                                                                                                                                                                                                                                            EMBL; AF056002; AAC12781.1; -. HSSP; Q13485; 1DD1.
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Best Local Similarity 25.7%
Matches 38; Conservative
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552 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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CAH3_RAT
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTFGEALKQPDG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP-----TEPEG 70
                                                                                                                                                                  Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A.; "cbNa sequence of rat liver carbonic anhydrase III."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                    Edwards Y.H.;
rat muscle carbonic anhydrase
                                                                                                                                                                                                                                                                     DB 1; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
A -> G (IN REF. 1).
FG -> SE (IN REF. 1).
KL -> NV (IN REF. 1).
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27.1%; Pred. No. 0.87;
ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF037072; AAB92558.1; --
EMBL, AB030829; BAB08111.1; --
HSSP; P00918; 1CIM.
InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
ProDom; P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
                    Kelly C.D., Carter N.D., Jeffery S., "Characterisation of cDNA clones for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
MEDLINE-89166882; PubMed-2852973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUNC_CELFI STANDARD; IP14090; OI-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29300 MW;
                                                                                   Biosci. Rep. 8:401-406(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22413; AAA40846.1; -.
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Best Local Similarity 2/...,
Local Similarity 2/...,
Local Similarity 2/...,
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223
259 AA;
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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95
118
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Mikuni O., Ito K., Mofatt J., Matsumura K., McCaughan K., Nobukuni T., Tate W., Nakamura Y.; "Identification of the prfc gene, which encodes peptide-chain-release factor 3 of Escherichia coli:";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 RALFRAGTAPLVAFLDRTDKLVPLGQEHTL------GDFDGNLEDALGRILAEE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 RTAFEQGSAPLTG-----EPATREYAFTSNLTFPPDGDAPGQVAFHLGKAGAYE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-KI2 / W3110;
MEDLINE-94286535; PubMed-8016077;
Grentzmann G., Brechemier-Baey D., Heurgue V., Mora L.,
Buckingham R.H.;
"Localization and characterization of the gene encoding release
                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; FALSE_NEG.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat;
Immunoglobulin domain; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELLULOSE-BINDING 1. CELLULOSE-BINDING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pepride chain release factor 3 (RF-3).
PRFC OR TOS OR MIAD OR B4375 OR 25976 OR ECS5333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 91:5798-5802(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLULOSE-BINDING 2
CATALYTIC
IG-LIKE DOMAIN 1.
IG-LIKE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDOGLUCANASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.2%; Score 78.5; Di 27.4%; Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.
                                                                                 InterPro; IPR003305; CBD_6.
InterPro; IPR001701; Glyco_hydro_9.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR004197; celD_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                   Pfam; PF02977; celD_N; 1.
Pfam; PF000759; Glyco_hydro_9; 1.
Pfam; PF00047; 19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115216 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1101
173
318
880
1006
PIR; S15271; S15271.
PDB; 1ULO; 01-APR-97.
PDB; 1ULP; 01-APR-97.
                                                                                                                                                                                                                                 Pfam; PF02018; CBD_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                      SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local Simi
Matches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RF3_ECOLI
P33998;
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ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 1-64 FROM N.A., AND SEQUENCE OF 625-641.
MEDLINE-90103465; PubMed-2604391;
MSDLINE-90103465; R. Kilburn D.G., Warren R.A.J., Miller R.C. Jr.;
MOSER B., Glikes N.R., Kilburn D.G., Warren C.A.J., Miller R.C. Jr.;
"Purification and characterization of endoglucanase C of Cellulomonas
"Purification and characterization of endoglucanase C of Cellulomonas
fini, cloning of the gene, and analysis of in vivo transcripts of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coutinho J.B., Gilkes N.R., Warren R.A.J., Kilburn D.G., Miller R.C. Jr.; "The binding of Cellulomonas fimi endoglucanase C (CenC) to cellulose and Sephadex is mediated by the N-terminal repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linkages in cellulose.
SIMILARITY: BELONGS TO CELLULASE FAMILY E (FAMILY 9 OF GLYCOSYL HYDROLASES).
SIMILARITY: CONTAINS 2 CELLULOSE-BINDING DOMAIN (CBD) REMOTELY RELATED TO BACTERIAL-TYPE CBD'S.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE DOMAINS.
                              16-OCT-2001 (Rel. 40, Last annotation update)
Endoglucanase C precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase C)
                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97035265; PubMed-8880921; Bateman A., Eddy S.R., Chothia C.; Members of the immunoglobulin superfamily in bacteria."; Protein Sci. 5:1939-1942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl. Environ. Microbiol. 55:2480-2487(1989).
[3]
CELLULOSE-BINDING DOMAINS.
      Last sequence update)
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 33-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. Microbiol. 6:1243-1252(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X57858; CAA40993.1; -.
EMBL; M29707; AAA23087.1; ALT_TERM.
EMBL; M29708; AAA23088.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
IDENTIFICATION OF IG-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 484;
MEDLINE=92065819; Pubmed=1956299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1375311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
STRUCTURE BY NMR OF 33-184
   01-MAR-1992 (Rel. 21,
                                                                                                                                                Cellulomonas fimi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92269585;
                                                                                                                                                                                                                                    NCBI_TaxID=1708;
                                                                                          (Cellulase C).
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5

Gaps

25;

45;

DB 1; Length 1101; Indels

1FBAD189CC5F8B5D CRC64;

us-09-749-185-3.rsp

EMBL; AP002569; BAB38756.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLIRE-21156231; PubMed-11258796; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tobe T., Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stop signals.";
J. Biol. Chem. 270:10595-10600(1995).
-!- FUNCTION: INCREASES THE FORMATION OF RIBOSOMAL TERMINATION
COMPLEXES AND STIMULATES ACTIVITIES OF RF-1 AND RF-2. IT BINDS
GUANINE NUCLEOTIDES AND HAS STRONG PREFERENCE FOR UGA STOP CODONS.
IT MAY INTERACT DIRECTLY WITH THE RIBOSOME. THE STIMULATION OF RF-1 AND RF-2 IS SIGNIFICANTLY REDUCED BY GTP AND GDP, BUT NOT BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Osmo-expression and fast two-step purification of Escherichia coli
translation termination factor RF-3.";
Eur. J. Biochem. 234:732-736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21074935; PubMed=11206551;
Berna N.T., Plunkett G. III. Butland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                               "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mortensen K.K., Hansen H.F., Grentzmann G., Buckingham R.H., Sperling-Petersen H.U.;
                                                                                                               SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                   Proc. Natl. Acad. Sci. U.S.A. 91:5848-5852(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95256223; PubMed=7737996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96163454; PubMed=8575429;
factor RF3 in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D17724; BAA04578.1; -. EMBL; Z26313; CAA81223.1; -. EMBL; U14003; AAA97271.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRFC SUBFAMILY.
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SEQUENCE OF 1-18.
                                                                                                                                                                                                                                                                                            Blattner F.R.;
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AE000508; AAC77328.1; -. AE005668; AAG59555.1; -.

EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 YLYQSGKGHTIQEVRIVKGLNNP--DLDAANGEDLAQQLRD-ELELVKGASNEFDKELFL 246
                                                                                                                                                                                                                                                                                                                                                                                  ::|: : | |:|| || : | | :|| 137 LTFMNKLDRDIRDPMELLDEVENELKI -----GCAPITWPIGCGKLFKGVYHLYKDET 189
                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=R1, MEDLINE=20036896; PubMed=10567266; MEDLINE=20036896; Particle Description J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----REL-LLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGA----DRALFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : - SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus
                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                    11.1%; Score 78; DB 1; Length 528; 26.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                        18; Mismatches 46; Indels
                                                                                                                                                                                                              -> L (IN REF. 2).
3EE94DE2B4C6B1C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                             1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG----
             EcoGene; EG12114; prfC.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR000161; GTP_EFTU.D2.
Pfam; PF00009; GTP_EFTU.D1.
Pfam; PF03144; GTP_EFTU.D2.
PROSTIE; PS00301; EFACTOR GTP; 1.
Protein blosynthesis; GTP-binding; Complete proteome.
                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247.AGEITPVFF---GTALGNFGVDHML---DGLVE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 AGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                                                                                                                                                                                                   59443 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans
                                                                                                                                                            26
91
144
314
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Best Local Similarity
Matches 41; Conserva
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528 AA;
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CONFLICT
SEQUENCE
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NP_BIND
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us-09-749-185-3.rsp

Length 259;

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Query Match
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                                                                                                                                                                                                                                                                                                     75 PAPAPLPAQSEWETVVEGAAQPVS----HLAKRRQELQSDLEVDRTYGDAVRALAR---- 126
                                                                                                                                                                                                                                                                     PGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVG-ADRALFRAGTA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                         InterPro; IPR002490; V_ATPase_sub_a.
Pfam; PF01496; V_ATPase_sub_a.1.
Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
SEQUENCE 690 AA; 75223 WW; 3007785EFF388RA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       studies.";
Biochem. Genet. 27:17-30(1989).
-!- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-!- CATALYTIC ACTIVITY: H(2)(3) = CO(2) + H(2)0.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse carbonic anhydrase III: nucleotide sequence and expression
                                                                                                                                                                                  Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E35B5CDDC4A54A93 CRC64;
                                                                                                                                                                                  i; DB 1;
                                                                                                                                                                                                                                                                                                                                                          93 PLVAFLDRTDK--LVP--LGQEHTLGDFDGNLEDALG 125
                                                                                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 AA.
                                                                                                                                                                              11.1%; Score 78; DB :
1larity 30.9%; Pred. No. 3.1;
Conservative 14; Mismatches
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Probom; P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001148; Carb_anhydrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89227981; PubMed=2496681; Tweedie S., Edwards Y.;
EMBL; AE001926; AAF10273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29397 MW;
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SWISS-2DPAGE; P16015; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:88270; Car3.
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95
118
259 AA;
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Best Local Similarity
Matches 30; Conserv
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SEQUENCE FROM N.A.
                      IGR; DR0695;
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                                                               'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392.353-358(1998).

-I- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN PRESENCE OF ATP. HYDROLYZES TWO ATPS FOR EACH PEPTIDE BOND CLEAVED IN THE PROTEIN SUBSTRATE (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: HYDROLYSIS Of large proteins such as globin, casein and denaturated serum albumin, in presence of ATP.

-I- SUBDINIT: HOMOTERRAMER (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI6; ALSO KNOWN AS THE LON FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                             Gaps
                                                                                                                       24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP-----TEPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWART: SM00464; LUN; 1.
PROSITE; PS01046; LUN.SER; 1.
Hydrolase; Serine protease; ATP-binding; Complete proteome.
NP_BIND 370 377 ATP (POTENTIAL).
ACT_SITE 692 692 BY SIMILARITY.
ACT_SITE 692 692 BY SIMILARITY.
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                                                           37; Indels
                                                                                                                                                                                                                                                                                     71 LGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFD 117
11.0%; Score 77.5; DB 1; 27.1%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-dependent protease La (EC 3.4.21.53)
LON OR AQ_242.
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InterPro; IPR003393; AAA.
InterPro; IPR003393; AAA_subfam.
InterPro; IPR003111; LON.
InterPro; IPR001311; LON.
Pfam; PF00004; AAA; 1.
Pfam; PF01309; LON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
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SMART; SM00464; LON; 1.
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998
15-DEC-1998
                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LON_AQUAE
O66605;
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10.9%; 27.7%;

Best Local Similarity

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 5:
                                      -1- SUBUNTT: HOMOTETRAMER.
-1- SUBCELLULAR LOCATION: CYLOPIASMIC.
-1- DEVELOPMENTAL STAGE: EXPRESSED DURING BOTH VEGETATIVE GROWTH AND
 30; Gaps
                        -----ALFRAGTA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   required for developmental gene transcription and intercellular signaling.";
J. Bacteriol. 175:4538-4544(1993).
-!- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS.
ESSENTAL FOR FRUITING BODY FORMATION AND DEVELOPMENT.
-!- CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin, casein and denaturated serum albumin, in presence of ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE LON FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93322334; PubMed-8331082;
Gill R.E., Karlok M., Benton D.;
"Myxococcus xanthus encodes an ATP-dependent protease which is
                                                                                                                                                                                                                                                                                                                                                                          for the development of
34; Indels
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                  Tojo N., Inouye S., Komano T.; "The lonD gene is homologous to the lon gene encoding an
                                                                        93 PLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQN 133
                                                                                                431 NPVIMLDEIDKLAI-----SFQGDPAAALLEVLDPEQN 463
                                                                                                                                                         D1002_MYXXA STANDARD; PRT; 826 AA. P36774; 01-JUV 4 (Rel. 29, Created) PFEB-1995 (Rel. 31, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) ATP-dependent protease La 2 (EC 3.4.21.53).
 Mismatches
                        PSGDGDVHIGPTEPEGLGDVHIRLQVGADR -----
                                                                                                                                                                                                                                                                                                                                                                          ATP-dependent protease and is essential Myxococcus xanthus.";
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 175:4545-4549(1993).
                                                                                                                                                                                                                                                                                                                           STRAIN=DZF1;
MEDLINE~93322335; PubMed=8331083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR003111; LON.
InterPro; IPR001984; Lon_endopep.
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D13204; BAA02491.1; -. EMBL; L19301; AAA72018.1; -.
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; 1.
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MEROPS; S16.003; -.
                                                                                                                                                                                                                                                  Myxococcus xanthus
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENT.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 LVGPPGVGKTSLGQSVAKATGRKFVRLSLGGVRDEAEIRGHRRTYVGALPGRFIQSMKKA 435
                                                                                                                                                                                                                                                                                                                                                                          30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: Periplasmic (Probable).
-:- INDUCTION: BY (GLCNAC)2.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       furnissii. Molecular cloning, isolation, and characterization of a periplasmic chicodextrinase.";
J. Biol. Chem. 271:33414-33424(1996).
J. Biol. Chem. 271:33414-33424(1996).
J. GLONACION: HYDROLYSES CHITIN OLIGOSACCHARIDES; (GLCNAC)4 TO (GLCNAC)2 AND (GLCNAC)5. FO (GLCNAC)2 AND (GLCNAC)3. TRACTIVE TOWARDS CHITIN, GLUCOSAMINE OLIGOSACCHARIDES, GLYCOPROPIEINS AND GLYCOPPEPTIDES CONPAINING (GLCNAC)2. HAS OPTIMONA ACTIVITY AT PHORECATURE OF 35-37 DEGREES CELSTUS.
J. CAPALYTIC ACTIVITY: HYDROLYSIS of the 1.4-beta-linkages of Nacetyl-D-glucosamine polymers of chilin.
acetyl-D-glucosamine polymers of chilin.
--- ENZYME REGULATION: INHIBITED BY (GLCNAC)4, (GLCNAC)5, (GLCNAC)5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keyhani N.O., Roseman S.;
"The chitin catabolic cascade in the marine bacterium Vibrio
SMART; SM00464; LON; 1.
PROSITE; PS01046; LON_SER; 1.
Hydrolase; Serine protease; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                             10.9%; Score 77; DB 1; Length 826; 26.9%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                          36; Indels
                                                                                                                                                   ATP (POTENTIAL).
BY SIMILARITY.
: F6765E0D91C948D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 GTKNPVMMLDEIDKLG-----ADFRGDPSAALLEVLDPEQN 471
                                                                                                                            GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chitodextrinase precursor (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1046 AA
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MEDLINE-97125982; Pubmed-8969204;
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InterPro; IPR001579; Chitinase_2.
InterPro; IPR00123; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18.
SMART; SM00704; Glyco_hydro_18; 3.
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-!- PATHWAY: CHITIN CATABOLISM.
                                                                                                                                                                                                                      MW.
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.9%
Matches 28; Conservative
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385
701
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701 7
826 AA;
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                                                                                                                         261
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P96156;
15-JUL-1999 (
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STRAINE-CV. COLUBRIA;
STRAINE-CV. COLUBRIA;
STATIA R., Lyznik R., MacKenzie S.;
Surnia R., Lyznik R., MacKenzie S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELULLAR LOCATION: Mitochondrial matrix.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE LON FAMILY OF ATP-DEPENDENT PROTREASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lon protease homolog 2, mitochondrial precursor (EC 3.4.21.-).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                         19; Gaps
                                                                                                                                                                                                  9 LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Indels 30; Gaps
                                                                                                                           Query Match
10.7%; Score 75.5; DB 1; Length 1046;
Best Local Similarity 30.5%; Pred. No. 9.2;
Matches 25; Conservative 8; Mismatches 30; Indels 19
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Hydrolase; Serine protease; ATP-binding; Multigene family;
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10.5%; Score 74; DB 1; Length 941;
Best Local Similarity 31.4%; Pred. No. 11;
Matches 33; Conservative 8; Mismatches 34; Indels
                                                      CHITODEXTRINASE.

fW; 40680F1642D55A1F CRC64;
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PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Hydrolase; Glycosidase; Signal; Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                         941 AA.
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InterPro; IPR003593; AAA.
InterPro; IPR00359; AAA.
InterPro; IPR003111; LON.
InterPro; IPR001941; Lon_endopep.
Proson Proson AAA; 1.
Proson Proson AAA; 1.
                                                                       SEQUENCE 1046 AA; 112380 MW;
                                                                                                                                                                                                                                                                                               980 GGGTGGGTTEP---GDV 998
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SMART; SM00382; AAA; 1.
SMART; SM00464; LON; 1.
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941 AA;
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Search completed: July 18, 2002, 14:31:53 Job time: 942 sec

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092y75 rhizobium m
09c6z1 arabidopsis
09v1j1 drosophila
093nx7 streptomyce
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090yal cyprinus ca
090ya0 cyprinus ca
034003 rhodobacter
0541R2 streptomyce
090y98 cyprinus ca
09sna4 arabidopsis
                                                                                                                                                                                                                                                O26636 methanother
O04954 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-B2682;
Shinichi K., Ensign J.;
"Cloning and characterization of a gene involved in sporulation and
                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=B2682;
Kawamoto S., Ensign J.C.;
"Cloning and characterization of a gene involved in regulation of
sporulation and cell division of Streptomyces griseus.";
Nippon Hosenkin Gakkaishi 9:136-151(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=B2682;
Kawamoto S., Ensign J.C.;
"Isolation of mutants of Streptomyces griseus that sporulate in
nutrient rich media.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B2682;
MEDLINE-97286526; PubMed-9141673;
Kawamoto S., Watanabe H., Hesketh A., Ensign J.C., Ochi K.;
"Expression analysis of a ssgA gene product associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell,division of Streptomyces griseus.";
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                  136 AA
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                                                                                                                                                                                                                                                                                                                                  PRT;
                          Q90YA1
Q90YA0
O34003
O54182
Q90Y98
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99ERN8
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NCBI_TaxID=1911;
72.5
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P95753
091906 streptomyce 091268 streptomyce 09277 streptomyce 095770 streptomyce 095771 streptomyce 09751 streptomyce 09751 streptomyce 09751 streptomyce 09751 halobacteri
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Q93jf9 streptomyce
Q9byg6 homo sapien
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Copyright (c) 1993 - 2000 Compugen Ltd
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Gapop 10.0 , Gapext 0.5
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Q9L268
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sp_bacteria:*
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sp_archeap:*
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Gaps

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Length 135;

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SEQUENCE FROM N.A.

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF195770; AAG28481.1. -.

SEQUENCE 135 AA; 14843 MW; 32006CC86BDE4ED6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=121022;
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van Wezel G.P., Rousseau C., Kraal B.;

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";

Submitted (OCT-1899) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195772: AAG28483.1; -.

SEQUENCE 145 AA; 15838 MW; 92AC0F30DF3D2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptoverticillium netropsis (Streptoverticillium flavopersicus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=55404;
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                                                                                                                                      Length 136;
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Pred. No. 5.6e-52;
7; Mismatches 12; Indels
      sporulation and cell division in Streptomyces griseus.";
Microbiology 143:1077-1086(1997).
EMBL; D50051; BAA21558.1; -.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                      14783 MW; C6A28A7823AD7C8B CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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85.9%;
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Matches 135; Conservative
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Matches 116; Conserv
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Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinshi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL096833; CAB46964.1; -.

SEQUENCE 136 AA; 14920 MW; 4867CIFIEOBECC88 CRC64:
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Bacteria; Firmloutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
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77.8%; Pred. No. 4e-46;
Live 12; Mismatches 1
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MEDLINE=97000351; PubMed=8843436;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                       van Wezel G.P., Rousseau C., Kraal B.; van Wezel G.P., Rousseau C., Kraal B.; "Cloning and sequencing of the Streptomyces albus ssgA gubmitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF19571; AAG38482.1; -
SEQUENCE 135 AA; 14735 MW; OFCBF4BDB2BA201B CRC64;
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65.9%; Pred. No. 4.5e-38;
ive 18; Mismatches 28;
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01-0CT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
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121 DDALNRSLAEEQSAG 135
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Seeger K.J., Harris D
Submitted (JAN-2000)
                            121 EDALGRILAEEQNAG
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SEQUENCE FROM N.A.
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinshi H., Hopwood D.A.;
Kinshi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL137778; CAB70943.1;
SEQUENCE 159 AA: 17472 MW; BA41013F940D7315 CRC64;
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SCE19A.24.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL096852; CAB51005.1; -.
SEQUENCE 142 AA; 15364 MW; 857862390AA51CCB CRC64;
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                                                                                                                                                                                                                                                 Length 159;
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                                                                                                                                                                                                                                              Query Match 35.4%; Score 249; DB 2; Length 15 Best Local Similarity 43.1%; Pred. No. 7.1e-17; Matches 56; Conservative 14; Mismatches 56; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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MEDLINE-97000351; PubMed-8843436;
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Best Local Similarity 37.74
Matches 49; Conservative
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149 DQELSHILAE 158
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STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Kinashi H., Hopwood D.N.;
"A set of ordered cosmids and a detailed genetic and physical methe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
BMBL: A1391041; CAOL575:1; ---
SEQUENCE 156 AA; 17188 MW; 7181972EE7F33FB0 CRC64;
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MEDLINE=97000351; PubMed-8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical me
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CRA4202811; -.
SEQUENCE 142 AA; 15741 MW; E24AA52C00AF40F1 CRC64;
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the EMBL/GenBank/DDBJ databases.
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Oliver K., Harris D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
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34.7%; Pred. No. 3.6e-07;
tive 14; Mismatches 50;
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                                    STRAIN-A3(2);
Saunders D.C., Harris D.
Submitted (AUG-2000) to
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Streptomyces coelicolor.
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Best Local Similarity
                    SEQUENCE FROM N.A.
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                                                                                                              SEQUENCE FROM N.A.
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77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLG---- 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLDGLNSPSGDGDVHIGP-----TEPEGLGDVHIRLQVGADRALFRAGTAPLVAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Klesser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map the 8 MD Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL049587; CAB40672.1;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                   138 AA
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                                                                                                                                                                                                       Created)
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                 PRELIMINARY;
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                                  120 LEDALGRILA 129
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132 IDDGLAELLA 141
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1902;
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Best Local Simi
Matches 46;
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EMBL; A132674; CAB59654.1; -.
Hypothetical protein.
SEQUENCE 126 AA; 13742 MW; D54A8574D28B4D69 CRC64;
                                                                                          70 GLGDVHIRLQVGAD-----RALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                  21 RFPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRP-ESR 79
                    Gaps
                                      12 RIPV--ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE 69
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                    18;
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Kinashi H., Hopwood D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                        Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                   51; Indels
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-heq 30; Indels
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Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MCPOTHETICAL 13.7 KDA PROTEIN.
SCE87.091
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Last annotation update)
         3.1e-06;
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                   Mismatches
        Pred. No.
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31.0%; Pre-
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MEDLINE=97000351; PubMed=8843436;
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                   40; Conservative
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         Best Local Similarity
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01-MAR-2001 (
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MEDLINE-2050483; PubMed-11016950;

MEDLINE-2050483; PubMed-11016950;

MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swarzell S., Weil D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 IGPTEPEGLGDVHIRLQVGADRA---LFRAGTAPLV-------AFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AAAT------ADRARSLLARRHTAPKTRHWCGAIADRVREAVADRGPAVPP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 FRIPVELRYEVGD-----PYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGD-GDVH 62
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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Best Local Similarity 26.6%; Pred. No. 4.7; Matches 41; Conservative 11; Mismatches 45; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Genome sequence of the nematode C.elegans: A platform for
                                                                Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 LGQEHT------LGDF-----DGNLED 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR000619; Guanylate_kin.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
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InterPro; IPR000223; Peptidase_S26A.
Pfam; PF00461; Peptidase_S26; 1.
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TYPE II SECRETION SYSTEM PROTEIN. GSPE1 OR VNG0218G.
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Science 282:2012-2018(1998).
EMBL; 281475; CAB03913.1; -.
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                                                                                                                                                                NCBI_TaxID=64091;
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C24H11.6.
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402 AA.

PRT;

PRELIMINARY;

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Search completed: July 18, 2002, 14:30:54
Job time: 943 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                              20; Gaps
                                                                                                                                                                                                                            22 GDPYAIRMTFHL--PGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Gaps
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Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RArabidopsis thaliana chromosome III BAC F7018 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
HSSP, P53041; JAJ.
InterPor: IPR02110; ANK.
InterPor: IPR02110; ANK.
Pfam: PF00023; ank; 7.
Pfam: PF00515; TPR: 3.
                                                                                                                                                                                                                                                                                                                           80 VGADRALFRAGTAPLVAFLDRTDKLVPLGQEHT-----LGDFDGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                          : ; ; ; ; ; 108 IWPPE---RAGWISDHWFWDKTQKLLKMADRMTQLQDMINEWAGLMTNAIGVLQA 159
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                                                                                                                                Length 261;
                                                                                                                                                                              47; Indels
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PRINTS; PR00727; LEADERPTASE.
PROSITE; PS00761; SPASE_I_3; 1.
SEQUENCE 261 AA; 28732 MW; E13FFA7E14CC1FA2 CRC64;
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456 Aa; 49259 MW; BABCB372E8A0A531 CRC64;
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Last annotation update)
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                                                                                                                             11.9%; Score 84; DB 5; 28.7%; Pred. No. 2.1;
                                                                                                                                                                           15; Mismatches
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PROSITE; PS50297; ANK_REP_REGION; 1.
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Best Local Similarity 25.0%,
Matches 35; Conservative
                                                                                                                                                                              Conservative
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STRAIN-CV. COLUMBIA;
                                                                                                                        Query Match
Best Local Similarity
Matches 33; Conserv
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SEQUENCE 4
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62 HIGPTEPEGLGDVHIRLQVGAD-----RALFRAGTAPLVAFLDRTDKLVPLGQEHTLGD 115
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                                                                                                                                                        Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyces. NCBI_TaxID=1902;
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"A set of ordered cosmids and a detailed genetic and physical methe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21.77-96(1996).
EMBL, AL596162; CAC44582.1;
SEQUENCE 402 AA; 41429 MW; 06572345E802539A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE BLDA-REGULATED NUCLEOTIDE BINDING PROTEIN.
  Created)
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MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                       Streptomyces coelicolor.
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Submitted (JUL-2001)
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Best Local Similarity
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01-DEC-2001
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LUITEN RUDOLF GIJSBERTUS MARIA (NL); WEZEL GILLES PHILIPPUS
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          AF195771 Streptomy
AL0096823 Streptomy
AX007228 Sequence
AX007216 Sequence
AX007216 Sequence
D50051 Streptomy
AE19577 Streptomy
AE19577 Streptomy
AE19572 Streptomy
AL096852 Streptomy
AL096852 Streptomy
AL040587 Streptomy
AL0505416 Sequence
AL051556 Streptomy
Confinuation (8 of
AL066633 Oryza sat
AL079355 Streptomy
Confinuation (7 of
AP004279 Oryza sat
AC026815 Oryza sat
AR57520 Streptomy
AF875702 Streptomy
AF875702 Streptomy
AN004279 Oryza sat
AC026815 Oryza sat
Confinuation (7 of
AF875702 Streptomy
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AL08898 Streptomy
AL085206 Streptomy
AL390975 Streptomy
Z46913 Streptomy
AF210249 Streptomy
AL38852 Streptomy
AL38852 Streptomy
AL355832 Streptomy
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AL35882 Streptomy
AL35882 Streptomy
AF14372 Myobacte
U10405 Streptomyce
AC074105 Oryza sat
AY033407 Myxococcu
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Streptomyces albus G.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetaceae; Streptomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 407)
Read.pa. Luiten.R.G. and Van Wezel,G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: wo 0000613.4 S 06-JAN-2000;
UNIV LEIDEN (NL); RRAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARI.
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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1. .407
/organism="Streptomyces albus /db_xref="taxon:1962"
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LMFLCHR32_06
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AC026815
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AF357202
AP002484
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OSJN00060
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Sequence 5 from Patent WO0000613.
AX007220
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ACCESSION
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KEYWORDS
SOURCE
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AX007220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
LOCUS
                                                                                July 18, 2002, 11:21:43; Search time 4085.76 Seconds (without alignments) 2084.582 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             atgagcttcctcgtctccga......gaggagcagagcgccggctg 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                    3595312
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                           1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                             summaries
                                                           - nucleic search, using sw model
                                                                                                                                                                                     IDENTITY_NUC Gaport 1.0
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em_htg_inv:*
em_htg_other:*
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Maximum Match 100%
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Maximum DB seq length: 200000000
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gb_pat:*
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Post-processing:

Database

Total number of

Searched:

Title: Perfect score:

Sequence:

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ou:

Run

Scoring table:

21. 22. 22. 24. 25. 27. 30. 33. 33.

Score

Result No.

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QGLSIGSERAHADDSHLDDDLNRSLAEEQSAG"
219 c 192 g 80 t
                                                                                                              /note="similar to Streptomyces griseus SsgA; possible cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 08-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycescaes; Streptomyces. 1 (bases 1 to 1544)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 accytogatecytacycygtycygetyacyttecaectececygagacycecegyteaec 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 accgaccaggottgtcgctcgcaggagcgagcgggcacacgccgacttcgacagccactc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 TGGGTCTTCGGGCGTGAACTGCTGGTCGAGGGAGTCCTGGACGCCGCGGGCGACGAC
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                                                                                                                                                                                                                                                                                                                                            Length 566;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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/db_xref-"taxon:1888"
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Streptomyces coelicolor A3(2)
                                                                                                                                division protein"
                                                                                                                                                 /codon_start=1
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26. .433
                              /gene="ssgA"
16. .20
                                                                                              /gene="ssgA"
                                                                                                                                                                                                                                                                               .75
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                              1. .>405 /
/gene="ssgA" /
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/ a 150 c 139 g 61 t
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Submitted (18-OCT-1999) Biochemistry, University of Leiden, PO 9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
1. .566
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'an Wazel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces albus ssgA gene (mpublished)

2 bases 1 to 566)

van Wezel, G.P.,
                                                                                                                                                                                                                                                                                                                                              1 atgagetteetegteteegaggagetegeetteegeateeeggtggagetgeggg
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Streptomyces albus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                 Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces albus SsgA (ssgA) gene, complete cds. AF195771
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 407; DB 6;
Pred. No. 1.9e-36;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces albus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF195771.1 GI:11066160
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ilarity 100.0%;
Conservative 0
                /gene="ssgA"
                            .>405
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AUTHORS JOURNAL

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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon:

Wising a specially developed Hidden Markov Model (Kroph et al., Nuclet Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Int(201-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon gity, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the Asel-Q genomic restriction fragment.
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//gene="SCO11.01c" hypothetical protein, partial CDS, len:
//note="SCO11.01c, hypothetical protein, partial CDS, len:
//note="SCO11.01c, hypothetical protein constraint function, previously sequenced as
//note="SCO11.01c" hypothetical protein constraint function in phosphotyrosine protein phosphatase
(159 aa). Weak similarity to the N-terminus of TR:06988
(EMBL:AL023797) Streptomyces coelicolor hypothetical
protein (172 aa), fasta scores; opt: 158 z-score: 206.4
EC): 0.00036, 46.2% identity in 65 aa overlap. Continues
as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                                                                                                    Submitted (08-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                  3 (bases 1 to 15441)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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complement(1. .289)
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1. .15441
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                                                                                                                                                           Seeger, K. and Harris, D.
                                                                                                                     (bases 1 to 15441)
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                                                          MOI. MIC
97000351
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gene

FEATURES

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complement(360. .1265)

complement(360. .1265)

/gene="SCQ11.02c"
/note="SCQ11.02c"

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RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAFTGLEDDSTLRTLHLAGPPEFTA
ERALLSAGELTGBEDGARALRSFSGNAEETLEGLAAGHTBLAGTTRPRGALHTRATPL
CDEVHYLVATPHWAERAGVEDVRDTDASALKHUPVVEVHESLEPVGRYRASVEDARPA
SPATVVAPDLRAVLACAVAGGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
COMPLEMENT (831. 1256)
/gene="SCQ11.02c"
/note="Match to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"
/gene="SCQ11.02c"
/gene="SCQ11.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma synthase/lyase, left 392 as; previously sequenced as SW.CYSA_STROO (EMBL:037580), cysA, S.coellcolor putative cystathionine gamma-lyase (392 aa). Similar to many e.g. SW.EMECL_PSEU (EMBL:08554), mdeA, Pseudomonas putida methionine gamma-lyase (398 aa), fasta scores; opt: 608 a-score: 653.6 E(): 4.5e-29.36.9% identity in 404 aa overlap. Highly similar to TR:03568 (EMBL:X91393) Streptomyces antibioticus hypothetical protein found upstream of the abab gene (322 aa) (87.1% identity in 232 aa overlap). Contains Pfam match to PF01053
CYS_MEL_Meta_PP, Cys/Met_metabolism PLP-dependent enzyme
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/protein_id="CAB46958.1"
/db_xref="G1:5457270"
/translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
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/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="G1:5457269"
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                                                     complement(1. .4279)
/note="sequence corresponding to EMBL:U37580 from 1 to
                                                                                                                                                                                                                                                                             /note="overlap with Streptomyces coelicolor cosmid H24 (EMBL-AL049826) from 41528 to 41625" (complement(350, .1265) /gene="SCQ11.02c"
DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
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/gene="SC011.03c"
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/transl_table=11
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CDS

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/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFG
RELIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPLGGERSLADPLLDEALDRIAPEDATA"
135 c 145 q 71 t
                                                                                                                                                                                                                                 filamentous microorganisms
Patent: WO 0006013-A 7 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
   PAT 06-SEP-2000
                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces 1 (bases 1 to 407)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggctccgagcaggcgctcttccgcgtcggcaaggcgccgctgctcgccttcctcgaccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ssgA"
/note="strain ATCC of Streptomyces goldeniensis"
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                                                                                                Streptomyces goldeniensis.
Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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     linear
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/organism="Streptomyces goldeniensis"
/db_xref="taxon:121022"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 243.8; DB 6;
Pred. No. 1.7e-18;
0; Mismatches 102;
                                                                                                                                                                                        Kraal, B., Luiten, R.G. and Van Wezel, G.P.
       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="SsgA"
/protein_id="CAC07387.1"
/db_xref="G1:9995089"
     AX007222
Sequence 7 from Patent WO0000613,
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                          GI:9995088
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ssgA"
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74.98;
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Best Local Similarity
Matches 305; Conserv
                                                            AX007222.1
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                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                   source
                     DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                          REFERENCE
AUTHORS
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AF195770
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                                                          VERSION
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SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLM
IETPENPGILDVCDVRRLVBAAHAGGALVAVDNTLATPLGQRPLELGADPSVASGTKQL
TGHGDVLLGYVAGRDAGAMAAVRRWRTVGAIPGEMBAWLAHRSIATLQLRVDRQDST
ALKYAEALRTRPETTGRRYGELDDPSHKNASQQMLRYGCYVSFTLBSRARDRFLDA
LRLVBGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mykrycfyctgnicrspwaeavfraryedaglghlyeadsagg
GWHEGEGADPRTEAVLADHGYGLDHAARQFQQSWFSRLDLVVALDAGHLRALRRLAPT
ERDAAKVRLLRSYDPAVAGGDLDVPDPYYGGRDGFEECLEMYEAASTGLLAAVREQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                              match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine-phosphatase (164 aa). Contains Pfam mi
to PF01451 LMWPc, Low molecular weight phosphotyrosine
protein phosphatase"
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/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
protein-tyrosine-phosphatase, len: 164 aa; previously
sequenced as Sw:PTPA_STRCO (EMBL.U37880), ptpA,
S.coelicolor low molecular weight
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                                                                                                              complement(1533. .2624)
/gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
complement(2031. .2075)
/gene="SCQ11.03c"
/note="SCQ11.03c"
/note="PSQ086 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
/gene="SCQ11.04c"
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Pred. No. 1.6e-19;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-tyrosine-phosphatase"
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/db_xref="GI:5457271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/trans1_table=11
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75.78;
                                                                                                                                                                                                                                                                                                          /note="ptpA"
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Matches 308; Conserv
                                                                                                                 misc_feature
                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to Streptomyces griseus SsgA; possible cell
division protein"
/codon_start=1
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 BCT 01-NOV-2000
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                                                                Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescace; Streptomyces.

( pases 1 to 408)
van Wezel, G.P., Rousseau, C. and Kraal, B.
                                                                                                                      Cloning and sequencing of the Streptomyces goldeniensis ssgA gene Unpublished
2 (bases 1 to 408)
van Wezel, G.P.
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                                                                                                                                                                    Direct Submission
Submitted (18-OCT-1999) Biochemistry, University of Leiden,
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
     Streptomyces goldeniensis SsgA (ssgA) gene, complete cds AF195770
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/db_xref="ATCC:21386"
/db_xref="taxon:121022"
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Pred. No. 1.7e-18;
0; Mismatches 102;
 DNA
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/product="SsgA"
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/db_xref="G1:11066159"
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goldeniensis
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74.9%;
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Best Local Similarity 74.9
Matches 305; Conservative
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Patent: WO 0000613-A 3 06-7AN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL OKGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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RELLLDGLNSPSGDGDVHIGPTEPEGIGDVHTRLQVGADRALFRAGTAPLVAFLDRTD
KLVPLGGEHTLGDFDGNLEDALGRILAEEQNAG"
139 c 142 g 66 t
  PAT 06-SEP-2000
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Reducing branching and enhancing fragmentation in culturing
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                                                                                                                                         Actinobacteridae,
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Pred. No. 5.9e-18;
0; Mismatches 105; Indels
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/db_xref="taxon:1911"
    DNA
                                                                                                                                     Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
1 (bases 1 to 407)
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/protein_id="CAC07385.1"
/db_xref="G1:9995085"
AX007218 407 bp
Sequence 3 from Patent W00000613.
AX007218
AX007218.1 GI:9995084
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/note="strain ATTC
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                                                                                                  Streptomyces griseus.
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/translation="MMSFLVSEELSFRIPVELRYEVGDPYAIRWTFHLPGDAPVTWAF
GRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRT
DKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG"
                                    BCT 19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 1513)
Shinichi,K. and Ensign,J.
Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus
Unpublished (1995)
5 (bases 1 to 1513)
Shinichi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-APR-1995) Kawamoto Shinichi, National Food Research Institute. Biomolecular Transfunction Laboratory; Kannondal 2-1-2, Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996) Location/Qualifiers
1. 1513
/ Organism="Streptomyces griseus" / Strain="B2682"
                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                       1 (sites)
Kawamoto,S. and Ensign,J.C.
Cloning and characterization of a gene involved in regulation of
sporulation and cell division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
                                                                                                                                                                                                                                                                                               2 (sites)
Kawamoto,S. and Ensign,J.C.
Isolation of mutants of Streptomyces griseus that sporulate in
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Expression analysis of the sagh gene product, associated with
sporulation and cell division in Screptomyces griseus
Microbiology (Reading, England) 143 (Pt 4), 1077-1086 (1997)
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Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 3.9e-18;
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/db_xref="G1:2281004"
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Actinomycetol. 9, 124-135 (1995)
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                                  Streptomyces griseus DNA for a D50051
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D50051. GI:1772323
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/codon_start=1
/transl_table=11
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                                                                                                                                             Streptomyces griseus
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomyces.
1 (bases 1 to 438)
Kraal,B., Luiten,R.G. and Van Wezel,G.P.
Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms
Grisment: WO 00006613-A 1 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MRESVQAEVMMSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLP GDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTA PLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGR"
                                      06-SEP-2000
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/gene="ssgA"
/note="strain ATTC of Streptomyces griseus"
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Pred. No. 5.7e-18;
0; Mismatches 105; Indels
                                        linear

    .438
    /organism="Streptomyces griseus"
/db_xref="taxon:1911"

                                        DNA
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/protein_id="CAC07384.1"
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                                AX007216 438 bp
Sequence 1 from Patent WO0000613.
AX007216
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ilarity 74.2%;
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Matches 302;
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Streptomyces netropsis SsgA (ssgA) gene, complete cds. AF195772
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/db_xref="G1:11066163"
/db_xref="G1:11066163"
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PLVARLLAFTDVKSVPGGQFLGDFEDSLEAALGKILAEEQNAG"
158 c 142 g 68 t
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Streptomyces netropsis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (18-CCT-1999) Biochemistry, University of Leiden, PO
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ACGGACAAGTCGGTGCCGCTCGGTCAGGAACAGACTCTGGGTGACTTCGAGGACAGCCTG 360
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                                                                                                                           gtccgggtctgcccggtggggaggcgaccaccagggaggtgcacatcaccctccaggtc
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/db_xref="taxon:55404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 438)
van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces
Unpublished
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Pred. No. 2.2e-16;
0; Mismatches 114;
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/product="SsgA"
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/note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF195772.1 GI:11066162
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ilarity 72.0%;
Conservative (
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van Wezel, G.P.
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SOURNAL
AUTHORS
TITLE
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Rraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS VAN (NL)
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0
301 accgaccagggettgtcgetcggcagcgagcgggcacacgccgacttcgacagccacete 360
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/db_xref="taxon:55404"
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Pred. No. 2.3e-16;
0; Mismatches 114;
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1. .407
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142 ctggtcgagggagtcctgg 160
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Cerdeno, A.M., Parkhil
98.68;
 Best Local Similarity 98.6
Matches 137; Conservative
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LDRNGEFLSRRILYTQDDVEQADGAGPETGKPQNLANAQLTVEELCEVSITASDNCAA
NLMLRELGGPAAVTRFVRSLGDRVTRLDRWEPELNSAEPGRVTDTTSPRAITRTYGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAA26775.1"
/db_xref="GI:153339"
/translation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
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PGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG"
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Dehottay,P., Duasart,J., De Meester,F., Joris,B., Van Beeumen,J., Erpicum,T., Fere,J.,M. and Ghuysen,J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G Beta-lactamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
 TGGCCGTTCGGCCGGGAGCTGCTCGACGGGATCAACCGCCCGAGCGGCGACGGCGAC
                                                                                                                  gtccgggtctgcccggtgggggagacggccaccaggggaggtgcacatcacctccaggtc 240
                                                                                                                                                                                                       accgaccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctc 360
                                                                                                                                                                                                                                                                                   331 ACGGACAAGTCGGTGCCGCTCGGTCAGGAACAGACTCTGGGTGACTTCGAGGACAGCCTG 390
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                                                  tgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcgggggacgcgac
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Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
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1. .1410
/organism="Streptomyces albus"
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540 c 496 g 1
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/gene="beta-lactamase"
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/db_xref="taxon:1888"
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Length 1410;

DB 1;

33.4%; Score 135.8;

Query Match

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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codons.

The position is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4478(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
iun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
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phosphoribosiltransferase; DNA helicase; DNA polymerase III;
elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase;
membrane protein; membrane transferase; protein-export membrane
protein; regulator; secreted protein; sugar transferase;
threonine-tRNA synthetase; transport system inner membrane protein.
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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Submitted (28-JAN-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
Actinomycetales; Streptomycineae; Streptomyces.
I (bases 1 to 30640)
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
Ast of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is funded
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                                                                                                                                                                                                                                                                                              82 eggetgaegttecaceteceeggagaegeceeggteacetgggtettegggegtgaaetg 141
                                                                             81
    Gaps
                                                                                                                            Streptomyces coelicolor sequencing at The Sanger Centre is fuby the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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                                                                                 gagetegeetteegeateeeggtggagetgeggtaegagaeegtegateegtaegeggtg
Indels
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Seeger, K.J. and Harris, D.
Unpublished
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identical to previously sequenced SW.RELA_STRCO (EMBL:X87267) Streptomyces coelicolor GTP pyrophosphokinase (EC 2.7.6.5) RelA, 847 aa and highly pyrophosphokinase (EC 2.7.6.5) RelA, 847 aa and highly similar to SW.RELA_STRAT (EMBL:AF072829) Streptomyces antibioticus RelA protein, 841 aa; fasta scores: opt: 4969 z-score: 4966.2 E(): 0; 90.3% identity in 848 aa overlap and to SW.RELA_CORGL (EMBL:AF038651) Corynebacterium glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA, 760 aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.7% identity in 774 aa overlap. Contains Pfam match to entry PRO1842 ACT, ACT domain and match to prosite entry PS00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar to TR:03325 (EMBL:298209) Mycobacterium tuberculosis hypothetical 49.8 kD protein MTCY174.11, len: 45.9% identity in 296 aa overlap. Contains possible coiled-coils region"
codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
/transl_table=11
/product=hypothetical protein SCL2.01"
/protein_id="Cap70913.1"
/db_xref="d1:6822207"
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AVBHLREQVDAHHAVGDLEARRARLOQUALUVETRREEKRAQRAKQSDEARGAEALV
AEAEELARSDQWAAGERLERSLVDTWKGLPFLDRKSDDELWHRFSHARSAFSKRRQH
FAQLDAQREEARRIKERLVSEAEALSNSTDWGPTAARYRDLMSEWKAAGRAQREHEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWNRFRGAQDVFFAARSSVFAERDAEQSENLKLKEELVTEAEKLVPVTDLKSARAAFR
SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGPTPRHARVPRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MDKLRSQVEQARAQGNDAKADKLARELEGRQALLDQALKGLHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="SCL2.03c, relA, GTP pyrophosphokinase, len: 847 aa;
                                                                                                                      IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SCL2.01"
/note="SCL2.01, hypothetical protein, len: >328 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="previously sequenced region SW:SCAPTRELA EMBL:X87267 S.coelicolor apt & relA genes" complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein SCL2.02"
/protein_id="CaB70914.1"
/db_xref="G1:6822208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1010. 1150
/gene="SCL2.02"
1010. 7gene="SCL2.02"
/note="SCL2.02, unknown, len: 46 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="GTP pyrophosphokinase"
/protein_id="CAB70915.1"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1229, .3772)
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                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="cosmid L2"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                          .38640
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/gene="apt"/
/gene="apt"/
/gene="apt"/
/gene="gcli2.04c, apt, adenine phosphoribosiltransferase,
len: 182 aa; identical to previously sequenced
SW.APT_STRCO (EMBL:887267) Streptomyces coelicolor adenine
phosphoribosyltransferase (EC 2.4.2.7) Apt, 182 aa and
highly smilar to SW.APT_ECOLI (EMBL:M4040) Escherichia
coli adenine phosphoribosyltransferase (EC 2.4.2.7) Apt,
13 aa; fasta scores: opt: 600 z-score: 682.8 E():
1.2e-30; 54.8% identity in 168 aa overlap. Contains Pfam
match to entry PF00156 Pribosyltran, Phosphoribosyl
transferase domain and match to Prosite entry PS00103
Purine/pyrimidine phosphoribosyl transferases signature"
                                                                                                                                                                                                                                                                                                                                AAGACPSRDWIGFVKSPRARNKIRAWFSKERRDEAIEOGKDAIVRAMRKONLPIQRIL
TGDSLVTLAHEWRYSDISALYAAIGEGHVSAPNIVOKLVOALGGEBAATEELDESVPP
SERGRKRRANADPGVVVKOVEDVWYKLARCCTPVPGDP IJGFVTRGSGVSVHRSDCV
NVDSLSREPER ILLEWAPPTOSSVELVAIOVEALDRSRLLSDVTRVLSDQHVNILSAA
VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3273. .7460)
/note="previously sequenced region SW:SCSECAPT EMBL:X85969
S.coellcolor secb, secf & apt genes"
complement(3778. .3781)
                                                                                               AELGMDPATLMAGLLHDTVEDTEÏGLEDLRRDFGDVYTLLVDGYTKLDKVKFGEAAQA
ETVRKMYVAMAKDPRVLVIKLADRLHNMRTMRYLKREKQEKKARETLEIYAPLAHRLG
MNTIKWELEDLAFAILYPKMYDEIVRLVAERAPKRDEYLAVYTDEVQQDLRAARIKAT
                                                                                                                                                                                              VTGRPKHYYSVYQKMIVRGRDFAEIYDLVGIRVLVDTVRDCYAALGTVHARWNPVPGR
FRDY IAMPEKPMYQSLHTYLGPGGRPYELQIRFEDMIRRAFGIABARAG
ASK'RTDAPKSGRSKDDHLNDMAWRQLLDWQKETBDFGEFLESLRFDLSRBSVFVP
TPKGDVIALPAGATAVDFAYAHTEVGHRTIGARVNGRLVPLESTLDNGDLVBFFTS
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                               PVDKPAEQQPRPKPLPAERPQNAPVVRAPAGQPARSGSSNRVRARLARLGVQRANPYN
PVLEPLLRIVRGNDPKIETSTLRQIERAYQVAERWHRGQKRKSGDPYITHPLAVTTIL
/translation="MPDEAQPLTAAKPESASASAAKPAPSAPQAKNDTHGPIQHAPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15"
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/note="Pfam match to entry PF00156 Pribosyltran,
Phosphoribosyl transferase domain, score 150.30, E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3904. .4568)
/note="previously sequenced region SW:SCAPTRELA
EMBL:X87267 S.coelicolor apt & relA genes"
complement(3956. .4453)
/gene="apt"
complement(3956. .4453)
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/protein_id="CaB70916.1"
/db_xref="G1:6822210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1256..1474)
/gene="relA"
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complement(4468, .4503)
complement(4501, .5622)
/gene="secF"
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/gene="secF"
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/trans1_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. (bases, 1 to 35284)
Redenbach, M., Kleser, H. M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-hydroxyphenylpyruvate dioxygenase; ABC transporter; amino acid permease; asnC-family; cysteine synthase; nicctinamidase; osmocregulation; osmotolerance; oxidoreductase; permease; phosphoenolpyruvate-dependent; protease; regulator; ribonuclease PH; rph; sugar phosphotransferase system; transcriptional regulator; transposase; tRNA Leu; zinc metallopeptidase. Streptomyces coalicolor A3(2)
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                                                                                                           35149
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                                                                                                                                                                      ccytcyatccytacycygtyccygttyacyttccacctccccygagacyccccygtcacct 121
                                           Gaps
                                                                                 2 tgagcttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgaga 61
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by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                        tccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtcg
                                                                                                                                                                                                                                                                                                                                                                              35210 TCCGTGTCTGGCCGTCCCGCAGTCACGGCCAGGGCGTCGTGTGCATCGCTCTCAGCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                         getecgageaggegetettecgegteggeaaggegeeggetgetegeetteetegaeegea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccgaccagggcttgtcgctcggcagcgagcggggcacacgccgacttcgacagccacctcg
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James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (16-JUL-1999) Streptomyces coelicolor sequencin
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DB 1; Length 38640; 0.00022;
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                                         0; Mismatches 175;
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  Score 110;
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                        Pred. No.
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Unpublished
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27.0%;
55.1%;
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                                         Conservative
                     Similarity
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                     Best Local Sim
Matches 215;
  Query Match
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ACCESSION
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JOURNAL
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(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)

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correct initiation coden. Where possible we choose an initiation coden (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation coden). If this cannot be identified we choose the most upstream initiation coden. If this cannot be the entire insert of the sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the Asel-E genomic restriction fragment.
                                                                                                                            are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Gusually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Which is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4766-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCE19A.01, hypothetical protein, partial CDS, len: >31 aa; unknown function, similar to members of the alkyl hydroperoxide reductase C/thiol-specific antioxidant family e.g. TR:053226 (EMBL:AL021185), bcp, Mycobacterium tuberculosis bacterioferritin comigratory protein (157 aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06, 63.3% identity in 30 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                       The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140. .226
/note="tRNA Leu anticodon TAG, Cove score 69.78"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces coelicolor A3(2)"
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/protein_id="CAB50982.1"
/db_xref="GI:5531350"
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/protein_id="CAB50983.1"
/db_xref="GI:5531351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxón:100226"
/clone="cosmid E19A"
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complement(243. .845)
/gene="SCE19A.02c"
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1. .35284
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="A3(2)"
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/translation="MASKAEKIVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK
AAGAHGVVKMGTAIQVVIGTDADPIAAEIEDMM"
complement(2385. 2489)
/gene="SCE19A.05c"
/note="SCE19A.05c"
/note="Fam match to entry pr00367 PTS_EIIB,
phosphotransferase system, EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL391041.1 GI:9716211
amino acid transport integral membran protein; branched amino acid
binding secreted protein; branched amino acid transport system
ATP-binding protein; branched amino acid transport system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 32704)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SCE19A.06, possible PTS transmembrane component, len: 431 aa; similar to many PTS (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20202 CGGACGATCCCTACGCGTGCACATCACCTTCCACATCGACTCGGCCACCGGTGCACT 20261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGGCATTCCGGTGCCGGCCCGGCTCGGCTACCACA 20201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ccgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgcccggtcacct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tgagcttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20382 GGGACGGCGACGCCCTCCTGGAGGCGCCCCACGCCCCAGGTGTCGGCCTGGCTGAGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgaccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 gggtcttcggggcgtgaactgctggtcgagggagtcctggacgccgcggggggacgcgacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 getecgageagegetetteegegteggeaaggegeegetgetegeetteetegaeegea
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109.6; DB 1
Pred. No. 0.00025;
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       /protein_id="CAB50986.1"
/db_xref="G1:5531354"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCE19A.06"
/note="SCE19A.06,
                                                                                                                                                                                                                                                                                                                   2660. .3955
/gene="SCE19A.06"
2660. .3955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%;
56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 205; Conservative
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SC8A11
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ADAIADSYTELQAVENADPTQWEESLNSTDKNLDRIGDQTDNTDVNKAVDDLGKAV
BNVRTSVENGDETPDLSPYTDAAGELTKVCTP"
COMPLement (1201. .1233)
/gene="SCE19A.03c"
/note="PSCE19A.03c"
attachment site"
complement site"
complement (1444, .2191)
/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1454. .2191)
/gene="SCE19A.04c"
/note="SCE19A.04c"
/note="S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown function, sinilar to parts of many sugar permeases e.g. TR:P96159 (EMBL:U65013), malx, Vibrio furnissii PTS (phosphoenolpyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 217 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
TGVTFAENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARWAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGQLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTABEKKALISHRGKAFRALVPVVRELLG"
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TOYRALGEWIYVLDCOVLQADGGTFRTAAITGRYVALADAVARAGGRKLIKANRKFLTG
TVSAVSOTVDGTPLLDLRYEEDVRADTDMNVVCTGDGRFVEVQGTAEARPFARDELN
TLLDLATAGCTELAELQRKALDATLER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ribonuclease PH"
protein_id="CABSO981."
/db_xref="G131353"
/translation="MSRIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV
                                                                                                                                                                                                                                          /note="SCE19A.03c, possible secreted protein, len: 134 aa;
                                                                                                                                                                                                                                                                               unknown function, probable CDS suggested by GC frameplot, positional base preference and amino acid composition. Contains probable V-terminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
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/gene="SCE19A.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1511. .2185)
/gene="SCE19A.04c"
/note="Pfam match to entry PF01138 RNase_PH, 3'
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complement(2268. .2501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative secreted protein"
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complement/???
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/note="ccm1"
                                                                                                            complement(892. .1296)
/gene="SCE19A.03c"
                                                                                                                                                                                 complement(892. .1296)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="rph"
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                                                                                                                gene
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TITLE

COMMENT

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NAHGDIAIFSLLVPELEEWINFYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
complement(3297. .7058)
/gene="SC8A11.04c"
/gene="SC8A11.04c"
/gene="SC8A11.04c"
/note="SC8A11.04c"

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/gene="SCBAll.03"
/note="SCBAll.03, possible regulator, len: 156 aa; similar
to TR:Q9S2F7 (EMBL:AL096852) Streptomyces coelicolor
putative regulator SCB19A.24, 142 aa; fasta scores: opt:
272 z-score: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                                                                                                                                                                                YTRATVADRLSTHRALAETLEGSPGRRLVHLÄAATLGPDDELAGQLERFADDAQKRGQ
LAAAVPALRQAGELVHDPRRQTGLLVRAAELASEINDRVQAQILLNRADLAEPGPTER
ARLMLVSDKAAFEPDEPQRRIQDMIDAAAGAFDVGSTSVAENLLWRAAARCFFQDGDA
                                                                                                                                                                                                                                                                                                                                                                     RVRAQAAAELDRWKPDPDAPHVLTVRAYTEPYRRGTDL1ARLEKLRPDREDGRLLHYL
GSGSWAIGDVGRATRYLAQAASVWRSOGRIGLLARSLAGSWRRLKLGDLAQAREBSAAE
GIALAEETGWIVWLGILKATSATTAVLRGEREAAARSVRELRAHSLFPVWPFASVWAO
QVEGILAALFDSRAVARAARAFDKTDPHYHSTSRWLLVPDLVDAAAAAGRNEGARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIVELPELADRLPSEMMIVARTYSTAVLAPDDTAEDCYDSALSALPDTWPLARARLHL
VGRRLLRRORRNYDARKPLRLARDEFDRVGAQPWADDAREQLRAAGESDGRRRPSKGE
SLTVQERQIABLASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
LGDDQPTSGG"
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VRAFILORAAGNPLALVELPRAAGGISPPLDDLPLTORLETAFASRTDSLTRECRTFL
                                                                                                                                                                LVLAAEPTAPLNOLLDVASRLAGSEVTVYALQEAVDAGLVVLTGRTPEFRHPLMRSAI
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/gene="SCBA11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteases, subtilase family, aspartic acid active site, PS00137 Serine proteases, subtilase family, histidine active site and PS00138 Serine proteases, subtilase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 49.10, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2184. .2453)
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complement(2184. .2453)
/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2042. .2239
/gene="SC8A11.01"
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/gene="SC8A11.03"
2787. .3257
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The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Kroph et al., Nucleic Acids Research, 22(22):478-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nin.go.jp/

in/Cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation rodon giff is sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most thorman initiation codon.
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/gene="SC8A11.01"
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/gene="Scalar"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL: http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrellGeanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, 13 John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                           3 (bases 1 to 32704)
Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
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          Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                Saunders, D.C. and Harris, D.
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                                                                                                          (bases 1 to 32704)
                                                                                                                                                                                                                          Unpublished
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                Mol. Micr
97000351
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Cosmid 5F2A.
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                                                                                                                 REFERENCE
                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                   IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGE
LLGEDVNERIVWVGGLSPGPRPYRLVLEGSRNLPDRPYSTRTRTVWDFTSATTDPTRL
TPLPLVQLDYAVAVDLSGRAHRRTELTVTASHLEGAAGAGAIRTATVEVSYDDGATWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT 05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC transporter; amino acid permease; BCCT family; carboxypeptidase; D-amino acid oxidase; ddh, dimethylarginine dimethylaminohydrolase; dehydrogenase; efflux protein; endouuclease; enoyl CoA hydratase; IPP isomerase; metallopeptidase;
                                                                                                                                                            /translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPTAPA
GPTRVLTLITGDRVTVTGEDGAETVLSVTDPHGRSGGAHVMTVGSDTYVYPDAAVPTL
GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTVQSRSPQLPEGTRAYRAVWAGDGSATEFRCAEVRDRVAVVRRSDTVAPTDQAAAAE
KAGARQLLILNDGYGKFDPWADLPEAAPLPVASLGTDDSARLLARFRGAGTTTLRVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSQGRAVEYRQDISLLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLGIVPTQVRAQGELTSWVTADDDVRWVSFASRPDLGQRGVARSYEPRSTTRETWFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                IRGAAISAEHSRAADFWTSLTGTGDAAAGGSAARSATSGGRLAGGIAKVWLDGKVRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4374. 4613)
/gene="SCBAll.04c"
/note="Pfam match to entry PF02225 PA, PA domain, score
19.00, E-value 0.058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2894 CGTICCGGCGGAGIICCGIIACGAICCCGACCACCCCCTCCTCGICACGAICCGCIICGC 2953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3014 GCGCACCACGAGCGGCCTGGGGGACGTCCAGGTGTGGGCCCGACACCCCCACACGGGGA 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 cetececeggagaegececeggteacettgggtettegggeegtgaaetgetggtegagggagt 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geogetyctcycetteetegaecycaecyaecayygettytegeteggeagegayegggge 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 catcccggtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttcca 95
family, serine active site. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGVGQTLIRAFGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2954 CCCCGAGGCCCCCCACCGGTCACCTGGCATGTCGCCCGTGACCTGCTGCACGAGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggaggtgcacatcaccetecaggteggetecgageaggegetetteegegteggeaagge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3074 GACCGCGTGGCTCCAGGTCAACGCACACGGTGACATAGCCATCTTCAGCCTGCCCGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 32704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                           /product="putative secreted peptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 77.2; DB Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor cosmid 5F2A, AL049587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3194 GCGGCTCGGAACCGACGCCTTCCTCTCCAA 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 acacgccgacttcgacagccacctcgacga 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37245 bp
                                                                                                                                    'db_xref="GI:9716215"
                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.0%;
52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.0 Best Local Similarity 52.1 Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC5F2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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á d ò a ŏ a ò g ŏ q δ 용

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codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                        Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 37245).
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-APR-1999) Streptomyces coelicolor sequencing proje Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
On May 10, 2000 this sequence version replaced gi:4584464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /jote="SC5F2A.O1c, ddah, dimethylarginine
dimethylaminohydrolase, len: 258 as; hydrolyses
asymmetrically methylated arginine with preference
dimethylated arginine over monomethylated arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 37245)
Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
regulator; thiolase; transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .37245
/organism="Streptomyces coelicolor A3(2)"

    .105
/note="Nominal overlap with cosmid 4C6"

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oxidoreductase; racemase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 37245)
Oliver, K. and Harris, D.
Unpublished
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gene

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/gene="SC5F2A.02c"
/gene="Sc
                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB40668 1"
Ab_xxref="G1:4584465"
Ab_xref="G1:4584465"
Ab_xref="SWISS-PROY: D3X7M4"
/translation="MPSKKALVRRPSPRLAEGLVTHVEREKVDHGLALEQWDAYVEAL
AGHGWETLEVEVDPADDCCPDSVFVENDAVVFRNVALITRECAESRRAEFRACKDERVARLG
CSVNNWWEPGTLDGGDYLKTGDTTYVGRGGFRNAAGVQQLRAAFEDLGARVVAPVSK
VLHLKSAVTALPDGTVIGHIPLTDVPSLFPRFLPVPEESGAHVVLLGGSRLLMAASAP
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/protein_id="CAB40669.1"
/db_xreff"Gl:4584466"
/db_xref="SPTREMBL:09X7M5"
/translation="WSEFISITGARENNLQDVTLRIPKGRLTVFTGVSGSGKSSVVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTWSTEYEGLADRFERLYLKRDLSGMSERTRDLVRGFLVEARCPDCGGARLNAAALAS
RIDGHSIADCSRMQITDLIAVLRGIDDPVALPVAGAAVAALERVEAIGLGYLSLDRET
ATLSGGEGGRLKTVRHLGSSLTGMTYIFDEPSVGLHPRDVGRLGDLLLRLRDKGNTVL
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ADGAVRFPPFAAGTWQGQTYTNTEELDTGKPYGDFTAAERAFLMRGRPGSKVTVSGSG
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VRAPTGELWYKGAERHNLREVTVAFPTGVLTAVTGVAGSGKSTLVAELTGAHPDAVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOSAIGISARSTPATYLGIMDTVRKVFARETGAEPGFFSFNSAGACGTCEGRGIIHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAFMDPVTTTCHDCEGRRFREEVLRLTVDGRSVADVLAMTAGQALGFFSDPGVRRRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALRDVGLTYLTLGQPLSTLSGGERQRIKLATRLHRTGAVYVLDEPTTGLHMSDVEGLL
ALLDRLVDAGNTVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIAVESRRQLNETFTWFVRNRLPKYERPHADALEGLTPAIVVDQRPVGGHSRSTVGTM
                                           NG.NG-dimethylarginine dimethylaminohydrolase from Homo sapiens (285 aa) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 aa overlap)." /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SC5F2A.03c, probable ABC transporter, len: 544aa; similar to many involved in antibiotic resistance egs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF00005 ABC_tran, ABC transporter, score 35.60, E-value 4e-08."
complement(3118." 3141)
/gene="SC5Ex.02c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
complement(3245. 4879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1090. .1803)
/gene="SC5F2A.02c"
/note="Pfam match to entry PF00005 ABC_tran, ABC
transporter, score 101.40, E-value 1.7e-26."
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/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
/gene="SC5F2A.02c"
(experimental). Similar to TR:D1038106 (EMBL:AB001915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (P-loop). Also contains possible membrane spanning hydrophobic regions."
                                                                                                                                                                                                                                                                                                                        /product="dimethylarginine dimethylaminohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTAELLADLGHEPVLVDIGEFEKLEGCVTCLSVRLRELYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC5F2A.03c"
/note="sc5F2A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(976. .3234)
/gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SC5F2A.02c
                                                                                                                                                                                                                             /transl_table=11
/label-ddah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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RRPDVLLLDEPTNNLDVYARRRLYAAVESWPCYMVVVSHDRELLDRVDQIADLRAGSV
TWYGGNLTAYEBALAVEQEAAERWRYAESSDLRROKRELADAQVYLARRRYGQKMYD
TKREPRAVMKLIARTAQQSAGKYRIMHEEKLAGAKERLDDAYEAVRDDDEIRVDLPYT
TYRPERAVYLTLRALEIRAVERTAGOLHGPERIALLGRNGAGTTLLRTVAGELAPV
AGEATAHVELRELDRYGLDVCLYVAENVARRAPGATNNR IRALLARRELFRGARADQ
QAATLSGGERFRAALAALMAEPAPQLLMLDBETNNLDMASVRQLTGALLARELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:09X7M6"
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GKSTLLKLIAGRLTPADGTVRVAGQVGYLPQNVTLDTALRVDEALGIDGRRAALHAIE
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TR:054381 (EMBL:X79146) from the lincomycin-production gene cluster of Streptomyces lincolnessis 78-11 (578 as) fasts accores; opt: 1624, 2-score: 1696.3, E(): 0, (50.3% identity in 541 as overlap). Contains two Pfam matches to entry PF00005 ABC_tran, ABC transporter, two Prosite matches to PS00017 AFP/GTP-binding site motif & (P-loop) and Prosite match to PS00211 ABC transporters family signature. Also contains a possible coiled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    romplement(4703...447)
/gene="SC5F2A.03c"
/note="PS00211 ABC transporters family signature."
complement(4739...4762)
/gene="SC5F2A.03c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry PF00005 ABC_tran, ABC transporter, score 122.30, E-value 9e-33" complement(3743. 3766) /gene="SCF2A.03c" /note="PS00017" ransporter pS00017" ransporter pS00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6237 CGCCGACCCGTTCGCCGTCGCATGACCTTCCCGGCCCCGGCCCTCGAGGGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgtcgatccgtacgcggtgcggctgacgttcc----acctcccggagacgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6177 GGTCTGCTGGACCTTCTCCCGCGAGCTGCTCATCGCCGGGATGCAGGAGCCGAACGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cggcgacgtccgggtcgccggtggggcagacggccaccaggggaggtgcacatcaccct
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Pred. No. 1.8;
0; Mismatches 161; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Jose="Pfam match to entry PF00005 ABC_tran, transporter, score 143.80, E-value 3.1e-39" complement(4403. .4447)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative ABC transporter"
/protein_id="CAB40670.1"
/db_xref="G1:4584467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3290. .3787)
/gene="SC5F2A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
/label=SC5F2A.03c
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/gene="SC5F2A.04"
4942. .5850
                                                                                                                                                                                                                                                                                                                                                                                                                                around 250aa.
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18.3%;
Best Local Similarity 53.9%;
Matches 209; Conservative
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Db 6006 CCAGGCGGCGGCGAGCTGGTGCCGGTGGGTCTCGAGCACCTCCAGCTGGACCTGGACCA 5947

Search completed: July 18, 2002, 11:22:05 Job time: 13735 sec

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N-methyl-D-a NMDAR2 subun

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NMDAE2C

Human Human Human

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NMDAE2C enco N-methyl-D-a N-methyl-D-a NMDAR2 subun NMDAE2C enco N-methyl-D-a N-methyl-D-a nqns NMDA recepto N-methyl-D-a N-methyl-D-a unqns

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N-methyl-D-a N-methyl-D-a unqns enco N-methyl-D-a

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clone NMDA22 NMDA recepto

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mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 3004; bioinsecticide; receptor agonist; antagonist; biomass; ds.
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AAQ79400
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AAZ38726
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/label= SsgA_protein
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 AAZ49729 standard; DNA; 407
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Sinds for godata/geneseq/geneseqn-embl/NA1981.DAT:*

Sinds for godata/geneseq/geneseqn-embl/NA1991.DAT:*

Sinds for godata/geneseq/geneseqn-embl/NA1992.DAT:*

Sinds for godata/geneseq/geneseqn-embl/NA1993.DAT:*

Sinds for godata/geneseq/geneseqn-embl/NA2001.DAT:*

Sinds for godata/geneseq/geneseqn-embl/NA2001.DAT:*

Sinds for godata/geneseq/geneseqn-embl/NA2001.DAT:*

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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WETENSCHAPPELIJK ONDERZO.
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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
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                                                                                                                                                                                                                                                                                                                                                                                                            NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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                                                                                                     a
SsgA_protein
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                                             Location/Qualifiers 1..405
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goldeniensis
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/label= 9
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Matches 305; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY44651
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                                                                                                                                                                           WO200000613-A1
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                                                                                                                                                                                                                                                                                                                                     mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesteroleamic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agents; antagonist; biomass; ds.
                                                                                                                                                                                                                                                                                                               liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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/label= SsgA_protein
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                                                                                                                                                                                                                                                           griseus ssgA gene-2.
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                                                                                                 AAZ49728 standard; DNA; 407 BP
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                                                                                                                                                                                                        (first entry)
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P-PSDB; AAY44649.
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mat_peptide
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparaslite agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibictic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                                                            accgaccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctc 360
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                                                                                        gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc
                                                                       ggetecgageaggegetetteegegteggeaaggegeegetgetegeetteetegaeege
                                  181 gtgcacatcggcccgaccgagcccgagggcttcggagatgtccacatccggctccaggtc
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                                                                                                                                                                                                                  (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces griseus ssgA gene-1.
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105;

Length 407; Indels

Score 239; DB 21; Pred. No. 1.2e-32;); Mismatches 105;

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Conservative

Similarity

Query Match Best Local Simi Matches 302;

58.7%; 74.2%;

61 accgrcgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacc 120 gleggegatecgtatgecatecggatgaegttecaeetteeeggegatgeeeetgtgaee 120 tgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcgggcgacggcgac 180

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P-PSDB; AAY44652
                                              Disclosure; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ssgA: liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agonist; antagonist; blomass; ds.
                                                                                                    accgicgatecgiaegeggiegegetgaegitecaecteceeggagaegeeeeeggieaee 120
                                                                                                              gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc 240
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                                                Gaps
                                                                          1 atgagetteetegteteegaggagetegeetteegeateeeggtggagetgeggtaegag 60
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                           Length 438;
                                              Indels
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                                                                                                                                                                                                                                                                                                       72 T; 0 other;
                           Score 239; DB 21;
Pred. No. 1.2e-32;
0; Mismatches 105;
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A; 145 C; 153
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces netropsis ssgA gene.
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                          58.7%;
ilarity 74.2%;
Conservative
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(NEWE-) NEDERLANDSE ORG W
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                           Query Match
Best Local Similarity
Matches 302; Conserv
BP;
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Sequence 438
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transgenic plant; insect resistance;
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 407 BP; 63 A; 151 C; 131 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 224.6; DB 2
Pred. No. 3.3e-30;
                                                                                      5; 60pp; English.
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Best Local Similarity 72.0%;
Matches 293; Conservative (
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Saccharopolyspora spinosa.

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                                                                                                                                                                                                                                                                                                     This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide corresponding calycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raise specific antibodies, useful for identifying corpusations of the significantly increased levels or produce new derivatives of (II) at significantly increased levels or produce new derivatives of contains the coding regions for proteins involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                               New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21072 TCAACCTGGTAGCCCCGGCGGGGTGTATCGCGCCAGTCGGCGTGGAGCTGCGGTACGACA 21013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 cogtogatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacct 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forosamine; trimethylrhamnose; polyketide synthase; biosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance; macrolide; insecticidal; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 22; Length 45624;
Pred. No. 0.00012;
0; Mismatches 75; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45624 BP; 7933 A; 14913 C; 14940 G; 7838 T; 0 other;
                                                                                                                   Salas JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corosamine and trimethylrhamnose biosynthesis.
                                                                                                                   Velten R,
                                                                                                                                                                                                                                                                             Claim 7; Page 58-74; 354pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. spinosa DNA fragment SEQ ID 1.
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                                                                                                                   Froede
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Best Local Similarity 61.1%;
Matches 118; Conservative
99DE-1057268
                                       99DE-1040596
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                                                                                                                Eberz G, Moehrle V,
                                                                                                                                                        WPI; 2001-267102/28.
                                                                            (FARB ) BAYER AG.
29-NOV-1999;
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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in blosynthesis of spinosyns. (I) are used (I) to identify, inactivate or modulate genes involved in the blosynthesis of adding forosamine or trimethylthamnose to a spinosyn or polyketide adding forosamine or trimethylthamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are marchides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding requines for proteins involved in forosamine, trimethylrhamnose and polyketide synthase biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
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                                                                                                                                                                                                                                                                                                          Salas JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 17.9%; Score 73; DB 22; Best Local Similarity 61.1%; Pred. No. 0.00012; Matches 118; Conservative 0; Mismatches 75;
                                                                                                                                                                                                                                                                                                      Velten R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 14-31; 354pp; German.
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                                                                      99DE-1057268
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                                                                                                                                                                                                                                                                                                      Moehrle V,
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                                                                                                                                                                                                                           (FARB ) BAYER AG.
                                                                                                                                                 27-AUG-1999;
                                                                      29-NOV-1999;
08-MAR-2001
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246 cgagcaggcgctcttccgcgtcggcaaggcgccgctgctcgccttcctcgaccgcaccga 305

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1375 cgtcaccggccgcggcggcgaggcctgcgcgcccaggcccggcgctgcacgaggccgt 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces venezuelae vep ORP1 (AAT68715) comprises the polyketide synthase (RKS) gene cluster encoding a polyene of 12 carbons (see also AAM19629-30 and AAW00918). It contains 5 PKS modules, with a 5'loading module and a 3' end domain. Each of the sequenced modules includes a keto-ACP, an acyltransferase, a dehydratase, a keto-reductase and an acyl carrier protein domain. The gene cluster was cloned using a heterologous hybridisation strategy from a genomic DNA library. A novel expression cassette encoding the first module from the vep gene cluster and module 7 from the Streptomyces tylp gene cluster has polyhydroxyalkanoate (PHA) monomer synthase activity and can be used for PHA prodn. in host (esp. insect) cells for use as a biodegradable polymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacctgggt 125
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                                 monomer synthase;
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                            Polyketide synthase; polyhydroxyalkanoate monomer syn
polyhydroxybutyrate; biodegradable polymer; vep gene;
Streptomyces venezuelae polyketide synthase vep ORF1,
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Pred. No. 0.017;
0; Mismatches 202;
                                                                                                                           Location/Qualifiers
20..13912
/*tag= a
14056..14136
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Best Local Similarity 47.4%;
Matches 182; Conservative C
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14148..15827
                                                                                                                                                                                                                                                                                                                            96WO-US20119.
                                                                                                                                                                                                                                                                                                                                                            95US-0008847.
                                                                metabolic engineering; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Williams MD,
                                                                                                Streptomyces venezuelae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        industrial use
                                                                                                                                                                                                                                                                                                                                                            19-DEC-1995;
                                                                                                                                                                                                                                                             WO9722711-A1
                                                                                                                                                                                                                                                                                                                            18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sherman DH,
                                                                                                                                                                                                                                                                                          26-JUN-1997
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comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic
                                                                                                                                                                                                                                                                                                                               synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Figure 23; 438pp; English.
                                                                                                                                                                                               P-PSDB; AAY77177, AAY77178, AAY77199
                                                                                Zhao L;
                                                                                     Xue Y,
(MINU ) UNIV MINNESOTA.
                                                                                Liu H,
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                                                                                     Sherman DH,
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1435 cgaagcggacccggagctcgcgccggccgcctcgcccggtcgctggtcaccaccaccgtac 1494

ggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtcggctc 245

ggtcttcacgcaccggtcggtcgtcctcgccccggaccgccccgcctcctcgacggcct 1554

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cttcgggcgtgaactgctggtcgagggagtcctggacgcggggggacggcgacgtccg 185

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(AAY77199)"
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                                                                                                                                                                                                                                                                                                                                                   /product= "vep ORF 1 amino acid sequence #1 (AAY77177)"
                                 The invention relates to an isolated and purified nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                                                                                                                                              Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromyc;
neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase;
biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma,
chronic obstructive pulmonary disease; respiratory inflammation;
hypercholesterolaemia; crop protection agent; ds.
1615 gegeetegeegteetgtteageggeeaagggtgeeeaaegtaegggeatgggeatggagtt
                     306 ccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctcgacga
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/product= "vep ORF 1 amino acid sequence #3
1467..15827
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                                                                                                                                                                                                          venezuelae vep ORF 1, SEQ ID NO:1.
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20..13912
                                                                           Streptomyces venezuelae ATCC15439
                                                               cgctctgaaccgcagcctcgccga 389
                                                                                                                                           AAZ87283 standard; DNA; 15872 BP.
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1..1155

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proteins are useful for synthesis of methymycin, pikromycin, comethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biomedically active agents, such as chemotherapeutics, in packaging or immunosuppressants, agents to treat asthma, chronic obstructive pulmonary cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents a Streptomyces venezuelae APCC 15439 DNA sequence, designated vep OMF 1 in the specification, which actually contains 3 open reading frames, which encode proteins AAY7177-Y7178 and AAY717199. The vep OMF 1 protein is defined in the specification as a PHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15872 BP; 2088 A; 6304 C; 5513 G; 1967 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.8; DB 21;
Pred. No. 0.017;
0; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a CalH transaminase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1735 cctcctcgaccggcccctcgccga 1758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.9%;
Best Local Similarity 47.4%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   monomer synthase
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Location/Qualifiers

Key

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polynuclectides and polypeptides can also be used to confer calicheamicin resistance to a subject, e.g. by using gene therapy. Human bone marrow cells can be transformed with calc gene and returned to the patient allowing the patient to tolerate calicheamicin treatment and be able to receive higher doses of calicheamicin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a CalH protein of Micromonospora echinospora. The protein is TDP-6 deoxy-D-glycerol-L-threo-4-hexulose 4-transaminase. The gene is present on the nonchromoprotein enediyne blosynthetic gene cluster. The calicheanicin gene cluster can be genetically manipulated to produce calicheanicin analogues. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 tacgoggtgcggctgacgttccacctccccggagacgccccggtcacctgggtcttcggg 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tacccggtggacctcaaccggctgcgcgccgtcgtggaccgggccacggcgggatacgac 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 ggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctcgacgacgc
                                                                                                                                                                                                                                                                                                                                                 Novel Micromonospora echinospora gene cluster which codes for calicheamicin biosynthesis polypeptides, used for production of calicheamicin compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.5%; Score 59; DB 21; LA Best Local Similarity 52.2%; Pred. No. 0.048; Matches 156; Conservative 0; Mismatches 140;
                              /product= "CalH protein"
/transl_except= (pos: 1..3, aa:
                                                                                                                                                                                                                       SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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                  /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                     Page 35; 53pp;
                                                                                                                                                                                                                                                                                                                                                                                   calicheamicin compounds
                                                                                                                                                                                                                                                                                            WPI; 2000-442652/38.
                                                                                                                                                                                                                                                                                                                P-PSDB; AAY93894
                                                                                   WO200037608-A2
                                                                                                                                                                                        07-DEC-1998;
                                                                                                                   29-JUN-2000
                                                                                                                                                                                                                                                             Thorson J;
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The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 31-40. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce
Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB07580, AAB07581, AAB07582, AAB07583, AAB07584, AAB07585,
AAB07586, AAB07587, AAB07588, AAB07589.
                      BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine; thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules -
                                                                                                                                  /transl_except= (pos: 1..3, aa: Met)
/note= "ORF31; encodes AAB07580"
925..9450
                                                                                                                                                                                                                                                                                                                                                                 transl_except= (pos: 1..3, aa: Met)
note= "ORF37; encodes AAB07586"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "ORF40; encodes AAB07589"
/note= "no termination codon given"
                                                                                                                                                                      /*tag= b
/note= "ORF32; encodes AAB07581"
9447..10802
                                                                                                                                                                                                        *tag= c
note= "ORF33; encodes AAB07582"
0864..11877
                                                                                                                                                                                                                                                      note= "ORF34; encodes AAB07583"
11888..12640
*tag= e
                                                                                                                                                                                                                                                                                           note= "ORF35; encodes AAB07584"
                                                                                                                                                                                                                                                                                                                              "ORF36; encodes AAB07585"
                                                                                                                                                                                                                                                                                                                                                                                                                 "ORF38; encodes AAB07587
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                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             'note= "ORF36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "ORF3
17646..18659
                                                                                                                                                                                                                                                                                                         ..13920
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05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
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                                                                        Streptomyces verticillus.
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/note=
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branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazolidne, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
                                                                                                                                                                                                                                                                                                                                                                                               5484
                                                                                                                                                                                                                                                                   5305 gagacgetgeggacggegttegtegageggaeggggtgeeeeaceaggtggteteggeg 5364
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                                                                                                                                                                                                                                                                                                                                   5365 cccgacgccgccggcgcgcgcgcgcgcggcggcggaggtcgtgcggatcgaggcggccgggcgg 5424
                                                                                                                                                                                                                                        43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctcccc 102
                                                                                                                                                                                                                                                                                                  103 ggagacgcccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac 162
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                163 gccgcgggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg
                                                                                                                                                                                                                                                                                                                                                                                             223 cacatcacctccaggtcggctccgagcaggcgctcttccgcgtcggcaaggcgccgctg
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/product= C-terminal 946 a.a of NMDAR2C receptor
                                                                                                                                                                            Length 18660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 18660 BP; 2365 A; 7239 C; 6510 G; 2546 T; 0 other;
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                                                                                                                                                                          14.3%; Score 58.4; DB 21; Length 50.0%; Pred. No. 0.043; ive 0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NMDAR2 receptor subunit clone NMDA26 gene.
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189..3025
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                                                                                                                                                                                                           Matches 146; Conservative
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                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-341863/42.
P-PSDB; AAR66060.
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                                                           The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)

receptor 2C (NMDARAC) gene clone NWDA26. This clone covers bases 1-3025

of the complete NMDARAC gene (AAQ79372), thus lacks the 3' 1043 bases.

CT he NMDA receptor contains two subunits and lacks the 3' 1043 bases.

CT he NMDA receptor forms the subunits 2A (AAQ79375), 2B (AAQ79377), 2C

and 2D (AAQ79378). The receptor forms part of a family of NMDA receptors

WICH have cation-selective channels and bind glutamate and NMDA. The

NMDARC gene was obtained by amplifying cDNA derived from human brain

tissues with primers corresponding to sequences in the rat NMDAR2A

receptor DNA and using the resultant fragments as probes to screen a cDNA

receptor DNA and using the resultant fragments as probes to screen a cNMDA21 (AAQ79402). The clones are thought to be splice variants of each other.

Based on the sequence of the 4 clones, a series of variants of each other.

CS the NMDA21 creeptor were constructed. The expression of the genes

CA 110 can be used to identify compounds which bind or are antagonistic to the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNAl; NMDA receptor; antagonist; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggagacgccccggtcacctgggtcttcggggcgtgaactgctggtcgagggagtcctggac 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gccgcgggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctcccc 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccttcgccgtcatcaccagcctgcacccgggccacgcgctcttcctggagggcgtgcgc 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gccgtcgccgacgccagccacgtgagttggcggctgctggacgtggtcacgctggaactg 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 cacatcaccetecaggteggeteegageaggegetetteegegteggeaaggegeegetg 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          858 tttgtggcctactgctcgcggaggaggccgaggtgctcttcgccgaggcggcgaggcc 917
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaccogggagggccgcgcgcgcacgcagcgcctgctgcgccagctcgacgcgccgtg

    used as probes in the identification and isolation of

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0
                                                                                                                                                                                                                                                                                                                                                                        Length 3025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 gacticgacagccaccicgacgacgcictgaaccgcagccicgccgagg 391
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                             Sequence 3025 BP; 526 A; 1017 C; 926 G; 556 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               918 ggtctggtggggcccggccacgtgtggctggtgcccaacctggcgctgg
           nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                     Score 56.2; DB 15;
Pred. No. 0.13;
); Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NMDAR2 receptor subunit clone NMDA22.
                                      Claim 11; Page 99-104; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ79400 standard; cDNA; 3698 BP.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                     NMDA receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ79400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from human brain tissues with primers corresponding to sequences in the rat NMDAR2A receptor DNA and using the resultant fragments as probes to screen a cDNA library derived from human hippocampal RNA. 4 basic clones were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), MMDA24 (AAQ79401) and NMDA26 (AAQ79402). The clones are thought to be splice variants of each other Based on the sequence of the 4 clones, a series of variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of the genes allows the reconstruction of the NMDA receptor. The complete receptor can be used to identify compounds which bind or are antagonistic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 ggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 geettegeegteateaceageetgeaceegggeeacgegetetteetggagggegtgege 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                /*tag= c
/note= "15 bp deletion of NMDAR2C sequence between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 gtgtccctggagcagcagctgcaggtgctgttcaaggtgctggaagagtacgactggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 giggagetgeggtaegagaeegtegateegtaegeggtgeggetgaegtieeaeeteeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geogegggegaegteegggtetgeeegggggaggeagaeggeeagggaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 gecgtegecgaegecagecacgtgagttggeggetgetggaegtggteacgetggaaetg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                    /*tag= b
/note= "11 bp insertion found in this clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3698 BP; 610 A; 1280 C; 1164 G; 644 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56.2; DB 15;
Pred. No. 0.12;
0; Mismatches 183;
                              NMDA22 variant NMDAR2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 99-104; 156pp; English.
                                                                                                                                                                                                                                                                                              these bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liaw CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%;
47.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0052449
                              /product= N
1034..1045
/*tag= b
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                                                                                                                                                                              1604..1605
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Best Local Similarity 47.6
Matches 166; Conservative
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-341863/42.
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Sequence 3698 BP; 612 A; 1283 C; 1159 G; 644 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA95032;
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             AAA95032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human N-methyl-D-aspartate (NMDA) receptor subunit (NMDAR). The nucleic acid sequence does not contain the 366 5'-most nucleotides, has an additional 11 nucleotides between nucleotides 1300 and 1301, nor the 15 nucleotides at positions 1960-1974, nor the 1061 3' nucleotides, as set forth in AAV82889. The CDNA sequence is derived from clone NMDA22. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate receptors can be assembled from several NMDA receptor subunit proteins of one type (homomeric) or from combinations of subunit proteins of different types (heteromeric). The present invention also comprises methods for using such receptor subunits to identify and characterise compounds which affect the function of such receptors, e.g. agonists, and anagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are functional as NMDA receptor subunits.
            432 gacccgggagggccgcgcgcgcgcacgcagcctgctgctgcgccagctcgacgcgccgtg 491
                                                                                                                                                                                                                                                                                             NMDA-activated cation-selective ion channel; glutamate receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding N-methyl-D-aspartate receptor subunit - useful for the
                                                              tttgtggcctactgctcgcgcgaggaggccgaggtgctcttcgccgaggcggcgcaggcc
                                      gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg 391
                                                                                                     Human N-methyl-D-aspartate receptor subunit clone NMDA22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assembly of functional glutamate receptor subunits
                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= NMDA_receptor_subunit
/note= "no termination codon"
                                                                                                                                                                                                                                                                                  N-methyl-D-aspartate receptor; NMDAR2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Columns 253-262; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                              AAV82909 standard; cDNA; 3698 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0231193.
93US-0052449.
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                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                            .3698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ľ C;
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                                                                                                                                                                                                                                23-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-1994;
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                                                                                      343
                                     283
                                                              492
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AAV82909
ID AAV8
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/transl_except= (pos:3681..3683,aa:Xaa)
/note= "this sequence contains a number of in-frame
stop codons, represented by Xaa in the protein sequence"
/partial
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                                                                                                                                                                                              43. gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctcccc 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282
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                                                                                                                                                                                                                                                                                             252 gigicociggagcagcagcigcaggigcigitcaaggigcigcigaagagiacgaciggagc 311
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                                                                                                    Gaps
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glutamate receptor; drug screening; animal model; disease diagnosis;
genetic screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                            103 ggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 geogtegeogaegecagecacqtgagttggeggetgetggaegtggteacgetggaactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 gecttegeegteateaceageetgeaceegggeeacgegetetteetggagggggtgege
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432 gaccegggagggccgcgcgcgcgcacgcacgcctgctgcgccagctcgacgcgcccgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 tttgtggcctactgctcgcgcgaggaggccgaggtgctcttcgccgaggcgcgcaggcc
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Length 3698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 ggtctggtggggcccggccacgtgtggctggtgcccaacctggcgctgg 600
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (pos:912..914, aa:xaa)
(pos:978..986, aa:xaa)
(pos:1041..1043, aa:xaa)
(pos:1266..1268, aa:xaa)
(pos:1392..1394, aa:xaa)
(pos:1392..1394, aa:xaa)
(pos:1503..1508, aa:xaa)
(pos:1503..1508, aa:xaa)
(pos:2136..2237, aa:xaa)
(pos:2232..2237, aa:xaa)
(pos:22444..2546, aa:xaa)
(pos:2544..2546, aa:xaa)
(pos:3027..3029, aa:xaa)
(pos:3027..3029, aa:xaa)
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                                                                                               0; Mismatches 183;
Score 56.2; DB Pred. No. 0.12;
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                                                                                                    166; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit for identifying mutations and for developing drugs against various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctccc 102
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                                                                                      97US-0940086
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93US-0052449
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20-APR-1993;
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               US6111091-A.
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Search completed: July 18, 2002, 11:36:31 Job time: 11256 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries

    nucleic search, using sw model

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US-08-940-086A-43
US-08-940-086A-53
US-08-940-086A-53
US-08-940-035A-65
US-08-940-035A-69
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Sequence 5, Appli Sequence 5, Appli	Sequence 51, Appl Sequence 51, Appl	51,	Sequence 51, Appl Sequence 45, Appl	45, 1	45,	45,	Sequence 45, Appl	Sequence 1, Appli	Seguence 17, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 7, Appli
US-08-940-086A-5 US-08-940-035A-5	US-08-231-193A-51 US-08-486-273A-51	US-08-480-474-51 US-08-940-086A-51	US-08-940-035A-51 US-08-231-193A-45	US-08-486-273A-45	US-08-480-474-45	US-08-940-086A-45	US-U8-94U-U35A-45 TS-08-125-468-1	US-08-474-933-1	US-08-510-646B-17	US-09-103-840A-1	US-09-130-114-2	US-08-804-227C-7
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ALIGNMENTS

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1375 cgicaccggccgcggcggcgaggccctgcgcgcccaggcccggcgcctgcacgaggccgt 1434
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                                                                                                                  APPLICANT: JULY, H.
APPLICANT: LAW, Y.
APPLICANT: ALW, Y.
APPLICANT: Chao, L.
TILLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEO ID NOS: 43
SOFTWARE: FastSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60.8; DB 4;
Pred. No. 0.00059;
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                         Sequence 1, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces venezuelae US-09-105-537-1
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nilarity 47.4%;
Conservative
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Best Local Similarity
Matches 182; Conserv
                                                                         GENERAL INFORMATION: APPLICANT: Sherman,
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LENGTH: 15872
US-09-105-537-1
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APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involued In The
TITLE OF INVENTION: Bolsynthesis of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
86 tgacgitccaccicccggagacgccccggicaccigggicticggggggigaactgctgg 145
                                                                            146 tcgagggagtcctggacgccgcgggggacgcgacgtccgggtctgcccggtggggaga 205
                                                                                                        266 teggeaaggegeegetgetegeetteetegaeegeaeegaeeagggettgtegeteggea 325
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STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
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APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03806.0054-01000
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FILING DATE: 03-AUG-125.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-510-646B-14; Sequence 14, Application US/08510646B patent 0. 6077699; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blanc, Veronique
Blanche, Francis
Crouzet, Joel
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Thibaut, Denis
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                                                                                                                                                                                                                                                                                                                                                                                                               386 ccgaggagcag 396
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APPLICANT:
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PEPLICANT: De Crecy-Lagard, Valerie
PEPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
CORRESPONDENCE ADDRESS:
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STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/FR 93/00923 FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 92/11441 FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                          Sequence 14, Application US/08403852D
Patent No. 5811695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                        1735 cetectegaceggeeectegeega 1758
  366 cgctctgaaccgcagcctcgccga 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: _______USA
ZIP: ________SU005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS ________
SOFTWARE: Patania
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Nathalie
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Thibaut, Denis
                                                                                                                                                                                                                             Blanche, Francis
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TYPE: nucleic acid
STRANDEDNESS: double
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OTHER INFORMATION:
US-08-403-852D-14
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HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                Crouzet,
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                                                                                                   RESULT 2
US-08-403-852D-14
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Best Local Simi
Matches 152;
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APPLICANT:
APPLICANT:
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APPLICANT:
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STRANDEDNESS:
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US-08-231-193A-43
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VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide S
VENTION: Coding For These Polypeptides And Their Use
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STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                       Length 474;
                                                                                                                                                                                                                                                                                                                                                                   Score 56.6; DB 3; Length 4
Pred. No. 0.0039;
0; Mismatches 159; Indels
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Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                                                                                                                                                                                                        ORGANISM: S.pristinaespiralis
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APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
                   TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERSTICS:
LENGTH: 474 base pairs
(202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                   13.9%;
48.9%;
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Best Local Similarity 48.99
Matches 152; Conservative
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                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                          ; LOCATION: 1..474
; OTHER INFORMATION:
US-08-510-646B-14
                                                                                                                                            MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                           NAME/KEY: CDS
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 TELEPHONE:
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COUNTRY:
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APPLICANT:
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Pred. No. 0.0039;
0; Mismatches 159; Indels
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                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATOMNEY/AGENT INFORMATION:
NAME: MAYORS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
RELECOMMUNICATION: NEORMATION:
                                                                                                                                     US/09/231,818
COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.pristinaespiralis
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 48.9%;
Matches 152; Conservative
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                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
NO
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Sequence 43, Application US/08486273A
Patent No. 5985586
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Lils, Steven B.
APPLICANT: Lils, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES:
ADDRESSEE: Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · 43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctcccc 102
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                                                           Score 56.2; DB 2; Length 3 Pred. No. 0.0044; 0; Mismatches 183; Indels
                                       343 gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REALABLE FORPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,273A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 108/08/231,193
FILING BAPLICATION STAR:
APPLICATION NUMBER: 20-APR-1994
CLASSIFICATION STARS
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 6362-9383B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.6%;
Matches' 166; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence LOCATION: 3...3698
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 92101-2926
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Diego
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US-08-486-273A-43
                                                                                                                                                                       RESULT 6
US-08-486-273A-43
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                                                                                                                                        APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
WUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 cacatcaccctccaggtcggctccgagcaggcgctcttccgcgtcggcaaggcgccgctg
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CURRENT APPLICATION DATA:

APPLICATION NUBBER:

FILING DATE: 20-APP-1994

CLASSIFICATION NUBBER: US 08/052,459

FILING DATE: 20-APP-1994

CLASSIFICATION DATA:

APPLICATION NUBBER: US 08/052,459

FILING DATE: 20-APR-1993

CLASSIFICATION NUBBER: 33,79

REGISTRATION NUBBER: 33,779

REGISTRATION NUBBER: 33,779

REGISTRATION NUBBER: 33,779

REGISTRATION NUBBER: 33,779

RELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEPHONE: 619-238-0999
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                                                                                                                                                                                                                                                                                                    ADDRESSEE: Brown, Martin, Haller & McClain STREET: 1660 Union Street CITY: San Diego STATE: CA STATE: CA COUNTRY: U.S.A. ZIP: 92101-2926
Sequence 43, Application US/08231193A Patent No. 5849895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 166; Conserva
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APPLICANT:
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APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun W.
APPLICANT: Lu Chin-Chun W.
APPLICANT: Lu Chin-Chun Wann N.-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR THEREFOR CORRESPONDENCE ADDRESS:
ADDRESSE: Heller Ehrman White & McAuliffe
                                                                                                                                                 491
                                                                                                                                                                                                     283 ctcgccttcctcgaccgcaccgaccagggcttgtcgctcggcagcgaggggcacacgcc 342
  163 gccgcgggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg 222
                                                                                                  223 cacatcaccetecaggteggetecgageaggegetetteegegteggeaaggegeegetg 282
                                                                                                                                                                                                                                                    551
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                                                 372 GCCGTCGCCGACGCCACGTGAGTTGGCGGCTGCTGGACGTGGTCACGCTGGAACTG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,086A
FILING DATE: 29-SEPT-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/052,449
FILING DATE: 20-APR-1993
ATTORNEX/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Heller Ehrman White & McAuliffe : 4250 Executive Square, 7th Floor La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 56.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9383C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 43, Application US/08940086A
; Patent No. 6111091
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
TELEPHONE: (619) 450-8400
TELEPAX: (619) 450-8499
INFORMATION FOR SEQ ID NO: 43:
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; LOCATION: 3...3698
US-08-940-086A-43
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LENGTH: 3698 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lia, Chin-chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: Brown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
223 cacatcaccetecaggteggetecgageageagegetettecgegteggeaaggegeegetg 282
                                                                                                43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctccc 102
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                                              432 GACCCGGGAGGCCGCGCGCGCGCACGCAGCGCCTGCGCCCAGCTCGACGCGCGCCCGTG 491
                                                                                                                                    492 TITGIGGCCIACTGCTCGCGCGAGGAGGCCGAGGTGCTCTTCGCCCGAGGCGGCGCGAGGCC 551
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Pred. No. 0.0044;
0; Mismatches 183; Indels 0
                                                                                                                                                                                                343 gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6362-9382B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/480,474
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/08480474 Patent No. 6033865 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFRENCE/DOCKET NUMBER: 6362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPAX: 619-238-0962.
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 3698 base pairs
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Best Local Similarity 47.6%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 92101-2926
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; LOCATION:
US-08-480-474-43
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Sequence 53. Application US/08231193A
Patent No. 5849895
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 giggagoigoggiacgagaccgicgaiccgiacgcggiggcggcigacgiiccacciccc 102
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                                                                                                                                                                                                                                                                                                                                                                                                                        312 GCCTTCGCCGTCATCACCAGCCTGCACCCGGCCCACGCGCTTTCCTGGAGGCCGTGCGC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 gccgcgggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 grgrcccreeaecaecaecrecaegrecrerrcaaegrecresaaeaeracaecaece 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 GCGTCGCCGACGCCACGTGAGTTGGCGGCTGCTGGACGTGGTCACGCTGGAACTG
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                                                                                                                                                                                                  Length 3698;
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                                                                                                                                                                                                Score 56.2; DB 4; Length 3 Pred. No. 0.0044; 0; Mismatches 183; Indels
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COUNTRY:

IN S.A.

IP: 92101-2926

COMPUTER READABLE FORM:

MEDTION TYPE: FORD

OPERATING SYSTEM:

OPERATING SYSTEM:

OPERATION NUMBER: DETONORM:

APPLICATION NUMBER: US/08/231,193A

FILING DATE: 20-APR-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/231,193A

FILING DATE: 20-APR-1994

CLASSIFICATION: 536

PRIOR APPLICATION: 536

CLASSIFICATION: 536

CLASSIFICATION: 536
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STREET: 1660 Union Street
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NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
                                                                                         NAME/KEY: Coding Sequence LOCATION: 3...3698
                                                                                                                                                                                                  Query Match
Best Local Similarity 47.68;
                                                                                                                                                                                                                                                Conservative
  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                           MOLECULE TYPE: CDNA
                           linear
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US-08-940-035A-43
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US-08-231-193A-53
                                                                                                                                                                                                                                              Matches 166;
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                                                                    FEATURE
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: HUMAN N'METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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                                                                                                                                                       103 ggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac 162
                                                                    giggagcigcggiacgagaccgicgaiccgiacgcggigcggcigacgiiccacciccc 102
                                                                                                                                                                                     223 cacatcaccetecaggicggetecgageagegeteteegegegegegeaggegeegetg 282
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                           Gaps
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47.6%; Pred. No. 0.0044;
tive 0; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, 7th Floor CITY: La Jolla STATE: CA COUNTRY: U.S.A.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6362-9383E
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/08940035A Patent No. 6316611 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 33,779
RELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPAX: 610-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3698 base pairs
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                         Matches 166; Conservative
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    Best Local Similarity
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) NAME/KEY: CDS
; LOCATION: 189..3833
US-08-486-273A-53
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MOLECULE TYPE: cDNA
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CITY: San Diego
STATE: CA
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Sequence 53. Application US/08486273A
Patent No. 5985586
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            738 GCCGTCGCCGACGCCACGTGAGTTGGCGGCTGCTGGACGTGGTCACGCTGGAACTG 797
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Pred. No. 0.0044;
0; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Brown, Martin, Haller & McClain
1660 Union Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,273A
FILING DATE: 06-JUN-1995
REFERENCE/DOCKET NUMBER: 6362-9383
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-099
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                              Query Match 13.8%;
Best Local Similarity 47.6%;
Matches 166; Conservative
                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 189..3833
US-08-231-193A-53
                                                                                                                                                        TOPOLOGY: both
MOLECULE TYPE: CDNA
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STREET: 16
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Sequence 53, Application US/08480474
Patent No. 6033865
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chin-Chun
TITLE OF INVENTION: SAME AND USES THEREFOR
NUMBER OF SEQUENCES:
ADDRESSEE: Brown, Martin, Haller & McClain
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Pred. No. 0.0044;
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1660 Union Street
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                  NAME: Seidman, Stephanie
REGISTRATION UNUBER: 33,779
REFRENCE/DOCKET NUMBER: 6362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0099
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.8%;
Best Local Similarity 47.6%;
Matches 166; Conservative
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Patentin Release #1.0, Version #1.25
                                                                                                                                               OPERATION OF SECULDATION OF SECULDATION OF SECULDATION OF SECULDATION DATA:
APPLICATION NUMBER: US/08/940,086A FILING DATE: 29-SEPT-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
FILING DATE: 20-APR-1994
FILING DATE: 20-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Seephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9383C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 24735-9383C
TELECOMMUNICATION NUMBER: 24735-9383C
TELEFRAX: (619) 450-8499
INFORMATION FOR SEO ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base palis
                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     Floppy disk
                                                                                 COMPUTER READABLE FORM:
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       La Jolla
                                                                                                     MEDIUM TYPE:
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                                                             92037
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US-08-940-086A-53
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                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chu W.
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NATA:
APPLICATION NUMBER: US/08/480,474
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.2; DB 3;
Pred. No. 0.0044;
0; Mismatches 183;
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                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779-
REFERENCE/DOCKET NUMBER: 6362-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
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ilarity 47.6%;
Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                              both
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Best Local Simi
Matches 166;
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US-08-480-474-53
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  Length 4002;
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13.8%; Score 56.2; DB 3; Length 4 47.6%; Pred. No. 0.0044; tive 0; Mismatches 183; Indels
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US-08-940-035A-53
Sequence 53, Application US/08940035A
Patent No. 6316611
GENERAL INFORMATION:
                                                Matches 166; Conservative
                            Similarity
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APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 0.0044;
0; Mismatches 183; Indels 0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: J.C.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383
TELEPAN: 619-238-099
TELEPAN: 619-238-099
TELEPAN: 619-238-099
TELEFAX: 619-238-099
TELEFAX: 619-238-0962
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 4017 base pairs
                                                                                                         RESULT 15
US-08-231-193A-49
; Sequence 49, Application US/08231193A
; Patent No. 5849895
; Patent No BAPERALION:
APPLICANT: Daggett, Lorrie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.8%;
Best Local Similarity 47.6%;
Matches 166; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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US-08-231-193A-49
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                                                                 APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
UNMER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0044;
0; Mismatches 183; Indels 0
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: THE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,035A
FILING DATE: 29-SEPT-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                  E: Heller Ehrman White & McAuliffe 4250 Executive Square, 7th Floor
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NAME: Setionan, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362
FELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-099
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 4002 base pairs TYPE: nucleic acid STRANBONESS: both
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Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
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Best Local Similarity 47.6'
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 189..3833
US-08-940-035A-53
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MOLECULE TYPE: CDNA
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Search completed: July 18, 2002, 11:25:01 Job time: 10891 sec

AQ851215 LMAJEV1_] BG263173 WHE2337_F AQ848096 LMAJFV1_

Perfect score:

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Scoring table: Sequence:

Searched:

Database

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- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp., the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC chones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                    925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BARH9D16 of RPCI-98 library from Drosophila melanogaster (fruit AL053013 AL053013. I GI:4934461
                                                                                                                                               AG049228 Pan trog1
AO849292 LMAJFV1_1
BL953854 HVSMEM01
AL565998 AL569998
AL569103 AL569103
BF55377 HVSMEf000
BF483973 WHE2306_G
BG357234 OVZ_11_E0
BG357931 LG1_Z24_G
                                                            BI726984 1031088H0
AL106054 Drosophil
AM566001 LG1_354, H
BG366417 HVSME1000
AL066742 Drosophil
BE230578 99AS792 R
AI833435 605089D02
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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JOURNAL
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 (without alignments)
1139.217 Million cell updates/sec
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AQ846145 LMAJFV1_1
BE496966 WHE0763_A
BE593775 WS1_102_A
AV938413 AV938413
AL508175 AL508175
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AG076818 Pan trog1
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AL053013 Drosophil
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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/organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98"

AL066742 Drosophil BI511102 BB160004B BG263550 WHE2343_C AQ852321 LMAJFV1_1

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Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; no bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

| Location/Qualifiers | Location Gual/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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RESULT CNS0091P

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306

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

source

FEATURES

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Per 19 years of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical mappen of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jons's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 SBBSCTSTSSSSSSSSSSSTSSCCCCCSYSYSSSTSSSSSSTSWGSTSGSSSSSSSSS 797
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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                                                                                                                                                            Length 925;
511 others
                                                                                                                                                            Score 64.2; DB 12;
Pred. No. 0.88;
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3

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us-09-749-185-4.rst

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing: a resource for DNA microarrays and expression
filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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LMAJFV1_Im15c01.y1 Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm15c01 5' similar to contains element 212bp.2 leishmania repetitive element ; DNA
                                                                                                                                                                                                                                                                                                                                                                               ggctgacgttccacctccccggagacgccccggtcacctgggtcttcgggcgtgaactgc 142
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Leishmania.
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Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
                                                                          1. .935
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/clone_lib="RPCI-98"
/clone="BACR14N09"
/note="end: T7"
                                                                                                                                                                             250
                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                            Conservative 104; Mismatches 165;
                                                                                                                                                                                                                                                           Pred. No. 0.88;
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                                                                                                                                                                                                                                           15.8%; Score 64.2; 29.5%; Pred. No. 0.
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/clone="LmAJFV1_m15c01"
/clone="LmAJFV1_m15c01"
/clone=lib="Leishmania major FV1 random genomic library"
/lab_host="ToP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline Phosphatase and ligated into pZero-2 vector's EcoRV site."

12 c 167 g 30 t
                                                                                                                                                                                                                                     DNA Sequencing by: Washington University Genome Sequencing Center If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. Seq primer: -40RP from Gibco
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WHE0763_A05_A092S Wheat heat stressed seedling cDNA library Triticum aestivum cDNA clone WHE0763_A05_A09, mRNA sequence. BE496986.1 GI:9695603
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                                                          ington University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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                                                                                                                                                                                                                 Ph.D.
                                                                                                                                                                                    Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58.8; DB 12;
Pred. No. 5.6;
0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major"
   NS / Beverley, SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Friedlin strain V1"
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Location/Qualifiers
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/organism="Leishmania
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                                                                Washington University School
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Contact: Akopyants, NS /
WashU Leishmania Project
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ilarity 48.8%;
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Query Match
Best Local Similarity
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1...394
/Organism="Triticum aestivum"
/cultivar="Chinese Spring"
/cultivar="Chinese Spring"
/clone="WHE0763_A05_A09"
/clone_lib="Whe0763_A05_A09"
/clone_lib="Whe0763_A05_A09"
/clone_lib="Wheoty heat-stressed seedling cDNA library"
/tissue_type="Leaf"
/dev_stage="Two-week old seedling"
/dev_stage="Two-week old seedling"
/lab_host="E. coli Solk"
/lab_host="E. coli Solk"
/lab_host="E. coli Solk"
/lab_host="E. coli Solk"
/lab_host="E. for I sole_2: Khol; Two-week old seedling were
heat treated at 37 C for 2 hr and cyclic heat treated at
37 C for 2 hr for two days at Texas Tech University (D.
Zhang, H. Nguyen lab). The tissue, total RNA, and poly(A)
RNA were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Pooideae; Tobases Triticeae; Triticeae; Pooideae; Tobases 1 to 554)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat genomes - Heat-stressed seedling cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GATGAAGATGATTCGCCCTCCAACGTCGCCGTCGACGATCGGCCGCACCTCGCGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 ggtcgagggagtcctggacgccgcgggcgacgcgacgtccgggtctgcccggtggggca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 GAAGGCCGGCGCCGAGGTCCTCAATGGCCTCTTCCTAAGGTATGAGGCCCCCGAAGGAGCG
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Pred. No. 5.6;
0; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.4%;
Best Local Similarity 47.1%;
Matches 180; Conservative C
                                      Triticum aestivum
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              SOURCE
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COMMENT
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KEYWORDS
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605 bp mRNA linear EST 18-AUG-2000 WS1_102_A09.gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jorganism="Sorghum bicolor"

Ada_xxef="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_l: XhOI;
Site_2: EcoRi; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 GCTGTTCGGGGAGGTGGCCGGCGCGCTTCAGCCCCGACGCGAGGCGCTGTTCGTCAG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gotgoggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctccccggaga 107
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     414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2502, Athens, GA 30602-7271, USA
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355 ceasaaccercerreaserceaccearcercececcesececcecarcececer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An EST database from Sorghum: water-stressed plants Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-Plant 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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168 c 225 g 128 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 605)
Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: PolyTMix
High quality sequence start: 98
High quality sequence stop: 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                 415 GCCCAAGGACATGGGCGCGGGC 436
                                                                                                                                                                                                                                                                                                                                                                      GI:9848848
                                                                 384 cgccgaggagcagagcgccggc
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us-09-749-185-4.rst

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Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp. 3 others
                                                                                                                                                                                                                                             AL508175 623 bp mRNA linear EST 04-JAN-2001 AL508175 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY07P24V 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
1 (bases 1 to 623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aichalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.

EST sequencing and analysis in barley
Unpublished (2000)
Unpublished (2000)
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Corrensstr. 3, D-06466 Gatersleben, Germany
Seq primer for 5'end.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Hordeum vulgare Barke developing caryopsis
59 GCTCTGCATGGNGTCCGAGTTCGACCTGCCGCTGGACCTCGTCGACAGAAGGGTCACCAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GATGAAGATGATTTCGCCCTCCAACGTCGCCGTCGACATCGGCCGCACGCTCGCCCCCCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gctcgccttccgcatcccggtggagctgcggtacgagaccgtcgatccgtacgcggtgcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (3.-15.DAP)"
/tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57.8; DB 9; 1
Pred. No. 7.8;
0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .623
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HY07P24V"
                                                                                                                                                                                                                                                                                                                   AL508175
AL508175.1 GI:12034390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.9%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    barley.
Hordeum vulgare
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Hordeum vulgare subsp. spontaneum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, Pooldeae
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/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
186 c 183 g 82 t
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                           cttcctcgaccgcaccgaccagggcttg---tcgctcggcagcgagcgggcacacgccga 344
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1 (bases 1 to 566)
Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1181 81-559-81-6856
Fax: 81-559-81-6855
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Pred. No. 6.4;
); Mismatches 191;
                                                                                                                                         CCTCGACACGTGTTTCTTCTGAGCTCTGA 352
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Location/Qualifiers
1. .566
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Best Local Similarity 47.5%;
Matches 173; Conservative
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns triamed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified CDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Choi))n the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Aktins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                                                                                                                                                                                                                                                                                                                                                                           BE603206 532 bp mRNA linear EST 22-OCT-2001
HVSWEh0102H24f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSWEh0102H24f,
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HVcDNA0009 ($ 10.45 DAP)"
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/lab_host="SOLR"
                                                                                                                                                  129 cgggcgtgaactgctggtcgagggagtcctggacgccgcggggcgacggcgacgtccgggt 188
                                                         189 ctgcccggtgggggaggcaccagggaggtgcacatcacctccaggtcggctccga
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/db_xref="taxon:4513"
/clone="HVSMEh0102H24f"
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Total hq bases = 418
                                                                                                                                                                                                                                                            384 VGSTCTTTKSSCTBSSGTSSBS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BE603206
BE603206.2 GI:13191055
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                        B44 bp DNA linear GSS 03-JUN-1999 BACSAILINE MELANTIPLE OF RPCT-98 Library from Drosophila melanogaster (fruit ALOS6652
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Ptertygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                              324 cagcgagcgggcacacgccgacttcgacagccacctcgacgacgctctgaaccgcagcct
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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112 c 92 g
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; C.I. 16155 (Mla13) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; T day old green seedlings were challenged with isolate A27 (AvrMla13) of Blumeria grammins f. Sp. hordei, and leaves were harvested 20 and 24 hr post-incoulation and snap frozen: uninoculated leaves were harvested 20 hr post-incoulation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/corders Also see Close TJ, wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 237 c 271 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
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                                                                                                                                                                                                                                                                                                                   /clone="HV_CEa0016G14f"
/clone_llb="Hordeum vulgare seedling green leaf EST
/lbrary HVCDNA0004 (Blumeria challenged)"
/tissue_type="seedling green leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctcgccttccgcatcccggtggagctgcggtacgagaccgtcgatccgtacgcggtgcg
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                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="C116155 (Mla13)"
/db_xref="taxon:4513"
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 473
Seq primer: AATTAACCCTCACTAAAGGG
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BF266913. GI:13263052
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1 (bases 1 to 761)
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                                                                             http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 166 c 179 g 78 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla13) unpublished (2001)

On Nov 17, 2000 this sequence version replaced gi:11197908.
        or
and contains a minimum of 100 bases of phred value 20 above. For more details on library preparation and
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Pred. No. 9.6;
0; Mismatches 203;
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100 Jordan Hall, Clemson, SC 29634, USA
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Clemson University Genomics Institute
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                                                                                                                                                                                                                                      GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-071C05.R.
Pan troglodytes
                                                                                                                                                                     GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC endwas generated during the R&D process and may have higher chance of
                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
gtgcggctgacgttccacctccccggagacgccccggtcacctgggtcttcggggcgtgaa 138
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Fuljyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fullyama A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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/clone_lib="PTB Chimpanzee Male BAC Librar
488 c 514 g 23 t 93 others
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1 . 1152
/organism="Pan troglodytes"
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/clone="PTB-071C05.R"
/sex="male"
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Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center
If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For Information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.

(beverley@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                  GSS 25-MAY-2001
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I (bases I to 474)

Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylle, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, T., Benett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvill, R., Willams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                      LMAJEVI_lm29c04.yl Leishmania major EVI random genomic library Leishmania major genomic clone LMAJEVI_lm29c04 5' similar to contains element V1-chl_type_II.2 V1-chl_type_I leishmania repetitive element ;, DNA sequence.
                                                    319 ctcggcaqcqaqcggcacacqccgacttcgacagccacctcgacgctctgaaccgc 378
Other_GSSs: lm29c04.x1
Contact: Acopyants, NS / Beverley, SM
Contact: Acopyants, NS / Beverley, SM
WashU Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
                                                                                       Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
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Location/Qualifiers
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                                                                                                                                                                                                           802 GGCGGGGGCCGCGCGGGGGGG 828
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Best Local Similarity
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Email: mmpratteuga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with PolyTMix or
T7 sequencing primer, are presented as the reverse complement.
High quality sequence stop: 469

POLYA-NO.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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Cordoniar-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
Sudman,M. and Pratt,L.H.
An EST database from Sorghum: plants infected with a compatible
                                                                                                                                 cgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacctgggt 125
                                                                                             186 ggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtcggctc 245
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                                Gaps
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
                                                              6 cttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgagaccgt 65
                                                                                                                                                                                                                                                                                 /db_xref="taxon:4558"
/clone_lib="Pathogen infected compatible 1 (PIC1)"
/tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
Colletotrichum graminicola"
                                ;
   Length 474;
                                  Indels
Score 55.6; DB 12;
Pred. No. 17;
); Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sorghum bicolor"/cultivar="BTx623"
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Contact: Cordonnier-Pratt MM
Department of Botany
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BM324683.1 GI:18063552
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Matches 148:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.

(Dases 1 to 615)
Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,
Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible
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PIC1_45_411.bl_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence.
/note="Vector: pBluescript II SK(-) from Lambda Zap II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 ggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggga 173
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Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55.2; DB 10;
Pred. No. 19;
0; Mismatches 148;
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49.38;
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Fax: 706 542 1805
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/db.xref="taxon:4558"
/db.xref="taxon:4558"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/tissue_type="Leaves"
/dev_stage="taeves"
/dev_stage="teaves"
/dev_stag
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T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 607 POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 TCTCGAGGTCAAGCAGCGGACGGTGTCGGACAAGGGGCAGTTCAGAGGCTACATCGGCCA 297
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                                                                                                                                                                                                                                                                               /organism="Sorghum bicolor"/cultivar="BTx623"
                                                                                                                                                                                           Location/Qualifiers
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Search completed: July 18, 2002, 10:12:49 Job time: 9969 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2002, 14:15:01; Search time 130.38 Seconds (without alignments) 115.010 Million cell updates/sec Run on:

US-09-749-185-5 687 Title: Perfect score:

1 MSFLVSEELAFRIPVELRYE......FDSHLDDALNRSLAEEQSAG 135 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

747574 seqs, 111073796 residues Searched: hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
			!	: 3		
¬	98/	7 OOT		7	AAY4465U	Streptomyces albus
2	481	70.0		21	AAY44651	Streptomyces golde
m	464	67.5		21	AAY44649	Streptomyces grise
4	446	64.9		21	AAY44652	Streptomyces netro
ហ	78	11.4		21	AAG35780	Arabidopsis thalia
9	78	11.4	258	21	AAG35779	Arabidopsis thalia
7	76.5			18	AAW55684	H. pylori ORF 02qe
80	16			22	ABB59950	Drosophila melanog
σ	75.5			22	AAU35800	Helicobacter pylor
10	75			22	AAG82257	S. epidermidis ope
11	74.5			22	AAB96082	Putative P. abvssi

WPI; 2000-147269/13. N-PSDB; AAZ49729.

Propionibacterium Trametes hirsuta p Novel human secret Rat type 2 methion Propionibacterium Fragment of human Rragment of human Human meghrin prot Human nephrin prot Human methionine a Human methionine a Human pf7 homologu Mouse type 2 methi Human type 2 methi Human type 2 methi elF-2-associated p Human colon cancer Human deleted in p Human deleted in p Human deleted in p Human deleted in p	Smad4 green iloure Smad4 green iloure Filamentous haemag Amino acid sequenc Fragment 7 of the FHA fragment 7 pol Bordetella pertuss Filamentous haemag Human colon cancer Rubella virus RA27 Adenylyl cyclase t Coriolus versicolo Human ORFX ORF2961
2 AAUS6042 2 AAB48832 2 AAU30706 2 AAU30706 2 AAU30706 2 AAU3220 0 AAU72219 1 AAB15495 0 AAU3220 0 AAW94765 0 AAW94765 0 AAW94765 0 AAW94765 0 AAW94765 1 AAU3073991 1 AAY6071 1 AAY6622	AAW850L AAW6509 AAY4356 AAY2396 AAY8740 AAR8740 AAR5033 AAR5333 AAW5927 AAW94300 AAW94310
540 22 622 22 22 622 22 22 22 22 22 22 22 2	798 19 798 19 10248 19 10248 20 11248 20 11248 21 1248 21 1258 21 1258 21 1258 21
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ALIGNMENTS

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SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antiblotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoctr; bioinsecticide; receptor agonist; antagonist; blomass.
                                                                                                                                                                                                                                                                                                       (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                         Luiten RGM;
                    AAY44650 standard; Protein; 135 AA.
                                                                                         Streptomyces albus G SsgA protein.
                                                                                                                                                                                                                                                         99WO-NL00395
                                                                                                                                                                                                                                                                                98EP-0202148
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                         Van Wezel GP, Kraal B,
                                                                                                                                                                                    Streptomyces albus G.
                                                                                                                                                                                                          WO200000613-A1
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                                           AAY44650;
          AAY44650
RESULT
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Streptomyces
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                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                AAY44649;
                                                                                                                                                           Query Match
                                                                                                                                                                     Best_Local
Matches 9
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                                                    The present sequence is S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                             VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                              1 MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          culture; filamentous bacteria; secondary metabolite;
Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                       Length 135;
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                                                                                                                                                                                                      100.0%; Score 687; DB 21; 100.0%; Pred. No. 4.1e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces goldeniensis SsgA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44651 standard; Protein; 135 AA.
                                Disclosure; Fig 5; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces goldeniensis.
                                                                                                                                                                                                                            Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                   DDALNRSLAEEQSAG 135
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                                                                                                                                                                                                                Similarity
                                                                                                                                                                    Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY44651;
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The present sequence is S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGD 60
                                                                                                                                                                       antiblotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhlbitors, antilmigraine agents, hybocholesterolaemic agents, ruminant growth promoters, bioinsecticides, receptor agonts, raminant growth promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SsgA: liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosupressive agent; mypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; Score 481; DB 21; Length 135; 71.1%; Pred. No. 3.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels
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N-PSDB; AAZ49727, AAZ49728.
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|dealdrilaeeqnag 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DDALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kraal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                            135 AA;
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99US-0134370
99US-0134768
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                                                                                                                                                                    85; Conservative
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121 eaalgkilaeeqnag 135
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                                                                                                                                                   Similarity
                                                                    135 AA;
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06-APR-1999;
08-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1999
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06-MAY-1999;
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                                                                    Sequence
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Best Local 9
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                                                                                                                                                                        Matches
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bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents,
                                                                                                                                                                                                                                                                                                                                                                                                  61 VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                     1 MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SsgA; liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                              Length 135;
                                                                                                                                                                                                                                                     28; Indels
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NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                          Score 464; DB 21;
Pred. No. 4.1e-48;
8; Mismatches 28;
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                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                            67.5%;
65.9%;
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edalgrilaeeqnag 135
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Best Local
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass
                                                                                                                     Length 135;
                                                                                                                                                              30; Indels
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                                                                                                                     64.9%; Score 446; DB 21;
63.0%; Pred. No. 6.2e-46;
ive 20; Mismatches 30;
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99US-0127462.
99US-0128134.
99US-0129845.
99US-0129845.
99US-0130619.
99US-0130891.
99US-0130891.
99US-0131449.
99US-0132449.
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99US-0132485.
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99US-0123180.
99US-0123548.
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905 - 0134941 905 - 0135124 905 - 0135235 905 - 0135629 905 - 0136021 905 - 0136021 905 - 0137528 905 - 0137528 905 - 0137502 905 - 0137502 905 - 0137502	990'S - 0139452 990'S - 0139453 990'S - 0139453 990'S - 0139455 990'S - 0139456 990'S - 0139458 990'S - 0139458 990'S - 0139461 990'S - 0139461 990'S - 0139461 990'S - 0139461 990'S - 0139462 990'S - 0139463 990'S - 0139899 990'S - 0140'S 3 990'S - 0141'S 7	905 - 0143547 905 - 0143547 905 - 0144085 905 - 0144086 905 - 0144333 905 - 0144333 905 - 0144334 905 - 0144334 905 - 0144335 905 - 0144635 905 - 0146588 905 - 0145218 905 - 0145218 905 - 0145218 905 - 0145218 905 - 0145218
9-MAY-1999 0-MAY-1999 1-MAY-1999 4-MAY-1999 7-MAY-1999 1-JUN-1999 4-JUN-1999 0-JUN-1999 0-JUN-1999	16-70N-1999) 16-70N-1999) 17-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 18-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 23-70N-1999) 24-70N-1999) 26-70L-1999) 01-70L-1999) 01-70L-1999) 06-70L-1999)	3. uct. 1999 6. uct. 1999 6. uct. 1999 9. uct. 1999 9. uct. 1999 9. uct. 1999 9. uct. 1999 9. uct. 1999 9. uct. 1999 1. uct. 1999 1. uct. 1999 1. uct. 1999 2. uct. 1999 2. uct. 1999 3. uct. 1999 3. uct. 1999 7. uct. 1999
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R 28-JUL-1999; R 02-AUG-1999; R 02-AUG-1999; R 02-AUG-1999; R 03-AUG-1999; R 03-AUG-1999; R 03-AUG-1999; R 05-AUG-1999; R 05-AUG-1999; R 05-AUG-1999; R 13-AUG-1999; R 13-CCT-1999; R 12-CCT-1999; R 13-CCT-1999;	905 - 0145951 905 - 0146386 905 - 0146389 905 - 0147038 905 - 0147204 905 - 0147204 905 - 0147303 905 - 0147303 905 - 0147303 905 - 0147303 905 - 0147303	905-0148541 905-0148654 905-0148686 905-01491368 905-0149125 905-0149125 905-0149920 905-0149930 905-0150566 905-015066 905-0151066 905-0151080 905-0151080 905-0151080 905-0151080 905-0151080 905-0151080 905-0151080 905-0151080	99US-0154779 99US-0155139 99US-0155659 99US-0155659 99US-015713 99US-0157753 99US-0157753 99US-0157753 99US-0158059 99US-0158059 99US-0158059 99US-0158369 99US-0159231 99US-0159231 99US-0159331 99US-0159331 99US-0159331 99US-0159331 99US-0159331 99US-0159331 99US-0159331 99US-0160741 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768 99US-0160768
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9905 - 0136021
9905 - 0136392
9905 - 0137222
9905 - 0137228
9905 - 0137528
9905 - 0137724
9905 - 0138540
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99US-0139817
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99US-0144085
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99US-0145088
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          25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
06-JUN-1999;
10-JUN-1999;
110-JUN-1999;
114-JUN-1999;
14-JUN-1999;
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02-AUG-1999;
                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                 50 EGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGS 109
                                                                                             22; Gaps
                                                                                                                                  39 dgtsdsdsdpdppk-pegdtrrqellari-----amigtskvrltdflderseyltkfa 91
                                                                       Query Match 11.4%; Score 78; DB 21; Length 257; Best Local Similarity 29.7%; Pred. No. 0.53; Matches 30; Conservative 14; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 43757.
                                                                                                                                                                     110 ERAHADFD-----SHLDDALNRSL-----AEEQSAG 135
                                                                                                                                                                                                                                 AAG35779 standard; Protein; 258 AA
          990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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990x-012548.
990x-0126264.
990x-0126785.
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99US-0130077.
99US-0130449.
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99US-0130891.
99US-0131449.
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99US-0132863.
99US-0134256.
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99US-0134941.
99US-0135124.
99US-0135353.
  99US-0161360
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                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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-MAY-1999;
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09-MAR-1999
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30-APR-1999
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99US-0147493.
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99US-0148171.
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99US-0149368.
99US-0149175.
99US-0149426.
99US-0149722.
99US-0149723.
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99US-0149930
99US-0150566
99US-0150884
99US-0151065
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99US-0151303.
99US-0151438.
99US-0151930.
99US-0153363.
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99US-0154779.
99US-0155139.
99US-0155486.
99US-0155659.
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99US-0157117.
99US-0157753.
99US-0157865.
99US-0158232.
99US-0158339.
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99US-0159294
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99US-0159330
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99US-0159584.
99US-0160741.
99US-0160767.
99US-0160770.
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9903-0160980.
9903-0160981.
9903-0161404.
9903-0161405.
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99US-0161360.
99US-0161361.
99US-0161920.
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           04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
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12-A0G-1999;
13-A0G-1999;
13-A0G-1999;
16-A0G-1999;
17-A0G-1999;
                                                                                                                               20 - AUG - 1999;
23 - AUG - 1999;
25 - AUG - 1999;
26 - AUG - 1999;
27 - AUG - 1999;
21 - AUG - 1999;
31 - AUG - 1999;
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-OCT-1999;
-OCT-1999;
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26-OCT-1999;
28-OCT-1999;
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                                                                                                                   20-AUG-1
20-AUG-1
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This sequence is a H. pylori cellular protein.

The protein may be used in a vaccine to prevent or treat H. pylori cellular protein.

The protein may be used in a vaccine to prevent or treat H. pylori collection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF
                                                                                                                ..
                                                                                                                                                   EGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGS 109
                                                                                                                Gaps
                                                                                                                                                                                        40 dgtsdsdsdpdppk-pegdtrrqellari----amiqtskvrltdflderseyltkfa 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
                                                                                                            35; Indels 22;
                                                                         ; DB 21; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. pylori ORF 02ge10116_23866562_c3_146 cellular protein.
                                                                                                                                                                                                                           110 ERAHADFD-----SHLDDALNRSL-----AEEQSAG 135
                                                                                                                                                                                                                                                                93 eeanaefdkvgedamkdldeastrilenieskmgafeesag 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claims 14,93; Pages 937-939; 1145pp; English.
                                                                                               Best Local Similarity 29.7%; Pred. No. 0.54 Matches 30; Conservative 14; Mismatches
                                                                           11.4%; Score 78; 29.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                           AAW55684 standard; Protein; 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0761318.
96US-0625811.
96US-0758731.
96US-0736905.
96US-0738859.
99US-0161992.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV25093
 28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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29-MAR-1996
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                                                                           Query Match
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR ampilfication for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                         215 gktllakav---ageahvpffsmggssfiemfvglgasrvrdlfetakkgapsiifidei 271
                                                                                                                                                                                                         44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                          11;
                                                                                                                                             Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 6642; 21pp + Sequence Listing; English.
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 6642.
                                                                                                                                           DB 18;
                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                   102 DQGLSLGSERAHADFDSHLDD----ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                        Score 76.5; D
Pred. No. 2.8;
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                               ABB59950 standard; Protein; 736 AA.
                                                                                                                                                                        15;
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                                                                                                                                           11.1%;
29.9%;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                              632 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical
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                                                                                                                                                                        29;
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                                                                                               Seguence
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                                                                                                                                           Query Match
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736 AA;

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                                                                                                 272 fttsngsvfriglgngve-vdpeeinvtfedvkgcdeakgelkevveflkspekfsnlgg 330
                                                                                                                                                                  331 klpkgvllvgppgtgktllarav---ageakvpffhaagpefdevlvgggarrvrdlfka 387
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ;
                                                                ---HLPG 35
                                                                                                                                 36 DAPVTWVF-----GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRV 89
                                  46;
                                                                                                                                                                                                   90 GK--APLLAFLDRTDQGLSLGSERAHADFDSHLDDALNRSLAE----EQSAG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                       pylori cellular proliferation protein #113.
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                                 62;
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DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Seq ID No 11393; 511pp; English.
                                 24; Mismatches
                                                                3 FLVSEELAFRIPVELRYETVDPYAVRLTF----
11.1%; Score 76; 23.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                      AAU35800 standard; Protein; 632 AA.
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2000US-207727P.
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2000US-253625P.
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2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
               Best Local Similarity 23.3%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS53659
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                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter
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27-NOV-2000;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
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26-MAY-2000;
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 Query Match
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us-09-749-185-5.rag

309 AA;

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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                         Sequence
                                                                                                                                                                                                                                            . 65
                                                                                                                                                                                                                                                                                                                   RESULT 1
AAB96082
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                                                                                                                                                                                                                                                                                                                                                                         ARH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the solution of vectors.

S. epidermidis polypeptides (II) via the production of vectors containing them whitch are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their crivity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH5509 represent oligonucleotide sequences from the present invention. AAH55091 to AAH55099 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                           4 ;
                                                                                                                                                                                                    44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                            215 gktllakav---ageahvpffsmggssfiemfvglgasrvrdlfetakkgapsiifidei 271
                                                                                                                                                                         11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

    S. epidermidis open reading frame protein sequence SEQ ID NO:1608.

    a wide variety of organisms. The present sequence represents an
                                                                                                                                             Length 632;
                 essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                         Indels
                                                                                                                                             DB 22;
                                                                                                                                                                        42;
                                                                                                                                                                                                                                                          102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                          Score 75.5; DB
Pred. No. 3.6;
5; Mismatches
                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 450; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                            Ā
                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                         AAG82257 standard; Protein; 309
                                                                                                                                            11.0%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2000; 2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-316495/33.
N-PSDB; AAH53107.
                                                                                                                                                            Local Similarity
                                                                                                   632 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200134809-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-2001
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                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                     AAG82257;
                                                                                                    Sequence
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                     272
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80 fnipisiqgktiqtipyalehiqprdfhvpgd----issaaffivaalitpg-sditih 133
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                                                                                                      FRIPVELRYETVD--PYAVR----LIFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVC 64
                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequences isolated from Pyrococcus abyssi encode
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  Length 309;
                                                     37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative P. abyssi ATPase subunit of ABC transporter #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thierry JC, Prieur D, Dietrich J, 1 Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
10.9%; Score 75; DB 22; 28.1%; Pred. No. 1.6; tive 13; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74.5; DE
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Pages 705-706; 1657pp; French.
                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                            PVGQTATRE - - VHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                              AAB96082 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%;
27.3%;
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                                                     Conservative
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Query Match
Best Local Similarity
Matches 25; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AA;
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999;
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P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and diagnostic agents for determining P. acnes proteins. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; udeltis; endophthalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                               | :| ||: :| || ::| || ::| || ::| || ::| || ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::| ||: ::|
                                                  SFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGV----LDAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
  35; Gaps
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  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #16938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitcham JL, Wany ... S, Carter D;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID No 17237; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ceiky YAW, Persing DH, Mitcham J
maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU56042 standard; Protein; 540 AA.
                                                                                                                                                                                                                                                      91 KAPLLAFLDRT---DQGLSLGSE 110
                                                                                                                                                                                                                                                                                                        309 gitlkafitrsslielgisegre 331
18;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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  Conservative
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39;
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  Matches
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 qiyystadgvderddvelptdahthmswafskpgvykavfaa----tlstpqgnasfga 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 VHITLQVGSEQALFRVGKAPLLAFLDRT--DQGLSLGSERAHADFDSHLDDALNRSLAEE 131
                                                                                                                                                                                                                                                                                                                                                               16 ELRYETVDPYAVRLTFHLPGDA--PVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTATRE 73
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                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                            10.8%; Score 74; DB 22; Length 540; 25.8%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                               51; Indels
                                                                                                                                                                                                                                                                                               17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB48832 standard; Protein; 622 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0305381.
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N-PSDB; AAC87518, AAC87519.
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                                                                                                                                                                                                                                                                                               32; Conservative
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                                                                                                                                     540 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1999;
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Query Match
Best Local Similarity
    416 AA;
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Best Local Si
Matches 32;
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                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy \cdot
(fungi or bacteria). The present sequence represents pyranose oxidase from the fungus Trametes hirsuta.
                                                                                                                                                                                                                                                                                                                                                                                           stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                         Gaps
                                                                                                                                26 AVRLTFHL-----PGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQ 79
                                                                                                                                                 22 akratahslpplpgpgdlp-----pgmnveydvaivgsg-----pigctyarel---ve 67
                                                                                                        30;
                                                                                Length 622;
                                                                                                                                                                                                                                                                                                                                                                               gene therapy; nutritional supplement;
                                                                                                        Indels
                                                                                                                                                                                                 | |:| :|: | :| 68 agfnvamfeige------idsglkigshkkntveygknidkfvn 105
                                                                                                                                                                                 80 VGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAH-ADFDSHLDDALN 125
                                                                                                        32;
                                                                                DB 22;
                                                                          Query Match 10.8%; Score /4; LL 2.8 Best Local Similarity 26.2%; Pred. No. 5.4; Matches 28; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #1197.
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                                                                                                                                                                                                                                                                        AAU30706 standard; Protein; 416
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26-JAN-2001; 2001US-0770160
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                                                                                                                                                                                                                                                                                                                                                                                vaccination;
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                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
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                                          Sequence
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inhibit type 2 methionine aminopeptidase (MeLR2). These inhibitors are useful for treating and/or diagnosing diseases involving abnormal angiogenesis (e.g. tumnours, diabetic retinopathy, inflammatory diseases, arteriosclerosis) or immune reactions which result in pathology (e.g. autoimmune disease, allergy and tissue graft rejection). The present sequence represents the amino acid sequence of rat MetAP2.
                                                                                                                                                                                                                                            The invention relates to ovalicin and fumagillin derivatives that can
                                                                                                                                                               133.pv11teaplnpkanrekmtgilcfetfntpghvp--wpiqavlslxslwagpigivmdsg 190
                                                                                                                                                                                                                58 DGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovalicin; fumagillin; type 2 methlonine aminopeptidase; inhibitor; MetAP2; angiogenesis; tumour; diabetic retinopathy; arteriosclerosis; inflammatory disease; immune reaction; autoimmune disease; allergy;
                                                      Gaps
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                                                                                                        14 PVELRYETVDPYAVR------GVLDAAG 57
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                                                    31;
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     Length 416;
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                                                      40;
     DB 22;
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Pred. No. 5.7;
(0; Mismatches
Score 73.5; D
Pred. No. 3.6;
                                                      18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW94764 standard; protein; 478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 99pp; English.
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27.0%;
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illarity 28.8%;
Conservative 2
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inflammatory disease; immune
tissue graft rejection; rat.
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es 32; Conserv
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Db 242 lqyddi----ckidfgthisgriidcaftvtfnpkydiilkavkdatntgikcagidvrl 297
Qy 64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDGGLSLGSERAHA 114
Db 298 cdvge-aiqevmesyeveidgktyqv--kpi----rnlnghsigpyriha 340
Search completed: July 18, 2002, 14:15:02
Job time: 10332 sec
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TYPE: PRT
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                                                                                                                July 18, 2002, 14:16:06; Search time 51.31 Seconds
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/pcTUS_COMB.pep:*
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-040-774-2

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US-09-093-448-1

US-09-093-448-1

US-08-093-448-1

US-08-093-448-1

US-08-01-1582D-14

US-09-005-532-2

US-09-005-532-2

US-09-096-765-965-17

US-08-465-965-17

US-08-465-966-17

US-08-465-966-17

US-08-127-499A-8

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US-09-320-878-3
US-09-105-537-35
US-09-105-537-6
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext
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28 65.5 9.5 989 4 US-09-199-637A-273 Sequence 273, Appl 29 65 9.5 184 2 US-08-737-825-10 Sequence 10, Appl 31 64.5 9.5 686 2 US-08-993-228-12 Sequence 12, Appl 32 64.5 9.4 411 4 US-09-189-930-302 Sequence 12, Appl 33 64.5 9.4 466 2 US-09-189-93 Sequence 12, Appl 33 64.5 9.4 529 3 US-09-080-044-2 Sequence 2, Appl 34 64 9.3 1064 1 US-08-95-138-7 Sequence 2, Appl 35 64 9.3 1064 2 US-09-080-289-5 Sequence 2, Appl 36 64 9.3 1064 2 US-09-080-59-5 Sequence 2, Appl 39 64 9.3 1082 1 US-08-357-598-5 Sequence 2, Appl 39 64 9.3 1082 2 US-09-003-289-5 Sequence 10, Appl 41 64 9.3 1082 2 US-09-003-289-5 Sequence 10, Appl 42 64 9.3 1082 2 US-09-003-289-10 Sequence 10, Appl 44 63.5 9.2 108-1 US-08-17-499A-1 Sequence 1, Appl 44 63.5 9.2 108-3 1 US-08-184-11 Sequence 1, Appl 44 63.5 9.2 108-3 1 US-08-184-1 Sequence 1, Appl 44 63.5 9.2 108-3 1 US-08-453B-3 Sequence 3, Appl 14 Phylician 1 US-08-09-453B-3 Sequence 1, Appl 14 63.5 9.2 108-3 1 US-08-453B-3 Sequence 3, Appl 14 Phylician 1 US-08-093-453B-3 Sequence 3, Appl 14 Phylician 1 US-08-093-453B-3
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ALIGNMENTS

us-09-749-185-5.rai

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Sequence 1, Application US/09093448A
Fatent No. 6207704
GENERAL INFORMATION:
APPLICANT: Liu, Jun O.
APPLICANT: Su, Zhuang
TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 0492611-0346
  103 LSDDAEYECQVGRSEMGPELVSPRVI-LSILVPPKLLLLTPEAGTMVTWVAGQEYVVNCV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 LQYDDI----CKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKVAGIDVRL 297
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                                                                                                                                                                                       Sequence 3, Application US/09040799
Patent No. 5885820
GENERAL INFORMATION:
APPLICANT CHANG, YIE-HWA
TITLE OF INVENTION: CLONE OF A NUCLEOTIDE SEQUENCE ENCODING
TITLE OF INVENTION: A PROTEIN HAVING TWO FUNCTIONS
NUMBER OF SEQUENCES: 5
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CURRENT APPLICATION DATA:
ELLCATION NUMBER: US/09/040,799
FILING DATE: 18-MAR-1998
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                                                                   53 L-DAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRV
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                                                                                                                                                                                                                                                                                                                                                             :: HOWELL & HAFERKAMP, L.C. 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY ACENT INFORMATION:
NAME: HOLLAND, DONALD R
RECISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 16153-4639
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEPHONE: 314-727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 28.89
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-040-799-3
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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CLASSIFICATION:
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US-09-093-448-1
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                                                                                                                                                                                                                                                                                                                    17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG-----DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GDAPVTWVFGRELLVEGV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.5; DB 4; Length 478;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                       64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/POCKET UNBER: 97,842
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, Suite 3200
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 71.5; DB 4; 28.6%; Pred. No. 6.7; tive 17; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09040774

Patent No. 6207811

GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Lenkkeri, Ulla
APPLICANT: Mannikko, Minna
TITLE OF INVENTION: Nephrin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    10.6%; Scor. 28.8%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VSEELAFRIPV---ELRYETVDPYAVRLTFHLP----
CURRENT APPLICATION NUMBER: US/09/093,448A CURRENT FILING DATE: 1998-06-08 WUMBER OF SEQ ID NOS: 4 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1241 amino acids
                                                                                                                          ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-093-448-2
                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.8%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.68.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-040-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                      LENGTH: 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-040-774-2
                                                                                   SEQ ID NO 2
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304 VHNELAROPPISNHPAPEYWCSIAYFEMD-VQVGETFKVPSSCPI------VTVDGYVD 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 69.5; DB 1; Length 552; 30.9%; Pred. No. 3.7; ive 15; Mismatches 27; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kern, Scott E.
APPLICANT: Hahn, Stephan A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/588,821 FILING DATE: 19-JAN-1996 CHASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/079001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,347
SER: 07265/079001
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APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-JAN-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,214
FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08915214
Patent No. 5814457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query, Match 10.1%
Best Local Similarity 30.9%
Matches 30; Conservative
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-588-821-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20 CLASSIFICATION:
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STATE: CP
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-915-214-2
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Patent No. 6207704
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jun O.
APPLICANT: Su, Zhuang
TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
FILE REFERENCE: 0492611-0346
CURRENT PELLING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 4
SECTIMENT OF SEQ ID NOS: 4
SECTIMENT PELLING DATE: 1998-06-08
                                                                                                                                                                                                                                                                                                                                                               25; Gaps
                                                                                                                                                                                                                                                                                                                                      17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG-----DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG------DVRV 63
                                                                                                                                                                                                                                             Query Match 10.3%; Score 70.5; DB 4; Length 478; Best Local Similarity 28.8%; Pred. No. 2.3; Matches 32; Conservative 19; Mismatches 35; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                              64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 CDVGE-AIQEVMESYEVEIDGKTYQV--KPI----RNLNGHSIGPYRIHA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.3%; Score 70.5; DB 4; Length 478; Best Local Similarity 28.8%; Pred. No. 2.3; Matches 32; Conservative 19; Mismatches 35; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 CDVGE-AIQEVMESYEVEIDGKTYQV--KPI----RNLNGHSIGQYRIHA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/0858821
| Patent No. 5712097
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Hahn, Stephan A. | ITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4 | NUMBER OF SEQUENCES: 91
| CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson P.C. | STREET: 4225 Executive Square, Suite 1400 | CITY: La Jolla | STATE: CA
CURRENT APPLICATION NUMBER: US/09/093,448A CURRENT FILING DATE: 1998-06-08 NUMBER OF SEO ID NOS: 4 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-093-448-3
                                                                                                                                                     ; ORGANISM: Mus musculus US-09-093-448-1
                                                                                                             LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-093-448-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 478
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US-08-588-821-2
                                                                                        SEQ ID NO 1
                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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25; Gaps

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5 VSEELAFRIPV-----ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
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                                                                                                                                                                                               Sequence 14, Application US/08701582D
Sequence 14, Application US/08701582D
Sequence 14, Application US/08701582D
GENERAL INFORMATION:
APPLICANT: WRANA, Jeffrey
APPLICANT: ATTISANO, Liliana
APPLICANT: SCHERER, Stephen W.
TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTNS, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/701,582D FILING DATE: 22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                  356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
                                                            55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.1%; Score 69.5; Di 30.9%; Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Miyazono, Kohei
APPLICANT: Kawabata, Masahiro
TITLE OF INVENTION: SMAD6 AND USES THEREOF
FILE REFERENCE: L0461/7038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-AUG-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: REA, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFRENCE/DOCKET NUMBER: 0249
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE:
US-08-701-582D-14
                                                                                                                                                                  RESULT 10
US-08-701-582D-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-096-776B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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Matches
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                                                                                                                                                                                                                                                                                                                                         304 VHNELARQPPISNHPAPEYWCSIAYFEMD-VQVGETFKVPSSCPI-----VIVDGYVD 355
                                                                                                                                                                                                                                                                                                                  5 VSEELAFRIPV-----ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VSEELAFRIPV------ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
                                                                                                                                                                                                                               10.1%; Score 69.5; DB 2; Length 552; 30.9%; Pred. No. 3.7; Live 15; Mismatches 27; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 69.5; DB 2; Length 552; 30.9%; Pred. No. 3.7; ive 15; Mismatches 27; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kern, Scott E.
APPLICANT: Hahn, Stephan A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,532
                                                                                                                                                                                                                                                                                                                                                                                                                          356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
                                                                                                                                                                                                                                                                                                                                                                                                    55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-JAN-1996
ATTORNEY AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/079001
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09005532
Patent No. 5955292
                 TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 30.9% (0); Conservative
                                                                                                                                                                                                                               Query Match 10.1%
Best Local Similarity 30.9%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                  , MOLECULE TYPE: protein US-08-915-214-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-005-532-2
                                                                                                      amino acid
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  TELEPHONE:
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Best Local Simi
Matches 30;
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Gaps

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Gaps

22;

37; Indels

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28.1%;

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Best Local Similarity 28.1% Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VSEELAFRIPV-----ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
                                                                                                                                                                                                                                                                                                                                                                         Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIAN
COMPUTER: TBM PC COMPATIAN
COMPUTER: TBM PC COMPATIAN
COMPUTER: PATENTING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
CLASSIFFCATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Jackson, David
RESISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                       Score 69.5; DB 4;
Pred. No. 3.7;
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CURRENT APPLICATION NUMBER: US/09/096,776B
CURRENT FILING DATE: 1998-06-12
FRIOR APPLICATION NUMBER: US 60/049,990
FRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-07-18
FRIOR FILING DATE: 1997-07-18
FRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN NUMBER: US 60/066,173
FRIOR FILING DATE: 1997-11-18
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
SEQUID NO 9
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08348353 Patent No. 5932217 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                     10.1%;
30.9%;
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                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-096-776B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey COUNTRY: U.S.A.
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Best Local Similarity
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US-08-348-353-17
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US-08-348-353-17
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Length 1248;

10.0%; Score 69; DB 2;

Query Match

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47 LLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLD----
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                                                                                                                                                                                                                                                                                               APPLICANT: Tuomanen, Elaine
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Indels
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                                                                                                                100 RTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600-1-097CIP1DIV2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCI/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 69; 28.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,965
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       Sequence 17, Application US/08465965 Patent No. 5968512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07/695,613
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411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 60
FELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6'
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
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TELEPHONE: ZULTUCK
TEMPAX: Z01-343-1684
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
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Best Local Similarity
Matches 27; Conserva
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US-08-465-965-17
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Texas
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                                                                                                                                     RESULT 15
US-08-726-214-2
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                    47 LLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLD-
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
WUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIPIDIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                   100 RTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 10.0%; Score 69; DB 3
Best Local Similarity 28.1%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRENT AFFLICATION NUMBER: US/08/465,966
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
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SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              Sequence 17, Application US/08465966 Patent No. 6015560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                     APPLICANT: Tuomanen, Elair
APPLICANT: Masure, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-465-966-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-08-465-966-17
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tang, Wel-Jen
APPLICANT: Gliman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                             100 RTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG 135
                                                                                        132 RAQQKLELGSVKSDGGLQAAAGGAL--SLAAAEVAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 68.5; Di
25.6%; Pred. No. 14;
:1ve 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: Concurrently Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: July 18, 2002, 14:16:07
Job time: 9697 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               . Sequence 2, Application US/08726214; Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1134 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.0%
Best Local Similarity 25.6%
Matches, 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                       NÚMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Gencore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
July 18, 2002, 14:17:33; Search time 73.98 Seconds
(without alignments)
175.345 Million cell updates/sec

Title:
Gapo-749-185-5
Sequence:
1 MSFLVSEELAFRIPVELRYE......FDSHLDDALNRSLAEEQSAG 135
Scoring table:
Gapop 10.0, Gapext 0.5
Searched:
283138 seqs, 96089334 residues
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Database: PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
Pred. No. is the number of results predicted by chance to have

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable regulator				hexokinase (EC 2.7	hypothetical prote	probable large ATP	thiamin monophosph	cell cycle protein	probable alcohol d	alpha-galactoside	hypothetical prote	ATP-dependent zinc	hypothetical prote	hypothetical prote	-	abc transporter, A	2,3-dihydroxybenzo	2,3-dihydroxybenzo	membrane bound zin		precorrin-3B C17-m	probable sugar upt	hypothetical prote	probable transcrip	cell division prot	cell division prot	methionyl aminopep	conserved hypothet
SUMMARIES	TD	T37179	T36147	T35247	T35319	S68694	A83271	T36380	AE2438	T47267	н69789	F96037	н70678	D71941	F97414	AB2632	E64653	G75203	A99708	E85558	G81315	н97694	AG2920	D96014	T36503	G83311	E64250	S73497	A46702	н87685
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, ,	score	498	203	155	117	90.5	82	79	78.5	78.5	78	7	76.5	76.5	75.5	75.5	75.5	4	74.5	4	74.5	74	7	73.5	73	73	73	73		72.5
Result	. ON .	1	7	Э	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

conserved hypothet	bynothetical prote	probable dihydroxy	nephrin - human	quinone oxidoreduc	probable glycosylt	hypothetical prote	hypothetical prote	methyltransferase	probable methyltra	methionyl aminopep	2,3-dihydroxybenzo	diol dehydratase-r	conserved hypothet	hypothetical prote
AE0332	A30232	E64752	T37190	G83766	AI0767	B83360	C84321	AE2776	C97556	DPHUM2	SYECEB	AD1219	G96034	A96710
2 0	4 C	1 (1	7	7	7	7	7	7	~	+	Н	7	7	7
921	707	655	1241	322	406	514	283	303	321	478	536	909	640	596
10.6		10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.2
72.5	4 C	71.5	71.5	71	71	71	70.5	. 70.5	70.5	70.5	. 70.5	70.5	70.5	70

ALIGNMENTS

RESULT T37179

283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

probable regulator - Streptomyces coelicolor C:Specias: Streptomyces coelicolor C:Specias: Streptomyces coelicolor C:Accession: T37179 #sequence_revision 03-Dec-1999 #sequence_revision 03-Dec-1999 #sequence_revision 03-Dec-1999 #sequence_revision 03-Dec-1999 #sequence_revision 03-Dec-1999 #sequence_revision 03-Dec-1999 #sequence_revision T37179 #sequence number: 221598 A:Reference number: 221598 A:Status: preliminary: translated from GB/EMBL/DDBJ	A; Molecule type: DNA A; Residues: 1-136 <see> A; Cross-references: EMBL:AL096823; PIDN:CAB46964.1; GSPDB:GN00070; SCOEDB:SCQ11.09 A; Experimental source: strain A3(2) C; Genetics: A; Gene: ssgA; SCOEDB:SCQ11.09</see>	Query Match Best.Local Similarity 75.6%; Pred. No. 1.1e-43; Matches 102; Conservative 9; Mismatches 24; Indels 0; Gaps 0; Ov. 1 MSFIVEFFIAPPIDVEIRPEMUNDANDIMFHIDCHADVEWVERPELLINECVIDAGINGD 60		QY 61 VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120 	Qy 121 DDALNRSLAEEQSAG 135 : : Db 122 DEALDRILAEEQSAG 136	RESULT 2 T36147 probable regulator - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 C;Accession: T36147 R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999 A;Reference number: 221598 A;Accession: T36147 A;Accession: T36147 A;Molecule type: DNA A;Residues: 1-142 <see> A;Cross-references: EMBL:AL096852; PIDN:CAB51005.1; GSPDB:GN00070; SCOEDB:SCE19A.24 A;Experimental source: strain A3(2) C;Genetics:</see>
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Conservative
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Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S68694
      C;Genetics:
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R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
S; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, April 1999
A; Accession: T35247
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-138 < OLI>
A; Coss-references: EMBL: ALO49587; PIDN: CAB40672.1; GSPDB: GN00070; SCOEDB: SC5F2A.05c
A; Genetics: A; Genetics: Strain A3(2)
C; Genetics: Strain A3(2)
C; Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           М.А.
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A;Cross-references: EMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: O5-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T35119
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, Submittee to the EMBL Data Library, May 1999
A;Reference number: Z21575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                 VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                                                          LVEGVLDAAGDGDVRVCPVGQTAT-REVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSFLVSEELAFR-----IPVELRYETVDPYAVRLTFHLPG---DAPVTWVFGREL 47
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A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
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:Gene: SCOEDB:SC5F2A.05c
;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                        Length 142;
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                                                                                                                                Indels
                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 22.6%; Score 155; DB 2; 1 Similarity 31.2%; Pred. No. 1.3e-08; 44; Conservative 16; Mismatches 63.
                                                                                   Query Match 29.5%; Score 203; DB 2; Best Local Similarity 37.3%; Pred. No. 1.7e-13; Matches 47; Conservative 16; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Matches 44; Conserv
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hexokinase (EC 2.7.1.1) 1 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: protein SPAC24H6.04
C;Species: Schizosaccharomyces pombe
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68694; T38360; S62406
R;Petit, T.: Blazquez, M.A.; Gancedo, C.
R;Petit, T.: Blazquez, M.A.; Gancedo, C.
A;Title: Schizosaccharomyces pombe possesses an unusual and a conventional hexokinase
A;Reference number: S68693; MUID:96140736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:254142; NID:9984697; PIDN:CAA90848.1; PID:9984701; GSPDB:GNO A;Experimental source: strain 972h-; cosmid c24H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-484 <PRS-
A; Residues: 1-484 <PRS-
A; Cross-references: EMBL: X92894; NID: 91160507; PIDN: CAA63487.1; PID: 91160508
A; Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, September 1995
A; Reference number: 221788
A; Reference number: 221788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A83271
hypothetical protein PA2984 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AGDGDVRVCPVGQTATREVHIT-----LQVGSEQALFRVGKAPLLAFLDRT----D 102
                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                   10 AFRIPV - - ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVG 67
                                                                                                                                                                                                                                                                                         19 ADREPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRPES 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ELAFRIPVELRYETVDPYAVRLTFHL---PGDAPV--TWVFGRELLVEG------VLDA
                                                                                                                                                                                                                                                                                                                                                                                    68 QTATREVHITLQVGS-----EQALFRVGKAPLLAFLDRTDQGLSLGSERAHAD 115
                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 484;
                                                                                                                   Length 142;
                                                                                                                ; Score 117; DB 2; Length 142; Pred. No. 0.00011; 15; Mismatches 54; Indels
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 90.5; DB
Pred. No. 0.23;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1L
C;Superfamily: hexokinase; hexokinase homology
C;Reywords: ATP; phosphotransferase
F;40-466/Domain: hexokinase homology <HXK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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31.3%;
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27.0%;
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139 VHPNRIIRRSTAQVGDAIAITGVHGA-
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A; Cross-references: EMBL:AJ001932;
A; Experimental source: strain ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                        32; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local S:
Matches 29,
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Biadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Nature 406, 959-964, 2007
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                               A;Residues: Ī-741 <STO>
A;Cross-references: GB:AE004724; GB:AE004091; NID:99949083; PIDN:AAG06372.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T36380

R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A; Reference number: 221573

A; Reference number: 221573

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule Lype: DNA

A; Residues: 1-862 < OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL049628; PIDN:CAB40869.1; GSPDB:GN00070; SCOEDB:SCE94.20
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable large ATP-binding protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DSTAARVVHTAVSVGSEAAL-------QFLSRFREHTGADVQEFLATS 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GRAEVRVLDVGQGLAVLVRTREHVLLYDS 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 LRYETVDPYAVR-----LIFHLPGDAPVTWVFGREL-----LVEGVLDAAGDG-DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 AVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQ-----TATREVHITLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thiamin monophosphate kinase [imported] – Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 741;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GSEQALFRVGK---APLLAFLD-RTDQGLSLGSERAHADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 GARQGAFDMGERVVVPVLRSLDLRRLDGLLL----SHADND 558
                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%; Score 79; DB 2. Ilarity 31.7%; Pred. No. 6.7; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.9%; Score 82; DB Best Local Similarity 32.7%; Pred. No. 2.8; Matches 33; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477 ALLLPALLPSSPPVEW----
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Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SCOEDB: SCE94.20
                                                                                                                                             A; Accession: A83271
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 LNR 126
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                                                                                                                                                                                                                                                                                                                       A; Gene: PA2984
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A.Reference number: AB1807; MUID:21595285; PMID:11759840
A.Accession: AE2438
A.Sholecule type: DNA
A.Residues: 1-332 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T47267
R;Bayle, D.; Wangler, S.; Weitzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M. Bayle, D.; Wangler, S.; Weitzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M. J. Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacte A;Reference number: 224437; MUID:99101471
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T47267
A;Rolecule type: DNA
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C;Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000019; PIDN:BAB76760.1; PID:g17134199; GSPDB:GN00179 A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Helicobacter felis
C;Date: 20-Apr_2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SHAGLELLLDPKIGK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; PLGITIALALPGDLSVSWV---ERLYQGITECLQKYHTPIVGGDVVRSPITTLSITAFGQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 VH-----ITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 PYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAG-----DGDVRVCPV---GQTATRE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 332;
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                                                                                                                                                                                                                                                                                                         C.Genetics:
A.Gene: alr5061
C;Superfamily: conserved hypothetical protein MJ0640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9 T47267 cell cycle protein [imported] - Helicobacter felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%; Score 78.5; DB 25.4%; Pred. No. 2.5;
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Llarity 29.9%; Pred. No. 5.3;
Conservative 16; Mismatches
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; 9

22;

Indels

39;

DB 2;

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-291 «COL» A;Residues: 1-291 «COL» A;Cross-references: GB:Z81451; GB:AL123456; NID:g3261662; PIDN:CAB03770.1; PID:g16661 A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70678
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Natures 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MulD:98295987
                                                                                                                                                                                                                                                                                                   453 TIYYPHD-----LEGAKVLLEKVGLKDTDGNGFVNF-PAGKLGGRDVEIVLLVNSDYSTD 506
                                                                                                                                                                                                                     30 TFHLPGDAPVTWVFGRELLVE--GVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
H70678
hypothetical protein Rv2426c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                     88'R----VG---KAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNRSLAE 130
                                       11.2%; Score //, 29.5%; Pred. No. 8.3; +ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: hypothetical protein MTH1814
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Best Local Similarity 28.6%;
Matches 36; Conservative 1
                                                                                                                                           Conservative
                                                        Query Match
Best Local Similarity
Matches 33; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 DKADIE 146
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C; Superfamil***
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Brouille, S.; Pruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd. A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Ladinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuell, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffono, F.; Tognoni, A.; Tosoto, Y.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffono, K.; Yastu, Y.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffono, K.; Yastu, Y.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Yasmanoto, M.; Yasta, K.; Yoshida, K.; Authors: Schleich, A.; Yamamoto, H.; Yamano, K.; Yastu, K.; Yoshida, K.; Authors: Voshikawa, H.F.; Zumstehn, E.; Yoshikawa, H.; Danchin, A.; Alter complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Anthors: Voshikawa, H.F.; Zumstehn, E.; Yoshikawa, H.; Danchin, A.; Alter complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Anthors: Preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-346 cKun>
A;Reperimental source: strain 168
C;Genetics:
A;Reperimental source: strain 168
C;Genetics:
A;Reperimental source: strain 168
C;Genetics:
A;Genetics:
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Frinan, T. M.; Wedidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9884, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F96037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-693 < KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49966.1; PID:g15141454; GSPDB:GN00167
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C;Specdes: 24-849-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F96037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain 1021, megaplasmid psymb
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Rieference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VSEELAFRIPVELRYE---TVDP-----YAVRLTFHLPGDAPVTWVFG---RELLVEGVL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.4%; Score 78; DB 1
Best Local Similarity 39.3%; Pred. No. 2.9;
Matches 33; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 KAAGATDIYAVELSPERQOKAEEL 212
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Holroyd

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ATP-dependent zinc metallopeptidase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Varlachy: strain J99
A;Varlachy: strain J99
C;Date: 12-Feb-1999 #text_change 21-Jan-2000
C;Accession: D71941
E;Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jing, Q.; Taylor, D.E.; Vovis, G.F Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-632 (ARN>
A;Cross-references: GB:AE001471; GB:AE001439; NID:g4154880; PIDN:AAD05932.1; PID:g415
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Title: Genomic sequence comparison of two unrelated isolates of the human gastric A; Reference number: A71800; MUID:99120557
                                                          ;
9
                                                                                                                                                                                                                                                          72 REVH-----ITLQVG-----SEQALFRVGKAPLLAFLDRTDQGLSLGSER 111
                                                             Gaps
                                                                                                                                             30 TFHLPGDAPVTWVF-----GRELLVEG-------VLDAAGDGDVRV-CPVGQTAT 71
                                                       41;
  Length 291;
                                                       36; Indels
     DB 2;
; Score 76.5; DE; Pred. No. 3.4; 13; Mismatches
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A; Status: preliminary
A; Molecule type: DNA
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A;Gene: agpA; SMb21647

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Search completed: July 18, 2002, 14:17:35 Job time: 9545 sec
C; Genetics:
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                        A;Gene: ftsH_2
C;Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain homd
F;184-395/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I stage, G.; Gillet, W.; Setubal, G.; Guenthner, D.; Kutyavin, T.; Levy, R.; Ll, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2333, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein AGR_C_807 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Atu0453 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ster, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; PMID:11743193
A.Recession: AB2632
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C;Genetics:
A;Gene: AGK_C_807
A;Map position: circular chromosome
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                             44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                    215 GKTLLAKAV -- - AGEAHVPFFSMGGSSFIEMFVGLGASRVRDLFETAKKQAPSIIFIDEI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVLDAAGDGDVR------VCPVGQTATR--EVHITLQVGSEQALFRVGKAPLLAFLD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 GVLDIAADGSLRTDKDFFISVYTDGSKLIEGLELRSLASPGQLDIVFEAGVTTAHAVTD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 248;
                                                                                                                                                                          Length 632;
                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                     42;
                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 -RTDQGLSLGSERAHADFDSHLD-----DALNRS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 75.5; DB
Pred. No. 3.6;
6; Mismatches
                                                                                                                                                                       11.1%; Score 76.5; DE 29.9%; Pred. No. 8.4; tive 15; Mismatches
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Best Local Similarity 31.2%;
Matches 30; Conservative
                                                                                                                                                              Query Match
Best Local Similarity 29.98
Matches 29; Conservative
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A;Molecule type: DNA
A;Residues: 1-248 <KUR>
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Residues: 1-248 <KUR>
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C;Genetics:
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51: GVLDAAGDGDVR-----VCPVGQTATR--EVHITLQVGSEQALFRVGKAPLLAFLD 99
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                                                                                                                                  19;
                                                                                       DB 2; Length 248;
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                                                                                     Score 75.5; DB 2; I
Pred. No. 3.6;
6; Mismatches 41;
                                                                                                                                                                                                                                                                       100 -RTDQGLSLGSERAHADFDSHLD-----DALNRS 127
                                                                                                                                                                                                                                                                                                   A;Gene: Atu0453
A;Map position: circular chromosome
                                                                                     Query Match 11.0%;
Best Local Similarity 31.2%;
Matches 30; Conservative
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Gaps

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2002, 14:31:53; Search time 45.63 Seconds (without alignments) 114.555 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-749-185-5 687 1 MSFLVSEELAFRIPVELRYE......FDSHLDDALNRSLAEEQSAG 135

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		helicobacte		helicobacte	_				_	barley mild		_	escherichia	mns musculu	homo	sus scrofa		c riboflavi	bordetella	human cytom				schistosoma	escherichia			rhizobium s	Ca	4			9 mycobacteri
	SCL	009756	032617	09x4y1	09zm <u>6</u> 6	P71408	P47695	P75120	P38062	P77596	P89684	P50579	008663	P10378	747	013485	gkg	043	plj(225	P16767	343	975	P26420	P46508	P40713	P98092	005615	P55653	P46550	014624	P40831	P19725	P9688
	De	8	03	6	8	P7	P4	P7	ь3	P7	P8	P5	8	P1	P9	01	8	0	6	P1	P1	P2	Ы	P2	P4	P4	P9	8	P5	Ρ4	01	ΡĄ	Pl	Ь
SUMMARIES	ID	HXX1_SCHPO	FTSH_HELFE	AGPA_RHIME	FTSH_HELPJ	FTSH_HELPY	FTSH_MYCGE	FTSH_MYCPN	AMP2_RAT	YAGF_ECOLI	POL2_BAMMN	AMP2_HUMAN	AMP2_MOUSE	ENTE_ECOLI	SMA4_MOUSE	SMA4_HUMAN	SMA4_PIG	SMA4_RAT	RIBD_CHLMU	FHAB_BORPE	UL36_HCMVA	CNRB_BOVIN	CYA1_BOVIN	SCRK_KLEPN	YME1_SCHMA	SCRK	HMCT	AROA	GABD_	TCPZ		GLMS	POLS	YW84_MYCTU
	DB		-	Н	Н	Н	Н	, ,	Н	-	_	-	-	Н	Н	7	Н	_	٦	Н	Н	Н	~	-	-							-		-
	Query Match Length	48	63	69		632																			662	302	3133	430	491	539	930	624	1063	143
dР	Query Match	13.2	11.4	11.2		11.0		10.6	10.6	10.4	10.3	10.3	10.3	10.3	10.3	10.1	10.1	10.1	10.0	10.0	10.0	10.0	10.0	9.0		9.7	9.7					•	9.5	
	Score	90.5	78.5	77	9	75.5	73	73	72.5	71.5	71	70.5	70.5	70.5	70.5	69.5	69.5	69.5	69	69	68.5	68.5	68.5	68	S	66.5		99	99	99	9	65.5	65.5	65
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Length 484;

Score 90.5; DB 1; Pred. No. 0.11;

13.2%; 27.0%;

Query Match Best Local Similarity

P20324 bacteriopha	007212 mycobacteri	P23531 lactococcus	Q9y4w6 homo sapien	P03235 epstein-bar	Q60024 thermoanaer	048414 bacteriopha	Q00813 haloarcula	P54813 caenorhabdi	Q01243 yersinia en	1	P80668 escherichia
VCAP_BPT3	STHA_MYCTU	PTLB_LACLA	AF32_HUMAN	YEC4_EBV	CH60_THEBR	GP60_BPSP1	RPOD_HALMA	YMEH_CAEEL	YSCB_YEREN	NOLF_RHIME	FEAB_ECOLI
г	-	~	Н	Н	٦	Н	7	7	-	П	П
310	468	268	797	289	540	73	259	9/9	137	367	499
9.5	9.5	9.5	9.5	9.4	9.4	9.3	9.3	9.3	9.5	9.5	9.5
. 65	65	65	65	64.5	64.5	64	64	64	63.5	63.5	63.5
34	35	36	37	38	39	40	41	42	43	44	45

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Query Match
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 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metalloprotease;
                                                                                                | ::||| | : |;
| GGT-NLRVCAVEVQGNGKFDITQSKYRLPQELKVGTREALFDYIADCIKKFVEEVHPGKS 150
                                                                                 AGDGDVRVCPVGQTATREVHIT----- LQVGSEQALFRVGKAPLLAFLDRT----D 102
                                                                                                                                                                                                                                                                                                                                                                                   29; Gaps
                            ELAFRIPVELRYETVDPYAVRLTFHL---PGDAPV--TWVFGRELLVEG-----VLDA 55
                                                    EEQFTIPTELLHRVIDRFVSELYKGLTINPGDVPMVPTWIIGTP---DGNEHGSYLALDL 91
                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
CAA4818021A243A0 CRC64;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1 COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-1 SUBCELLULAR LOCATION: Integral membrane protein.
-1 SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC.
METALLORPOTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERIPLASMIC (POTENTIAL).
 55;
                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cell division protein ftsH homolog (EC 3.4.24.-).
                                                                                                                                                                                                                                   638 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000642; Peptidase_M41.
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ001932; CAA05102.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA.
InterPro; IPR003959; AAA_subfam.
 19;
                                                                                                                                                        ONLEIGETFSYPCVQRSINDA 171
                                                                                                                                     103 QGLSLGSERAHADFDSHLDDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70245 MW;
 Conservative
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444
638 AA;
                                                                                                                                                                                                                                                                                                                                 Helicobacter felis
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=214;
                                                                                                                                                                                                                                                                                                                                                           Helicobacter.
38;
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FTSH_HELFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Periplasmic. SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                       221 GKTLLAKAV---AGEASVPFFSMGGSSFIEMFVGLGASRVRDLFDIAKKEAPSIIFIDEI 277
                                                       44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERIPLASMIC ALPHA-GALACTOSIDE BINDING
                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99009011; PubMed-9791127;

Gage D.J., Long S.R.;

"Alpha-galactoside uptake in Rhizobium meliloti: isolation and characterization of agpA, a gene encoding a periplasmic binding protein required for melibiose and raffinose utilization.";

J. Bacteriol. 180:5739-5748(1998).
                             11;
 Length 638;
                             41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Plasmid;
                                                                                                                                                                                                                                                                                   precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E -> K (IN REF. 1).
76F9B95708C2DF9F CRC64;
 DB 1;
                                                                                                             102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                               278 D---AIGKSRAAGGMISGNDEREQTLNQLLAEMDGFG 311
                                                                                                                                                                                                                                     01-MAY 2000 (Rel. 39, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
Periplasmic alpha-galactoside binding protein
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymb (megaplasmid 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF119834; AAD26274.1; -.
EMBL; AL603647; CAC49966.1; -.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 2.
PF00496; SBP_BACTERIAL_5; FALSE_NEG.
Sugar transport; Transport; Periplasmic; Sign
                                                                                                                                                                                                               693 AA
                           16; Mismatches
11.4%; Score 78.5; 29.9%; Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                           Conservative
                                                                                                                                                                                                               STANDARD;
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693
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              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693 AA;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                             29;
                                                                                                                                                                                                            AGPA_RHIME
Q9X4Y1;
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-1021
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                Best Local
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Venter J.C.;
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ID FTSH_H
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                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Hydrolase; Metalloprotease;
                                                                   MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
                                                    30 TFHLPGDAPVTWVFGRELLVE--GVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT 2INC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                 Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIAILARITY).
                                                                                                  R-----VG---KAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNRSLAE 130
                                                                                                               Length 693;
                              39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-C77-2001 (Rel. 40, Last annotation update)
Cell division protein ftsH homolog (BC 3.4.24.-).
        DB 1;
                                                                                                                                                                                   632 AA.
       ch 11.2%; Score 77; DB 1 Similarity 29.5%; Pred. No. 3.8; 33; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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InterPro; IPR003593; AAA.
InterPro; IPR003950; AAA_sub.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
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PROSITE; PS00674; AAA; 1.
Cell division; ATP-binding;
                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                      NCBI_TaxID=85963;
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138
210
434
435
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        Query Match
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                    Local
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FTSH_HELPJ
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
MEDLINE-97394467; PubMed-9252185;
Tomb J.F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.F., White O., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                      215.GKTLLAKAV---AGEAHVPFFSMGGSSFIEMFYGLGASRVRDLFETAKKQAPSIIFIDEI 271
                                                                                                                                                                                                                                                                 44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                   Gaps
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J. Biol. Chem. 271:446-457(1996).
-!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melchers K., Weitzenegger T., Buhmann A., Steinhilber W., Sachs G., Schafer K.P., "Cloning and membrane topology of a P type ATPase from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-CC016 17874 / NCTC 11638;
MEDLINE=97386403; PubMed=9244252;
Beier D., Spohn G., Rappuoli R., Scarlato V.;
Hidentification and characterization of an operon of Helicobacter pylori that is involved in motility and stress adaptation.";
J. Bacteriol. 179:4676-4683(1997).
                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequencing, expression, and genetic characterization of the Helicobacter pylori fish gene encoding a protein homologous to members of a novel putative ATPase family."; J. Bacteriol. 178:6151-6157(1996).
ZINC (CATALYTIC) (BY SIMILARITY).
2FB67B43C51559FB CRC64;
                                                                                                                                  Length 632;
                                                                                                                                                                                                42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P71408; O07679; 048268; 01-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 40, Last annotation update) Cell division protein ftsH homolog (EC 3.4.24.-). FTSH.OR HP1069.
                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 76.5; DI 29.9%; Pred. No. 3.8;
                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-NOTC 11639 / UA802;
MEDIINE-9704792; PubMed-8892813;
Ge Z., Taylor D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96132941; PubMed=8550601;
                              69765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 324-632 FROM N.A.
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
438 4
632 AA;
                                                                                                                                                                 Similarity 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=210;
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Bacillus/Clostridium group; Mollicutes;

Last sequence update)
Last annotation update)
ftsH homolog (EC 3.4.24.-).

Created)

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SEQUENCE FROM N.A.

STRAIN-ATCC 3353 / G-37;

STRAIN-B-6026346; PubMed-756993;

Fraser C.M., Gocsyne J.D., White O., Adams M.D., Clayton R.A.,

Fraser C.M., Gocsyne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Fritchman D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Forberson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,

Fritchman and A. Bott K.F., Hu P.-C., Lucier T.S.,

Feterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

(BY SIMILARITY).
                                                                                  Mycoplasmataceae; Mycoplasma
                                                           Mycoplasma genitalium.
Bacteria; Firmicutes;
                                   Cell division protein
  01-FEB-1996 (Rel.
                         16-OCT-2001 (Rel.
                                                                                               NCBI_TaxID-2097;
                                                 FTSH OR MG457
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TRANSMEM
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METAL
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Matches
  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA_sub.
InterPro; IPR003596; AAA_sub.
InterPro; IPR003595; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
PROSTE; PS00674; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease; Zinc; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
G -> P (IN REF. 1).
V -> MI (IN REF. 1).
L -> F (IN REF. 2).
H -> D (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%; Score 75.5; DB 1; Length 632; 29.9%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQ -> FE (IN REF. 1).
RQ -> KL (IN REF. 1).
R -> K (IN REF. 1).
I -> M (IN REF. 2).
A -> G (IN REF. 2).
S -> Y (IN REF. 2).
V -> F (IN REF. 2).
K -> E (IN REF. 1).
V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1D0674163FFC206D CRC64;
(BY SIMILARITY).

COFACTOR: BINDS 1 ZINC IÓN (POTENTIAL).

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 D---AIGKSRAAGGVVSGNDEREQTLNQLLAEMDGFG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 DOGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.
                                                                                                                                                                               EMBL; U59452; AAC44563.1; -. EMBL; U97567; AAB66377.1; -. EMBL; AE000614; AAD08115.1; -. EMBL; U58625; AAB05472.1; -. MEROPS; M41.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
4430
4430
455
455
616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354
                                                            METALLOPROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576
616
632 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3354
3366
401
430
449
455
                                                                                                                                                                                                                                         HP1069;
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TRANSMEM
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METAL
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NP_BIND
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003960; AAA_sub.
Interpro; IPR003959; AAA_subfam.
Interpro; IPR000642; Peptidase_M41.
Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
SMART; SM00382; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GRELLVEGVLDAAGDGDVRVCPVGQ-TATREVHITLQVGSEQA--LFRVGK--APLLAFL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ATP (POTENTIAL).
AID (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC (CATALYTIC) (BY SIMILARITY). ADB26C68CD780535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%; Score 73; DB 1; Length 702; 30.9%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
EXTRACELLULAR (POTENTIAL)
-:- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 DRTDQGLSLGSERAHADFDSH--LDDALNRSLAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76729 MW;
                                                                                                                                                                                                                                                                                                                           EMBL; U39732; AAB01647.1; -. EMBL; U39727; AAC72477.1; -. HSSP; P09372; IDKG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003593; AAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
45
179
197
702
278
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                                                                                                METALLOPROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493
494
497
702 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; M41.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; MG457; -
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702 AA.

PRT;

STANDARD;

FTSH_MYCGE P47695;

FTSH_MYCGE RESULT A D Ŋ

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8
                                                                                           RESULT
AMP2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                       "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
D07585386C8B4C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                  Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                       Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               (BY STATLARITY).
-!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-!- SUBCELDULAR LOCATION: INTEGTAL membrane protein.
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC METALLOPROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cell division protein [tsH homolog (EC 3.4.24.-).
FTSH OR MPN671 OR MP171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%; Score 73; DB 1; larity 30.9%; Pred. No. 9.8; Conservative 17; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
ZINC (CATALYTIC)
BY SIMILARITY.
330 DEID---SVGSKRGRVELSSYSVVEQTLNQLLAE 360
                                                                                           709 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA.
InterPro; IPR003509; AAA_sub.
InterPro; IPR00359; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
Pfam; PF00134; Peptidase_M41; 1.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000018; AAB95819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77735 MW;
                                                                                                                                                                                                                                 Mycoplasmataceae; Mycoplasma
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192
709
275
490
491
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709 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M41.001;
                                                                                                                                                                                                                                               NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc; Complete
                                                                                                                                                                                                                                                                                                                                          Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                        pneumoniae.
                                                                                         FTSH_MYCPN
P75120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
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NP_BIND
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                         FTSH_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=REUBER H35; TISSUE=Liver;
MEDLINE=93266517; PubMed=8496145;
Wu S., Gupta S., Chatterjee N., Hileman R.E., Kinzy T.G.,
Denslow N.D., Merrick W.C., Chakrabarti D., Osterman J.C., Gupta N.K.;
"Cloning and characterization of complementary DNA encoding the
eukaryotic initiation factor 2-associated 67-kDa protein (p67).";
J. Biol. Chem. 268:10796-10801(1993).
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                  01-0CT-1994 (Rel. 30, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Poftidase M 2)
METAP2 OR MNPEP OR P67EIF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
-!- PTM: CONTAINS 12 O-LINKED GLCNAC.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C; ALSO KNOWN AS THE
MAP FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS.
FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY
PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE
REGULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE
EIF-2 GAMMA-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)0 = L-METHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95372350; PubMed=7644482; Meaver L.H., Stewart A.E., Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E., Mattins S.M., Bradshaw R.A.; Bradshaw R.A.; "Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent enzymes." proc. Natl Acad. Sci. U.S.A. 92:7714-7718(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-LYS.
COBALT 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0599; MAPEPTIDASE.
PROSITE; PS01202; MAP_2; 1.
Hydrolase; Aminopeptidase; Cobalt; Glycoprotein.
                                                                                                                                  478 AA
99 DRTDQGLSLGSERAHADFDSH--LDDALNRSLAE 130
                      327. DEID---SVGSKRGRVELSSYSVVEQTLNQLLAE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR002468; MAP_2.
Interpro; IPR001714; Methamino_PTase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001714; Methamino_Prase
InterPro; IPR000994; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; 1.
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L10652; AAA41111.1; -.
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
106
251
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HSSP; P56218; 1XGS.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; M24.002;
                                                                                                                              AMP2_RAT
P38062:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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; 9

Gaps

16;

32; Indels

Similarity

Local

29;

44 Matches

δŏ

GRELLVEGVLDAAGDGDVRVCPVGQ-TATREVHITLQVGSEQA--LFRVGK--APLLAFL 98

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                                                                                                                                                                             8;
COBALT 1 AND 2 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 AND 2 (BY SIMILARITY).
LRPTCKEVVSRGDDY -> CAQPVKKLSAEEMTIKT (IN
                                                                                                                                                                                                                                       242 LQYDDI----CKIDFGTHISGRIIDCAFTVTFNPKYDILLKAVKDATNTGIKCAGIDVRL 297
                                                                                                                                                                              Gaps
                                                                                                                                                                                                           17 LRYETVDPYAVRLTF--HLPG----DAPVTWVFG--RELLVEGVLDAAGDG------DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Rlathg M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO E.COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chung E.,
urdi O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                           Score 72.5; DB 1; Length 478; Pred. No. 6.9;
                                                                                                                                                                                                                                                                        64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Lyase; Complete proteome.
SEQUENCE 655 AA; 69399 MW; 208AF2F6DB39EE8B CRC64;
                                                                                              BE1COE91E0CB3D74 CRC64;
                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                   ol-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yagF.
Eschart.
                                                                                                                                                                           20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD002691; ILVD_EDD; 1. PROSITE; PS00886; ILVD_EDD_1; 1 PROSITE; PS00887; ILVD_EDD_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE000134; AAC73372.1; -. EMBL; U70214; AAB08650.1; -. ECGENE, EG13345; yagF. InterPro; IPR000581; ILVD_EDD. Pfam; PF00920; ILVD_EDD; 1.
                                                                                              53052 MW;
                                                                                                                                          10.6%;
28.8%;
                                                                                                                                                                             Conservative
   262
331
364
459
478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                          Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                            478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
   262
331
364
459
464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YJHG.
                                                                                              SEQUENCE
                                                                  CONFLICT
   METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPLER COMPONENT PROTEINASE (POTENTIAL).
70 KDA PROTEIN.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 FGMTQNAGMGWDANKLTGKEVLIIGTQGGIRAGDGRPIALGYHTGHWEIGMQMQAAAKE- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AESLQFHVIDKRGVPGMWNILKAGRVYELLSLAADG---------VGCE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 QALFRVGKAPLLAF-----LDRTDQGLSLGSERAHA---DFDSHLDDALNRSLAEE 131
                                Gaps
                                                            31 FHLPGDAPVTW----VFGRELLVEGVLDAAGDGDVRVCPVG-QTATREVHITLQVGSEQA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 AVRLIFHLPG--DAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete nucleotide sequence and genome organization of barley
                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein 2 [Contains: Helper component proteinase
(EC 3.4.22.-) (HC-PRO); 70 kDa protein].
Barley mild mosaic virus (strain Nal) (BaMMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
                                                                                                                                             86 LFRVGKAPLLAFLDRTDQGLSLGSERAHADFDS--HLDDA-----LNRSL 128
 Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEAVAGE (BY HC-PRO PROTEASE)
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
A290247196822BE2 CRC64;
                              43;
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 AA
                                19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
Score 71.5; 1
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001337; TMV_coat.
Pfam; PF00721; TMV_coat; 1.
Polyprotein; Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97128984; PubMed-8973524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mild mosaic virus (Nal strain).";
Arch. virol. 141:2077-2089(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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28.2%;
10.4%;
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                                Conservative
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                                                                                                                                                                                                                                     STANDARD;
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        891 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Bymovirus.
NCBI_TaxID=103900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kashiwazaki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
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                                32;
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ACT_SITE
SITE
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POL2_BAMMN
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                                                                                                                                                                                                                              MEDLINE=95372350; PubMed=7644482;
Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,
Matthews B.W., Bradshaw R.A.;
"Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent
                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
(Initiation factor 2 associated 67 KDa glycoprotein) (p67) (p67eIF2).
METAP2 OR MNPEP OR P67EIF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C; ALSO KNOWN AS THE MAP FAMILY 2.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEINS.
-:- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)0 = L-METHIONINE + PEPTIDE.
+ PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 282:1324-1327(1998).
-!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.
MEDLINE-59030697; PubMed-9812898;
Liu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;
"Structure of human methionine aminopeptidase-2 complexed with fumagillin.";
                                                                                                                                                                                                                                                                                                                                                            Li X., Chang Y.;
Molecular cloning of a human complementary DNA encoding an
initiation factor 2-associated protein (p67).";
Biochim. Biophys. Acta 1260:333-336(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COBALT 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001714; Methamino_Prase.
InterPro; IPR000994; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; 1.
PRINTS; PR00599; MAPEPTIDASE.
PROSTTE; PS01202; MAP. 2; 1.
Hydrolase; Aminopeptidase; Cobalt; 3D-structure.
                                              478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-LYS.
                                              PRT;
                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
MEDLINE=95178556; PubMed=7873610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U29607; AAA82930.1; -. EMBL; U13261; AAC63402.1; -. PDB; 114-JAN-00. MEROPS; M44.002; -. MIM; 601870; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002468; MAP_2.
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
93
106
231
251
                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                       TISSUE=Brain;
                                              AMP2_HUMAN
P50579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
ACT_SITE
METAL
                                                                                                                                                                                                                                                                                      enzymes
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                                  AMP2_HUMAN
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                                                                                                                                                                                                                                                                                                                242 LQYDDI----CKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKCAGIDVRL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
(Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).
METAP2 OR MNPEP OR P67EIF2.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                   17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG------DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6 x CBA; TISSUE-Liver;
Sekiquchi S., Suzuki E.;
Sekiquchi S., Suzuki E.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS (BY SIMILARITY).
-!- FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE RECULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE EIF-2 GAMMA-SUBUNIT (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)O = L-METHIONINE
+ PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity). SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                 25;
COBALT 1 AND 2 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 AND 2 (BY SIMILARITY).
5788E4BBB35E48F9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                            10.3%; Score 70.5; DB 1; Length 478; 28.8%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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ASP/GLU-RICH (ACIDIC).
POLY-LYS.
COBALT 2 (BY SIMILARITY).
                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 AA.
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InterPro; IPR001714; Methamino_PTase.
InterPro; IPR000994; Peptidase_M24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB003144; BAA19789.1; -.
                                                                                                       MW.
  262
331
364
459
52891
                                                                                                                                                                                                                                 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
93
106
251
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262
331
364
459
478 AA;
                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMP2_MOUSE
008663;
                                                                                                    SEQUENCE
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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     METAL
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CONFLICT
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                                                                                                                                                                                                                                                                      P10378; P15049; P77773; 01-MRR-1989 (Rel. 10, Created) 01-NOV-1997 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 2,3-dihydroxybenzoate-AMP ligase (EC 6.3.2.) (Dihydroxybenzoic acidactivating enzyme) (Enterobactin synthetase component E) (Enterochelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ο,,
                                                                                                                                              Gaps
                                                                                                                                17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG-----DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-KI / MG1655,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 393-546 FROM N.A.
MEDLINE-89123155; PubMed-2521622;
Liu J., Duncan K., Walsh C.T.;
Inu Join Sequence of a cluster of Escherichia coli enterobactin biosynthesis genes: identification of entA and purification of its product 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase.";
J. Bacteriol. 171:791-798(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elkins M.F., Earhart C.F.; "Opacity factor from group A streptococci is an apoproteinase."; FEMS Microbiol. Lett. 56:35-40(1988).
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M. Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                         25;
COBALT 1 AND 2 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 AND 2 (BY SIMILARITY).
BBBB9A2AFC19952E8 CRC64;
                                                                                                                                                                                            298 CDVGE-AIQEVWESYEVEIDGKTYQV--KPI-----RNLNGHSIGPYRIHA 340
                                                                                10.3%; Score 70.5; DB 1; Length 478; 28.8%; Pred. No. 11;
                                                                                                                                                                            64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staab J.F., Elkins M.F., Earhart C.F.; "Nucleotide sequence of the Escherichia coli entE gene."; FEMS Microbiol. Lett. 50:15-19(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                         35; Indels
                                                                                                                                                                                                                                                               Ä.
                                                                                                         19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89290355; PubMed-2525505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90236256; PubMed-2110093;
262
331
364
CC
364
CC
459
CC
52921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-8 FROM N.A.
                                                                                                         Conservative
                                                                                                                                                                                                                                                               STANDARD;
262
331
364
459
478 AA;
                                                                                             Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        ENTE OR B0594.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                              synthase E)
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                                              SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 ITLQVGSEQALFRVGKAPLLAFLDRTDQGLS-----LGSERAHADFDSHLDDALN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 LTFHLPGDAPVTWVFGRELLVEGVLDAAGD------GDVRVCPVGQTATREVH 75
PUNCTION: ACTIVATION OF THE CARBOXYLATE GROUP OF 2,3-DIHYDROXY-BENZOATE (2,3-DHB), VIA ATP-DEPENDENT PPI EXCHANGE REACTIONS, TO THE ACTIVADENTLATE, PREPARING THAT MOLECULE FOR THE FINAL STAGES OF ENTEROBACTIN SYNTHESIS.

PATHWAY: ENTEROBACTIN BIOSYNTHESIS. ENTEROBACTIN IS AN IRON-CHELATING COMPOUND INVOLVED IN TRANSPORTING IRON FROM THE BACTERIAL ENVIRONMENT INTO THE CELL CYTOPLASM.

SUBUNIT: PROTEINS ENTE, ENTE, ENTE, AND ENTG FORM A MULTIENZYME COMPLEX CALLED ENTEROCHELIN SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWA4_MOUSE STANDARD; PRT; 551 AA.
P97471; Q9CW56;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 LIRHAASDS-IAVIDGERQLSYRELNQAADNLACSLRRQGIKPGETALVQLGNVA--ELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Enterobactin biosynthesis; Iron transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 70.5; DB 1; Length 536; 26.6%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAEGNPLPQG -> ECRRKSTAAR (IN F818942DFDDBDC99 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane; Complete proteome RANSMEM 86 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000165; AAC73695.1; -...
EMBL; X15058. CAA3158.1; -...
EMBL; M24148; AAA16101.1; -...
EMBL; M36700; AAA18492.1; -...
EMBL; M03070; SYECEB.
PIR; A00076; SYECEB.
PIR; A48308; A48308.
ECGENE; EGIOCÓS; entE.
InterPro; IPR000873; AMP-bind.
Pfam; PP050501; AMP-binding; 1...
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                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
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                                                                                                                                                                                           RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Winter 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disruption in mice.";
Cytokine Growth Factor Rev. 11:49-58(2000).
-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA (TRANSPORTHING GROWTH FACTOR) SUPERFAMILY; SMAD4 IS THE COMMON SMAD (CO-SMAD) (BY SIMILARITY). REQUIRED FOR GASTRULATION. MAY ACT AS A TUMOR SUPPRESSOR.
                                                                           Anna C.H., Devereux T.R.; "Sequence and chromosomal mapping of the mouse homolog (Madh4) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBUNIT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).
INTERACTS WITH C-SKI, MSG1 AND ATF2 (BY SIMILARITY).
-:- SUBCELLUIAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND, MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: BELONGS TO THE DWARFIN/SMAD FAMILY.
-!- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
-!- SIMILARITY: CONTAINS 1 DWB/MH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               franscription regulation; Multigene family.
                                                                                                                                                    SEQUENCE OF 67-551 FROM N.A.
STRAIN-C57BL/6J; TISSUE-Lung;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20175825; PubMed-10708952;
                                              STRAIN=A/J; TISSUE=Lung;
MEDLINE=97311184; PubMed=9166592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q13485; 1DD1.
MGD; MGI:894293; Madh4.
InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin.A.
                                                                                                        human DPC4/MADH4 gene.";
Mamm. Genome 8:443-444(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U79748; AAB57905.1; -. EMBL; AK004804; BAB23576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00968; Dwarfin; 1.
SWART; SM00523; DWA; 1.
SWART; SM00524; DWB; 1.
                                SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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MEDLINE-96371046; PubMed-8774881;
Zhang Y., Feng X.-H., Wu R.-Y., Derynck R.;
"Receptor-associated Mad homologues synergize as effectors of the TGF-
                                                                                                                                                                                                                                                                                                                                          303.VHNELAFQPPISNHPAPEYWCSIAYFEMD-VQVGETFKVPSSCPV------VTVDGYVD 354
                                                                                                                                                                                                                                                                                                             5 VSEELAFRIPV------ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against
DPP homolog 4) (Deletion target in pancreatic carcinoma 4) (hSMAD4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moskaluk C.A., Hruban R.H., Schutte M., Lietman A.S., Smyrk T., Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96144684; PubMed-8553070;
Hahn S.A., Schutte M., Shamsul Hoque A.T.M., Moskaluk C.A.,
da Costa L.T., Rozenblum E., Weinstein C.L., Fischer A., Yeo C.J.,
Hruban R.H., Kern S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu F., Pouponnot C., Massague J.;
"Dual roile of the Smad4/DPC4 tumor suppressor in TGFbeta-inducible
transcriptional complexes.";
Genes Dev. 11:3157-3167(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequencing of DPC4 in the analysis of familial pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
CHARACTERIZATION OF SAD DOMAIN.
MEDLINE=20102728; PubMed=10636916;
de Caestecker M.P., Yahata T., Wang D., Parks W.T., Huang S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hruban R.H., Kern S.E.;
"DPC4, a candidate tumor suppressor gene at human chromosome
18q21.1.";
                                                                                                                                                                                                         DB 1; Length 551;
                                                                        S -> A (IN REF. 2).
R -> P (IN REF. 2).
0835EF88D9C1C980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT CARCINOMA HIS-493
                                                                                                                                                                                                                                                                                                                                                                                                                                                355' PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 384
                                                                                                                                                                                                                                                                                                                                                                                                                55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 AA
                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                       10.3%; Score 70.5; I
32.0%; Pred. No. 13;
                                                     POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Diagn. Mol. Pathol. 6:85-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97253203; PubMed=9098646;
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                                                                                                                              60417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 271:350-353(1996).
                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 383:168-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
319
529
465
257
292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
274
320
450
257
292.
551 AA;
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                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissur=Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMA4_HUMAN
Q13485;
                                                                        CONFLICT
                                                                                                                              SEQUENCE
                                                                                                                                                                                                            Query Match
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Hill C.S., Shioda T., Roberts A.B., Lechleider R.J.;
"The Smad4 activation domain (SAD) is a proline-rich, p300-dependent transcriptional activation domain.";
J. Biol. Chem. 275:2115-2122(2000).
                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 285-552.
MEDLINE-20113477; PubMed-10647180;
Oin B., Lam S.S., Lin K.;
"Crystal structure of a transcriptionally active Smad4 fragment.";
Structure 7:1493-1503(1999).
                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS) OF 273-552.
MEDLINE-21127490; Pubmed-11224571;
Chacko B.M., Qin B., Correia J.J., Lam S.S., de Caestecker M.P.,
                                                                                                                                                                                                                                        The L3 loop and C-terminal phosphorylation jointly define Smad
                                                    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 319-543.
MEDLINE-97357157; PubMed-9214508;
Shi Y., Hata A., Lo R.S., Massague J., Pavletich N.P.;
"A structural basis for mutational inactivation of the tumour suppressor Smad4.";
Nature 388:87-93(1997).
                                                                                                                                                                                                                                                                                                                                                                     Verschueren K., Huylebroeck D.;
Remarkable versatlity of Smad proteins in the nucleus of
Transforming growth factor-beta activated cells.";
Cytokine Growth Factor Rev. 10:187-199(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine Growth Factor Rev. 11:5-13(2000).
                                                                                                                                                                                                                                                                                                               "TGF-beta signal transduction.";
Annu. Rev. Biochem. 67:753-791(1998).
                                                                                                                                                                                                                                                 protein trimerization.";
Nat. Struct. Biol. 8:248-253(2001).
                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20112302; PubMed-10647776;
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Wrana J.L., Attisano L.;
"The Smad pathway.";
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304 VHNELAFQPPISNHPAPEYWCSIAYFEMD-VQVGETFKVPSSCPI------VTVDGYVD 355
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D -> H (IN PANCREATIC CARCINOMA).
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DOMAIN 31 140 DWA.
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7EE3C4647712DA90 CRC64;
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30.9%; Pred. No. 16;
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                                                     EMBL; AF045441; AAC03051.1; JOINED. EMBL; AF045441; AAC03051.1; JOINED. EMBL; AF045444; AAC03051.1; JOINED. EMBL; AF045444; AAC03051.1; JOINED. EMBL; AF045445; AAC03051.1; JOINED. EMBL; AF045446; AAC03051.1; JOINED. EMBL; U44378; AAA91041.1; -. PDB; IDDI; 24.NOV-99. PDB; LDBB; 29-NOV-00.
                AF045440; AAC03051.1; JOINED. AF045440; AAC03051.1; JOINED.
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InterPro; IPR003619; Dwarfin_A.
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AAC03051.1;
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              AAC03051.1
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SMART; SM00524; DWB; 1.
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MIM; 600993;
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Search completed: July 18, 2002, 14:31:54 Job time: 943 sec

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; AF045447; AAC03051.1; -.

OM protein

Run on:

Sequence:

Searched:

Database

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043060 porphyridiu
043061 porphyridiu
0490h8 campylobact
092tw5 rhizobium n
098c85 rhizobium n
098c85 streptomyce
09xa56 streptomyce
09ya04 streptomyce
09stx6 treptomyce
09stx7 rhizobium n
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Q96ta2 homo sapien
Q60500 homo sapien
Q9keb8 bacillus ha
Q9kxv7 streptomyce
Q9zng9 pseudomonas
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1888;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces albus ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195771; AAG28482.1; ...
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100.0%; Pred. No. 1.2e-60;
ive 0; Mismatches 0;
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069245
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Q9L950
Q9NEK2
Q9V2C0
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Best Local Similarity 100.
Matches 135; Conservative
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Streptomyces albus
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Copyright (c) 1993 - 2000 Comp
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van Wezel G.P., Rousseau C., Kraal B.;

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";

submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF195770; AAG28481.1; -.

SEQUENCE 135 AA; 14843 MW; 32006CC86BDE4ED6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J., Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coellcolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96 (1996).
EEMBL. AL096823; CAB469641.1.
SEQUENCE 136 AA; 14920 MW; 4B67CIFIEOBECC88 CRC64;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          James K.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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75.6%; Pred. No. 6.9e-42;
iive 9; Mismatches 24;
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MEDLINE-97000351; PubMed-8843436;
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Matches 102; Conservative
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                                                                                               Shinichi K., Ensign J.; "Control of a gene involved in sporulation and "Cloning and characterization of Streptomyces griseus."; submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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EMBL: D50051; BAA21558.1: -. SEQUENCE 136 AA; 14783 MW; C6A28A7823AD7C8B CRC64;
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65.9%; Pred. No. 1.6e-38;
ive 18; Mismatches 28; Indels
  Length 135
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Score 481; DB 2;
Pred. No. 3.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA.
     Query Match 70.0%; Score 481; DB Best Local Similarity 71.1%; Pred. No. 3.36* Matches 96; Conservative 14; Mismatches
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Matches 89; Conservative
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MEDLINE=97000351; PubMed=8843436;
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Submitted (JUL-1999)
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Best Local Simi
Matches 51;
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"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";
"Embmitted (OCT-1929) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195772; AAG28483.1; -
SEQUENCE 145 AA; 15838 MW; 92AC0F30DF3D2620 CRC64;
                                                                                                                                                                                                                                                              Streptoverticillium netropsis (Streptoverticillium flavopersicus).
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Seeger K.J., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Cerdeno A.M., Parkhill J.,
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131 EAALGKILAEEQNAG 145
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122 EDALGRILAEEQNAG 136
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                                               DDALNRSLAEEQSAG
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Best Local Similarity
Matches 85; Conserv
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Wb Streptomyces coelicolor A3(2) chromosome.";
MOI. Microbiol. 21:77-96(1996).
EMBL; AL096652; CAB51005.1; -.
SEQUENCE 142 AA; 15364 MW; 857862390AA51CCB CRC64;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map is treptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL137778; CAB70943.1; -. SEQUENCE 159 AA; 17472 MW; BA41013F940D7315 CRC64;
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteridae;
Actinomycetalees; Streptomycineae, Streptomycetaceae; Streptomyces.
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Last annotation update)
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40.2%; Pred. No. 1.6e-14;
iive 12; Mismatches 64;
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MEDLINE=97000351; Pubmed=8843436;
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SEQUENCE FROM N.A.
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                     STRAIN-A3(2);
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL049587; CAB40672.1;
 77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLGIDDGL 136
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                   Streptomyces coelicolor.

Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-97000351; PubMed-8843436;
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                       121 DDALNR 126
                                          137 AELLAR 142
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                                                                                                                                                                                                                                                                                Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL391041; CAC01575.1; --
SEQUENCE 156 AA; 17188 MW; 7181972EEFF33FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical me the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL: ALOA9863; CAB42228.1; --
SEQUENCE 142 AA, 15741 MW; E24AA52C00AF40F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 156;
                                                                                                         STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 EVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%; Score 134; DB 2; Length 15
31.5%; Pred. No. 1.1e-05;
tive 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oliver K., Harris D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                         STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 31.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBL PUTATIVE REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-A3(2);
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SEQUENCE FROM N.A.
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                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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DB 2; Length 142;

17.0%; Score 117;

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Q9RKC9

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SERAIN—ATCC 15692 / PAO1;
STRAIN—ATCC 15692 / PAO1;
MEDLINE—2043737; Pubmed—10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brioth K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E., W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 MD Streptomyces coelicolor A3(2) chromosome.";
Mol..Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 ALLILPALLPSSPPVEW--------GRAEVRVLDVGQGLAVLVRTREHVLLYDS 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AVRLIFHILPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQ----TATREVHITLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 protein; Complete proteome.
741 AA; 79979 MW; 2C17D3850CEB98D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B380462A621C7BDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE LARGE ATP-BINDING PROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GSEQALFRVGK --- APLLAFLD - RTDQGLSLGSERAHADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%; Score 82; DB 16;
32.7%; Pred. No. 9.7;
Live 8; Mismatches 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 79; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 862 AA.
                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004724; AAG06372.1; -.
InterPro; IPR001279; Beta_lactam_met.
Pfam; PF00753; lactamase_B: 1.
Hypothetical protein; Complete proteon
SEQUENCE 741 AA; 79979 MW; 2C17D38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=97000351; Pubmed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOI..Microbiol. 21:77-96(19)
EMBL; AL049628; CAB40869.1;
ATP-binding.
SEQUENCE 862 AA; 94537 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 33; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
                                 NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2)
         Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCE94.20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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         OC SERVICE SER
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                                 3;
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                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                 19 ADRFPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRPES 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 IPVELRYE-TVDPYAVRLTFHLPG-----DAPVTWVFGRELLVEGVLDAAGDGDVRVCPV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AFRIPV -- ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A set of ordered cosmids and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL132674; Cabs.
Hypothetical protein.
SEQUENCE 126 AA; 13742 MW; D54A8574D28B4D69 CRC64;
                                                                                                                                                                                                        68 QTATREVHITLQVGS------EQALFRVGKAPLLAFLDRTDQGLSLGSERAHAD 115
                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%; Score 107.5; DB 2; Length 126; 36.1%; Pred. No. 0.0035; tive 13; Mismatches 34; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN PA2984.
      31.3%; Pred. No. 0.00046;
tive 15; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: | :: | |: | | | GR----VQAVVEFHSPQGCSVVQFENKALIRFLRRT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GQTATREVHITLQVGSEQ -- ALFRVGKAPLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              741 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL 13.7 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCE87.09C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9RKC9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HZM0
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                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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         9
                                                                       64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDA 123
                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 EGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGS 109
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 DGTSDSDSDPDPPK-PEGDTRRQELLARI-----AMIQTSKVRLTDFLDERSEYLTKFA 92
                              LRYETVDPYAVR-----LIFHLPGDAPVTWVFGREL-----LVEGVLDAAGDG-DVRV 63
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN—EV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Barnstead M.E.,
Romain C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.,
"Arabidopsis thaliana chromosome III Pl MZB10 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009326; AAD56321.1; -.
EMBL; AC009326; AAD56321.1; -.
                                                  LRYAAEVAPTVRGRVEDGLATHVP - - - PTTFEAAREVARAGGDLVLGLLPGPEDGID - - -
           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
DNA Res. 0:0-0(1997).
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 AA
                                                                                                                                                                                           258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
Pred. No. 23;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 78; 29.7%; Pred. No.
                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                Created)
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 31.7%; Pred.
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05,
19,
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           39; Conservative
                                                                                                                                                                                           PRELIMINARY;
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=MARBURG 168;
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Matches 30; Conserv
 Best Local Similarity
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RA Kunst E- 3044403; Fulmeu-33043/;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Broullet S., Bruschi C., Brans A., Braun M., Brignell S.C., Bron S.,
Broullet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Broullet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Gallazia A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollghtly E.J., Grandl G.,
RA Hilbert H., Holsappel S., Hosono S., Haloch J., Harwood C.R., Henaut A.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lepidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sato T., Wambult R., Wadler R., Wenler R., Vassarotti A.,
Varita A., Wambult R., Wadler E., Woshikawa H., Danchin A.;
RA Winters P., Wabbut A., Yamamoch H., Yamane K., Yasumoto K., Yatu K.,
RA Winters P., Wabbutt R., Wadler E., Woshikawa H., Danchin A.;
Phylic M., Tamamoch H., Yamane K., Yoshikawa H., Danchin A.;
Phylic M., Promice of the gram-positive bacterium Bacillus
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VSEELAFRIPVELRYE---TVDP----YAVRLTFHLPGDAPVTWVFG---RELLVEGVL 53
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Pred. No. 9.8;
6; Mismatches 29; Indels
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PROSITE; PS00059; ADH_ZINC; 1.
Complete proteome; Oxidoreductase; Zinc.
SEQUENCE 346 AA; 37341 MW; 5E327192D678F8A2 CRC64;
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Job time: 944 sec
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                                                                 MEDLINE-98044033; PubMed-9384377;
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InterPro; IPR002085; Adh_zn_fa
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HSSP; P07846; 1SDG.
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Best Local Similarity 39.3
Matches 33; Conservative
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FROM N.A.
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nucleic search, using sw model

nucleic

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1797656 seqs, 10463268293 residues hits satisfying chosen parameters:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

US-09-749-185-6 407

Perfect score:

Sequence:

Listing first 45 summaries

GenEmbl:*

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Minimum Match 0% Maximum Match 100%

Post-processing:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of

Searched:

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LUITEN RUDOLF GIJSBERTUS MARIA (NL); WEZEL GILLES PHILIPPUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                ALS96162 Streptomy
AL646086 Ralstonia
AL040587 Streptomy
AL341751 Streptomy
L14612 Pseudomonas
AE001952 Deinococc
AL163003 Streptomy
AL589708 Streptomy
AL589708 Streptomy
Continuation (3 of
                                             AX007218 Sequence
AX007218 Sequence
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AX07220 Sequence
AX07220 Sequence
AX087320 Sequence
AX08333 S.albus bet
AL33778 Streptomy
AL33778 Streptomy
AL33778 Streptomy
AL35178 Streptomy
AX089419 Sequence
AX089419 Sequence
AX089419 Sequence
AX089410 Sequence
AX089413 Streptomy
Continuation (7 of
AL66079 RA1sconia
AR070943 Streptomy
U52907 Thermus agu
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Streptomyces goldeniensis.
Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

(hases 1 to 407)

(hases
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AE005987 Caulobact
AL592292 Streptomy
AL049863 Streptomy
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AL079356 Streptomy
AL359988 Streptomy
AC078894 Oryza sat
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1. .407
/organism="Streptomyces goldeniensis"
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LMFLCHR16_03
LMFLCHR36_31
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Sequence 7 from Patent W00000613.
AX007222 4X007222.1 GI:9995088
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SCBAC16H6
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SC5F2A
SC9E12
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AP003575
AB070943
AX007222
AF195770
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AE001952
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AF195772
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13.3 40901
13.2 110000
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13.1 32608
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38640
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27.1
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259.8
248.6
248.6
243.8
110.4
95.6
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SOURCE
ORGANISM
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VERSION
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AX007222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                            4447
                                                                                                                July 18, 2002, 11:22:05; Search time 4085.76 Seconds (without alignments) 2084.582 Million cell updates/sec
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_htg_inv:*
em_htg_other:* em_htgo_inv:*

em_htg_hum:*

SUMMARIES

Score

Result

a Query Match Length DB

1.2

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Streptomyces griseus SsgA; possible cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomycineae; Streptomyceso.

1 (bases 1 to 15441).
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinsshi, H. and Hopwood, D.A.
Kinsahi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
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                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 407; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor cosmid Q11. AL096823 AL096823 GI:5457267
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/db_xref="ATCC:21386"
                                                                                       /note="similar to
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                                                                           /gene="ssgA"
/note="similar
                                                                                                                        /codon_start-1
                                             /gene="ssgA"
1. .408
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                                                                 /node= start=...
/codon_start=...
/transl_table=11
/transl_d="CaC07387.1"
/product="5sgA"
/protein_id="CaC07387.1."
/db_xref="ci:9995689"
/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLFHLPGDAPVTWAFG
RELLIDGGRRPGGDGDVHIAPADPEFFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPIGGERSLADFPALLDEALDRILAEEQNAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (18-OCT-1999) Biochemistry, University of Leiden, PO 3502, Leiden 2300 RA, Netherlands
Location/Qualifiers
1. .408
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                                                              of Streptomyces goldeniensis"
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Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                           Score 407; DB 6;
Pred. No. 5.3e-42;
Mismatches 0;
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                                             /gene="ssgA"
/note="strain ATCC
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0
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Best Local Similarity 100.0%;
Matches 407; Conservative 0
                 "ssgA"
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van Wezel, G.P.
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                    /gene≖'
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PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGVETLVFASGMAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLM
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complement(1, .4279)
           misc_feature
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/gene="SCQ11.01c"
/note="SCQ11.01c"
/note="SCQ11.01c, hypothetical protein, partial CDS, len: >95 aa; unknown function, previously sequenced as TR:053870 (EMBL:037380), S.coelicolor hypothetical protein ORF5 downstream of phosphotyrosine protein phosphatase (159 aa). Weak similarity to the N-terminus of TR:069888 (EMBL:AL023797) Streptomyces coelicolor hypothetical
                                                                                                                                                                                                                                                                        Submitted (08-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.nih.go.jp/
jun/Ggi-bin/frameplot.pl. CAUTION: We may not have predicted the
jun/Ggi-bin/frameplot.pl. or content of the correct initiation codon. Where possible we choose an initiation
codon (atg, gtg, ttg or (att)) which is preceded by an upstream
ribosome binding site sequence (optimally 5-13bp before the
initiation codon). If this cannot be identified we choose the most
upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given for SS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden markov model (krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
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DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the AseI-Q
                                                                                                                                                                                                                          Barrell, B.G. and Rajandream, M.A.
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/organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
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/protein_id="CAB46956.1"
/db_xref="G1:5457268"
   Microbiol. 21 (1), 77-96 (1996)
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Location/Qualifiers
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complement(1. .289)
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                                                                                                                                                                                3 (bases 1 to 15441)
James, K.D., Parkhill, J.,
Direct Submission
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                                                                                                              Seeger, K. and Harris, D.
                                                                            (bases 1 to 15441)
                                                                                                                                                     Unpublished
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TITLE
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gene

CDS

FEATURES

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transcriptional regulator, len: 301 as; previously sequenced as TR:053869 (EMBL:037580) S.coelicolor lysR-like protein (301 aa). Highly similar to SW:ARAB_STRAT (EMBL:037580), arab, Streptomyces antibioticus transcriptional regulatory protein (301 aa), fasta socres; opt: 1581 z-score: 1813.2 E(::0, 80.3% identity in 300 aa overlap. Similar to many other transcriptional regulators. Contains probable helix-turn-helix motif at aa 17-38 (Score 1659, 44.84 SD). Contains Pfam match to PF00126 HTM_1, Bacterial regulatory helix-turn-helix protein, lysR family and PS00004 Bacterial regulatory proteins, lysR family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDLALLRTFVTVHRAGSFTRAAALLGLSQPAVTSQIRTLERQLG
RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAETGLEDDSTLRTLHLAGPPBFFTA
ERALPALGELTGEDGQAFALRASFGNAEETLEGLAAGHHDLAIGTTRPRGALHTATPL
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SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
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/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="G1:5457269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="PS00044 Bacterial regulatory proteins, lysR family
note="sequence corresponding to EMBL: U37580 from 1 to
                                                           7...98
/note="overlap with Streptomyces coelicolor cosmid H24
(EMBL-AL049826) from 41528 to 41625"
complement(360. 1265)
/gene="SCQ11.02c"
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                                                                                                                                                                                                                                                                                                                   /gene="SCO11.02c"
/note="SCO11.02c, abaB, probable lysR-family
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/gene="SCQ11.02c"
/note="Match to PF00126 HTH_1,
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/gene="SCQ11.02c"
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/gene="SCQ11.03c"
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                /note="abaB
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PAT 06-SEP-2000
                                                                                                                                                                        Actinomycetales; Streptomycineae; Streptomycesos.

( bases. 1 to 407)

Kraal, B., Luiten, R.G. and Van Wezel, G.P.

Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms

patent: WO 0000613-A 3 06-74N-2000;

UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLE GIJSBERTUS MARI
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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                                                                                                         Streptomyces griseus.
Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 1e-23;
0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                       1. .407
/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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/protein_id="CAC07385.1"
Sequence 3 from Patent WO0000613.
AX007218
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/note="strain ATTC
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1. .>405
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llarity 77.4%;
Conservative
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Best Local S:
Matches 315,
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              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                 // Complement(2693. .3187)
/gene="SCO11.04c"
/gene="SCO11.04c"
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/fore="SCO11.04c"
/fo
                                  TGHGDVILGYVAGRDAGAMAAVRRWRKIVGAIPGPMEAWLAHRSIATLQLRVDRQDŠT
ALKVAEALRTRPEITGLRYPGLPDDPSHKVASQQMLRYGCVVSFTLPSRARADRFLDA
LRLVEGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
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GWHEGEGADPRTEAVLADHGYGLDHAARQFQQSWFSRLDLVVALDAGHLRALRRLAPT
ERDAAKVRLLRSYDFAVAGGDLDVPDPYYGGRDGFEECLEWVEAASTGLLAAVREQVE
GRAA"
            IETPSNPGLDVCDVRRLVEAAHAGGALVAVDNTLATPLGQRPLELGADFSVASGTKQL
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                                                                                                                     complement(1533. .2624)
/gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
/gene="SCQ11.03c"
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                                                                                                                                                                                                                                                                   /note="PS00868 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
complement(2693, .3187)
/gene="SCQ11.04c"
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Pred. No. 1.6e-28;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="low molecular weight
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/protein_id="CAB46959.1"
/db_xref="G1:5457271"
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82.8%;
                                                                                                                                                                                                                                                                                                                                                                  /note="ptpA"
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/translation="MMSFLVSBELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAF
GRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRT
DKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                           f. (bases 1 to 1513)
Shitchi, K. and Ensign, J.
Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus
Unpublished (1995)
Shinichi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-APR-1995) Kawamoto Shinichi, National Food Research
Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)
Location/Qualifiers
1. 1513
                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                 2 (sites)
Kawamoto, S. and Ensign, J.C.
Isolation of mutants of Streptomyces griseus that sporulate in nutrient rich media.
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                                                                                                                                              1 (sites)
Kawamcto,S. and Ensign,J.C.
Cloning and characterization of a gene involved in regulation of
Sporulation and cell division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
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/strain="B2682"
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/protein_id="BAA21558.1"
/db_xref="G1:2281004"
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                                                      Streptomyces griseus.
Streptomyces griseus
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 438)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
filamentcus microorganisms
Patent: WO 0000613-A 1 06-JAN-2000;
UNIY LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MRESVQAEVMMSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLP
GDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTA
PLVAFLDRTDKLVPLGOEHTGDFDGNLEDALGR"
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llarity 77.4%; Pred. No. 9.8e-24;
Conservative 0; Mismatches 92;
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/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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/db_xref="GI:9995083"
Sequence 1 from Patent WO0000513.
AX007216
AX007216.1 GI:9995082
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/product="SsgA"
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Streptomyces netropsis.

Actinobacteria; Actinobacteridae;
Actinomycetaceae; Streptomycineae;
Actinomycetaceae; Streptomycineae;
I (bases 1 to 407)

Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
Filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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RELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTD
KSVPLGGEQTLGDFEDSLEAALGKILAEEQNAG"
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 gtccacatcgcgcccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                       1 atgagettectegteteggaagaacteteetteegtatteegtggagetgegttaegag
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    /organism="Streptomyces netropsis"
/db_xref="taxon:55404"

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Pred. No. 2.5e-22;
0; Mismatches 99;
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/protein_id="CAC07388.1"
/db_xref="G1:9995091"
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Sequence 9 from Patent W00000613.
AX007224
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Best Local Similarity 75.7%;
Matches 308; Conservative
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AF195772 438 bp DNA linear BCT 01-NOV-2000
Streptomyces netropsis SsgA (ssgA) gene, complete cds.
AF195772
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GDAPVTWARGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAP
PLVAFLURTKSVPLGGPGTLGDFEDSLEAALGKILAEEQNAG"
158 c 142 g 68 t
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Submitted (18-OCT-1999) Biochemistry, University
9502, Leiden 2300 RA, Netherlands
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/db_xref="taxon:55404"
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Pred. No. 2.4e-22;
0; Mismatches 99;
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/db_xref="G1:11066163"
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/transl_table=11
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/translation="MSFLVSEELAFRIPVEERYETVDPYAVRLTFHLPGDAPVTWVFG
FELJVEGVLDAAGDGDVRVCPVGQTATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
GGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
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acggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctc
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                                                    gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
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Submitted (18-007-1999) Biochemistry, University
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
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Pred. No. 8.9e-22;
0; Mismatches 102;

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    /organism="Streptomyces albus"
    /db_xref="taxon:1888"

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/db_xref="G1:11066161"
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/product="SsgA"
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/note="similar
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van Wezel, G.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1...405
// Office "ssqa"
// Office "strain ATCC of Streptomyces albus G"
// Chote "strain ATCC of Streptomyces albus G"
// Chote "strain ATCC of Streptomyces albus G"
// Chote "ssqa"
// Product = ssga"
// Ab_xref = "GI:995087"
// Chotefin_ide "CACC07386.1"
// Chotefin_ide "GACUSELARIPVELRYETVDPYAVRLFHLPGDAPVTWVFG
// CHOSIGORON RELIVESTARE PHILLOWGSEQALFRVGRAPLIAFLDRIP
QGLSLGSERAHADFDAHLDDALNRSAAEEQSAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 5 06-JAN-2000;
UNIV LEIDEN (NL); RRAAL BAREND (NL); LUITEN RUDOLE GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces 1 (bases 1 to 407)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgc 300
                                                                                                                                     acggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctc 360
                                                                                                                                                                                                                      ACGGACAAGTCGGTGCCGCTCGGTCAGGAACAGACTCTGGGGTGACTTCGAGGACAGCCTG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 tgggcgttcgggcgggagttgctcatcgacggaggtccgcggccgtgcggggacggggac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atgagetteetegteteggaagaaeteteetteegtatteeggtggagetgegttaegag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                                                                                                                                                                                                                                                                                                                                                                          PAT (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces albus G.
Streptomyces albus G
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407;
                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                        gacgaggcgctggaccgcatcctggccgaggagcagaacgccggctg 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 243.8; DB 6;
Pred. No. 9.7e-22;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces albus G"
/db_xref="taxon:1962"
                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 from Patent WO0000613. AX007220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                            AX007220.1 GI:9995086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.98;
74.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .405
/gene="ssgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 305;
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DEFINITION ACCESSION

VERSION KEYWORDS

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RESULT AX007220 LOCUS

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

FEATURES

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Query Match Best Local

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BASE COUNT ORIGIN

gene

CDS

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jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (adg. gtg. ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGVTFÄENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARWAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGGLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(892. 1296)
Agene-"SCE19A.03c,
/note-"SCE19A.03c, possible secreted protein, len: 134 aa;
unknown function, probable CDS suggested by GC frameplot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCE19A.01"
/note="SCE19A.01"
/note="SCE19A.01, hypothetical protein, partial CDS, len:
>31 aa; unknown function, similar to members of the alkyl
hydroperoxide reductase C/thiol-specific antioxidant
family e.g. TR:053226 (EMBL:AL021185), bcp, Mycobacterium
tuberculosis bacterioferritin comigratory protein (157
aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06,
63.3% identity in 30 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 aa; unknown function, similar to many e.g.
SW:Y030_MYCTU (EMBL:Z73902) Mycobacterium tuberculosis
hypothetical protein (204 aa), fasta scores; opt: 633
z-score: 743: 6E(1: 0. 52.0% identity in 200 aa overlap.
Similar to SW:YGGV_ECOLI (EMBL:U28377), yggV, Escherichia
coli hypothetical protein (197 aa) (49.5% identity in 198
                             Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(243. .845)
/gene="SCE19A.02c"
/note="SCE19A.02c, conserved hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the Asel-E genomic restriction fragment.

Location/Qualifiers
      where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="tRNA Leu anticodon TAG, Cove score 69.78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="IVVDEOGKVERALYNVRATGHVAKIIKDLGI"
140. .226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"hypothetical protein"
/protein_id-"CAB50982.1"
/db_xref-"GI:5531350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/label=SCE19A.02c
/product="hypothetical protein"
/protein_id="CAB50983.1"
/db_xref="G1:5531351"
                                                                                                                                                             http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tRNA-Leu"
complement(243. .845)
/gene="SCE19A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cosmid E19A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCE19A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCE19A.01"
                                                                                                                                                                                                                                                                                                                                                         upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=2
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-SCE19A.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aa overlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-1999) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. (bases 1 to 35284)
Redenbach, M., Klaser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. Coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(WIL: http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-hydroxyphenylpyruvate dioxygenase; ABC transporter; amino acid permease; asnC-family; cysteine synthase; nicotinamidase; osmoregulation; osmotolerance; oxfdoreductase; permease; phosphoenolpyruvate-dependent; protease; regulator; ribonuclease PH; rph; sugar phosphotransferase system; transcriptional regulator; transposase; tRNA Leu; zinc metallopeptidase. Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1878 E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                              265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 ACCGACCAGGGCTTGTCGCTCGGCAGCGGGCACACACGCCGACTTCGACAGCCACCTC 385
gtccacatcgcgccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                                                                                                                                                                                                                                                                                       Greegerergecegeregecagaegecaccaegeagergeacarcaecerecagere
                                                                                                  tgggcgttcgggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacggggac
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James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 GACGACGCTCTGAACCGCAGCCTCGCCGAGGAGCAGAGCGCCGGCTG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gacgaggcgctggaccgcatcctggccgaggagcagaacgccggctg 407
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Streptomyces coelicolor cosmid E
AL096852
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Seeger, K. and Harris, D.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL096852.1 GI:5531349
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                                                                                                                                                             146
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AUTHORS
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SOURCE

LOCUS

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Gaps 61

Indels

Length 35284;

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Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescales;                                                                                                                                                                                                                                                                                                                                                           (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20202 CGGACGATCCCTACGCGTGCACATCACCTTCCACATCGACTCGGCCACCGGTGCACT 20261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20442 CCCTGCGGGCGGTGCCGCGGGGACGGCGCGCAGCTCGGGATCGACGGCTGG 20501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGGCATTCCGGTGCCGGCCCGGCTCGGCTACCACA 20201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20322 TGCGGGTGTGGCCCGTCGAAGACGGAGGCCGCAGCGTCGTACTCGTCGCGCTGAGCAGCC 20381
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                                                                                                                                                                                                                                                         possible PTS transmembrane component,
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phosphoribosiltransferase; DNA helicase; DNA polymerase III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tgagcttcctcgtctcggaagaactctccttccgtattccggtggagctgcgttacgaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                             len: 431 aa; similar to many PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 110.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor cosmid L2. AL137778
AL137778.1 GI:6822206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                              2660. .3955
/gene="SCE19A.06"
/note="SCE19A.06,
                                       2660. .3955
/qene="SCE19A.06"
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Seeger, K.J. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%;
55.9%;
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/product="putative ribonuclease PH"
/protein_id="CAB50985.1"
/do_xref="G1:5531353"
/translation="MSRIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV
TEGNPRWRKGSGEGWTYAALFANTNTRGDRESVKGRIGGRTHEISRLIGRSLRAV
IDYKALGENTVVLDCDVLQADGGTRTAAITGAYVALADAVAWAQGRKLIKANRKPLTG
TLLDLATAGCTELAELGRKALDATLER"
complement(1511. 2185)
/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown function, similar to parts of many sugar permeases eg. TR:P96159 (EMBL:165013), malx, vibrio furnissii PTS (phosphoenolpyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 217 z-score: 287.9 E(): 11-6-08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative secreted protein"
protein_id="CAB5O994.1"
/db_xref="GI:5531352"
/translation="MAASRHRRLRRTVTAVATVATIALFAGLFTGCDAVDKALDCVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAIADSVTELQQAVENADDPTQWEESLNSIDKNLDRIGDQTDNTDVNKAVDDLGKAV
DNVRTSVENGDETPDLSPVTDAAGELTKVCTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCE19A.04c, rph, probable ribonuclease PH, len: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MASKAEKIVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as; highly similar to many e.g. SW:RNPH_ECOLI (EMBL:X00781), rph, Escherichia coli ribonuclease PH (238 as), fasta scores; opt: 916 z-score: 1116.8 E(): 0, 60.8% identity in 240 as overlap. Contains Pfam match to entry PF01138 RNBse_PH, 3' excribonuclease family and PS01277 Ribonuclease PH signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exoribonuclease family, score 266.70, E-value 3.1e-76" complement(1805. 1843) / gene="SCE19A.04c" / note="PS0127 Ribonuclease PH signature" complement(2268. 2501) / gene="SCE19A.05c" complement(2268. 2501) / gene="SCE19A.05c" / note="SCE19A.05c" 
positional base preference and amino acid composition. Contains probable N-terminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1201. .1233)
/gene="SCE19A.03c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF00367 PTS_EIIB,
phosphotransferase system, EIIB, score 43.00, E-value
8.1e-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry PF01138 RNase_PH, 3'
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/protein_id="CaB50986.1"
/db_xref="G1:5531354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2489)
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/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1454. .2191)
/gene="SCE19A.04c"
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                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/label=SCE19A.03c
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us-09-749-185-6.rge

COMMENT

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/note="SCL2.03c, relA, GTP pyrophosphokinase, len: 847 aa; identical to previously sequenced SW:RELA_STRCO (EMBL.X87267) Streptomyces coelicolor GTP pyrophosphokinase (EC 2.7 6.5) RelA, 847 aa and highly similar to SW:RELA_STRAT (EMBL.AF072829) Streptomyces antibioticus RelA protein, 841 aa; fasta scores: opt: 4969 z-score: 4906.2 E(): 0; 90.38 identity in 848 aa overlap and to SW:RELA_CORGL (EMBL.AF038651) Corynebacterium glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA, 760 aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.78 identity in 774 aa overlap. Contains Pfam match to entry PF01842 ACT, ACT domain and match to Prosite entry PS00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / CLEAR 12 11 OH = "MPDEAQPLTAAK PESASASAK PAPSAPQAKNDTHGPIQHAPAA
PUDRAEQOPRYRILPAERRONAPVVRAPAGQPARSSSSNRYRALLARLGVORNNPIN
PVLREPLERILYRGNDPK IETSTLAGIERAVOVAERWHRGQKRKSGDPY ITHPLAVTTIL
AELGMDPATLLMAGLILHDYVRDTEVGLEDLRRDFGDVYTLLVOGVTKLDVKKFGBAQA
ETVRKWVVAMAKDPRVLVIKLADRLHNMRTMRYLKREKQEKKARETLEIYAPLAHRLG
MYTIKMELEDLAFATLYRKMYDEIVRLNAFBARRDETAAVVTDEVOGOTARATKAR
VTGRPKHYSVYOKMIVRGRPAET PIDLVGITRVLAVTOTYNDGYAALGTVHARWHPYPGR
FKDY IAMPKENMYOSLHTY IGPGGKRVELOURTFDMHRRAEYGIAAHWKYKQEAVAG
ASKVRTDAPKSSGKSKDDHLNDMAMLRQLLDWQKSTEDPGEFLESTLDNGDLVEVFT
TPKGDVIALPAGATPVDFAYATUTTYTGARVARKQULLFGATLDNGDLVEVFTSK
AGAGPSRDWLGFVKSPRARKIRAMFSKERRDEAIROGKLAVFTSK
AGAGPSRDWLGFVKSPRARKIRAMFSKERRDEAIROGKLAVFTGK
AGAGPSRDWLGFVKSPRARKIRAMFSKERRDEAIROGKDATVARAMKQULLFGEDESVPP
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complement(3273. .7460)
Anote="Previously sequenced region SW:SCSECAPT EMBL:X85969
S.coelicolor secD, secF & apt genes"
complement(3778. .3781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRGRGRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIIGFVTRGSGVSVHRSDCV
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VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3904. .4568)
/note="previously sequenced region SW:SCAPTRELA FORDEMS: 87267 S.coelicolor apt & relA genes" complement(3956. .4453)
                                                                                                                                /note="previously sequenced region SW:SCAPTRELA
EMBL:X87267 S.coelicolor apt & relA genes"
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/product="adenine phosphoribosiltransferase"
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/protein_id="CAB70915.1"
/db_xref="G1:6822209"
                                                                                                                                                                                                        complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1256. .1474)
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                                                                                                                                                                                                                                                                                complement(1229. .3772)
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                                                                                                                                                                                                                                                                                                                      /gene="relA"
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                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (adg., qg, ttq or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the sequence he entire insert of the sequence do not be sequenced to a shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
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/note="SCL2.01, hypothetical protein, len: >328 aa;
/note="SCL2.01, hypothetical protein, len: >328 aa;
similar to TR:033236 (EMBL:298209) Mycobacterium
tuberculosis hypothetical 49.8 kD protein MTCXI74.11, len:
450 aa; fasta scores: opt: 843 z-score: 874.7 E(): 0;
45.9% identity in 296 aa overlap. Contains possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given for sosition of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nfi-go.jb/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="SWQAGSPEEALAYFERKYEGLVVEIGLLEKRVKTTDLSAKDAQT
YOHHNEWOTOPHHAVGDLEALBALDOLVALVETRREEKRAQARAKQSDEARGAKEALV
AEAEELARSDQWRAAGERLESLVDTWKGLPFLDKSDDELWHRPEAHASAFSKRRKQH
FAQLDAQREEARRIKERLVSEAEALSNSTDWGPTAARYFDLMSEWKAAGRAQKEHEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein SCL2.02"
/product="hypothetical protein SCL2.02"
/db_xref-"G1:6822208"
/translation="MDKLRSQVEQARAQGNDAKADKLARELEGRQALLDQALKGLHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LWNRFRGAQDVFFAARSSVFAERDAEQSENLKLKEELVTEAEKLVPVTDLKSARAAFR
SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGPTPRHARVPRA"
                                                                                                                                                                      Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                               (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
Notes:
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/organism="Streptomyces coelicolor A3(2)"
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/protein_id="CaB70913.1"
/db_xref="G1:6822207"
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/gene="SCL2.02"
/note="SCL2.02, unknown, len: 46 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:100226"
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/gene="SCL2.01"
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/gene="SCL2.02"
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/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                strand).
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                                                      /translation="wadypeegvvekditplladpgaralidalabagrigatkvv
GLEARGFILGAPVALRAGLGFIPVRKAGKLPGATLSQAYDLEYGSAEIEVHAEDLTAG
DRVLVVDDVLATGGTAEASLELIRRAGAEVAGLAVLMELGFLGGRARLEPALAGAPLE
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Debottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J., Erpicum, T., Frere, J. M. and Ghuysen, J. -M. Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="sece"
/note="SCL2.05c, secF, protein-export membrane protein,
len: 373 aa; identical to previously sequenced
SW:SECF_STRCO (EMBL:X85969) Streptomyces coelicolor
protein-export membrane protein SecF, 373 aa and similar
                                                                                                                                                                                                                                                                                               E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35030 TGCGCCTCGTTGTGTCGAGCGAGTCCTCCCTGCCTGTCCCGCAGGCCTGCGGTACGACA 35089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35210 recererereces recedades as a series as a series as a series and a series as a series
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 cctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgcccggtgacct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 cggacaagatcgtgccgctgggggagggagcgttccctcgccgacttcgacgccctgctcg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tgagcttcctcgtctcggaagaactctccgtattccggtggagctgcgttacgaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 tecacategegecegecegagegagaegtteggegaggteetgateegeetgeaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgca
                                                                                                                                                                                                                                                             PF00156 Pribosyltran,
domain, score 150.30,
                                                                                                                                                                                                                                                                                                                                                                                            /gene="apt"
/note="PS00103 Purine/pyrimidine phosphoribosyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 95.6; DB 1; Length 38640; 52.8%; Pred. No. 0.0007; 1ve 0; Mismatches 184; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-lactamase.
Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
Bacteria; Firmicutes; Actinobacteriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                      /note="Pfam match to entry
Phosphoribosyl transferase
3.5e-41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35390 CGCACATCCTGGCGGAAAGCTAGGGCGGGG 35419
'protein_id="CAB70916.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="secF"
complement(4501. .5622)
                                                                                                                                                                                                                                                                                                                                                         complement(4103. .4141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      transferases signature complement(4468. .4503)
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                                                                                                                                                                                            complement(3980. .4429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4501. .5622)
                                  /db_xref="GI:6822210'
                                                                                                                                                                                                                                 'gene="apt
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M28303.1 GI:153338
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Matches 206; Conserv
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/translation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
SVSDAERRLAGLERASGARLGVYAYDTGSGRTVAYRADELFPMCSVFKTLSSAAVLRD
LDRNGFELSRR LLYTQDDVEQAAGAGFETGKPONLANAQLTVEELCEYSITASDNCAA
NLMLRELGGAAVTRFVRSLGBRYTRLDRWEPELNSAEPGRYTDTTSPRAITRTYGRL
VLGDALNPRDRALLTSWALLANTTSGDRRRAGLEPDWTLGAGRYGTNNDAGVTWP
PGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG"
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binding secreted protein; branched amino acid transport system
ATP-binding protein; branched amino acid transport system permease;
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Redenbach,M., Klaser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor; transcriptional regulator; transcriptional regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 gaactctccttccgtattccggtggagctgcgttacgagacctgtgatccctacgccgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94.6; DB 1; L
Pred. No. 0.0023;
                                                                                                                                 /organism="Streptomyces albus"
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Deta-Lactamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
87275916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA26775.1"
/db_xref="GI:153339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="inverted repeat"
1230. .1242
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540 c 496 g 1
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                                                                                                                                                                                                                          /gene="beta-lactamase"
243. .1187
                                                                                                                                                                                                                                                                                  /gene="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1204. .1216
/gene="beta-lactamase"
                                                                                                                                                                               /db_xref="taxon:1888"
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Streptomyces coelicolor A3(2)
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 ctcatcgacggaggtccgcgg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CTGGTCGAGGGAGTCAAGGGG 141
                                                                                                                                                                                                                                                                                                           /codon_start=1
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79.4%;
                                                                                                                                                             /strain="G"
                                                                                                                                                                                                           243. .1242
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Matches 112; Conservative
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LGDDQPTSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (adg. gr. datl) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If may be shorter because we only sequence NAV NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also included but some of these may be fortuitous.

The length in codons is given for each CDS.
Usually the highest scoring match found by fasta o is given for
USD which show significant similarity to other CDS in the database.

The position of possible ribosome binding site sequences are given
where these have been used to deduce the initiation codon.
Gene prediction is based on positional base preference in codons
using a specially developed Hidden Markov Model (Krogh et al.,
Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SC8A11.01"
/note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                  Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial regulatory proteins, luxR family and match to
Prosite entry PS00622 Bacterial regulatory proteins, luxR
family signature. Also contains a possible
helix-turn helix motif at residues 699. .720 (+3.25 SD)"
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/note="SC8A11.01"
/note="SC8A11.01, possible transcriptional regulator (fragment), len: >750 aa; similar to TR:09S124
(EMBL:AL109747) Streptomyces coelicolor probable
(EMBL:AL109747) Streptomyces coelicolor aa; fasta scores: opt: 818 z-score: 913.7 E(): 0; 32.6% identity in 775 aa overlag. Contains Pfam match to entry PF00196 GerE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), 01 (first CDS), c (complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                   Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                          Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Colney, Norwich, Norfolk NR4 7UH, UK Notes:
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where pc
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/db_xref="taxon:100226"
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                                                                                                     Saunders, D.C. and Harris, D.
Unpublished
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                                                                                                                                                                         (bases 1 to 32704)
                                                                    (bases 1 to 32704)
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GIALAEETGEWIVWLGLKATSALTAVLRGEREAAARSVRELRAHSLFPVWPFASVWAQ
QVEGLLALFDSRAVEAYDALARAFDKTDPHYHSTSRWLLVPDLVDAAAAAGRNEQARE
                                                                                                                                     YTRATVADRISTHRALAETLEGSPGRRLVHLAAATLGPDDELAGGLERRADDAQKRGG
LAAAVPALRQAGELVHDPRRQTGLLVRAAELASEINDRVQAQILLNRADLAEPGPTER
ARLMLVSDKAAFEPDEPQRRIQDMIDAAAGAFDVGSTSVAENLLWRAAARCFFQDGDA
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PDHPLLVTIRFAPEGAPPVTWHVGRDLLHEGLRTTSGLGDVQVWADTPTDRETAWLQV
NAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
                                                  VRARI LQRAAGNPLALVELPRAAQGI SPPLDDLPLTQRLETAFASRTDSLTRECRTFL
LVLAAEPTAPLNQLLDVASRLAGSEVTVYALQEAVDAGLVVLTGRTPEFRHPLMRSAI
                                                                                                                                                                                                                                                                                                                  RVRAQAAAELDRWKPDPDAPHVLTVRAYTEPYRRGTDLIARLEKLRPDREDGRLLHYL
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QHGRRLRRQRRNVDARKPLRLARDEFDRVGAQPWADMAREQLRAAGESDGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
/translation="IGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
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/gene="SCBA11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
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/gene="SC8A11.01"
/note="Pfam match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 49.10, E-value
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/transl_table=11
product="hypothetical protein SCBA11.02c"
/protein_id="CAC01574.1"
/db_xref="GI:9716213"
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/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
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/protein_id="CAC01575.1"
/db_xref="GI:9716214"
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/gene="SC8A11.02c"
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2787. .3257
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/gene="SC8A11.03"
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/trans1_table=11
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97000351
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AAAVRSTLLAASGDAFAQAHPYPTGQTVRRDVYTNGSPAPYALDLALSPAELDEBGLF
TLSBAQVYTVDAHGTASGVGVTTHLDAAEDNGAYATRLVASGADGAVLARTPVGVNKEGR
RATLALTAKDHHDKPLSGTVILKDVERNTAPKVYSVDASGRLDLRLSPSTYSVWMNSA
VPGVOGTHTALGFAWATTAGFWYDTDADDLKAAAAVTPRATAMQFLRIDGYRG
VTGLPPFMDSYVARFWXDSLWVTPPPEVPTGSYTTATTRRQIQPTGTATGYRG
VTGLPPFMDSYVARFSOLWYPPPPEVPTGSYTTATTRRQIQPTGTASGOTFDD
VTVQSRSPQLPBGTRAYRAWAGDGSATEFRGAEVRDKVAVFRSDTVAFTDQAAAAB
                                                                                                                                                                                                                                                                                                                                                                                           GPTRVLTLITGDRVTVTGEDGAETVLSVTDPHGRSGGAHVMTVGSDTYVYPDAAVPLL
GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
IRGAAISAEHSRAADFWTSLTGTGDAAAGGSAARSATSGGRLAGGIAKVWLDGKVRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSDTTAQIGAPDVWSGGNTGEGVGVAVLDTGVDAGHPDFAGRIAATASFVPDQDVTDR
NGGTHVASSTVAGTGAASGGVEKGVARGASLHIGKVLDNSGSGODSWATAVRD
QHAKIVSMSLGDSPPTGTPDLSEAVNMLSAETGALFVVAAGNGPEAYTVGTPAADA
ALTVGAVNGPGKGVDQIADFSSRGPRVGDNAVKPDLTAPGVGVLAARSRYAPGEGGAA
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IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGG
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TPLPLVQLDYAVAYDLSGRAHRRTELTYTASHLEGAAGAGAIRTATVEVSYDDGATWH
RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGYGQTLIRAFGLR"
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                                                                                                                                                                                                                                                                                                                                             /translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPTAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttccggtggagctgcgttacgagacctgtgatccctacgccgtgcggctgaccttcatc 97
family, serine active site. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgcggccgtgcgggacgggacgtccacatcgcgcccgccgacccggagacgttcggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 aggicoligatocgcoligoaggiggagogaccaggogalgiloogggicggogogogo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 32704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 tegeegacttegaegeectgetegaegaegaegetggaeegeateetggee 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.11;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                               /transl_table=11
/product="putative secreted peptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4374, .4613)
/gene="SC8A11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL159178.1 GI:7210989
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Best Local Similarity 51.4*
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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SCH22A/c
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VERSION
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1984) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Inn/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream cibosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid H22A Lies between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. (bases I to 29625)
Cerdeno, A. M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (07-MAR-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Jote="SCH22A.01, possible regulatory protein (fragment), len: >465 aa; similar to TR:CAB59599 (EMBL:AL132662) Streptomyces coelicolor hypothetical regulatory protein SCF11.22, 877 aa; fasta socres: opt: 708 z score: 765.1 E(): 0; 34.5% identity in 466 aa overlap. Contains Pfam match to entry PF01590 GAF, GAF domain and possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSKR and Beowulf Genomics.

Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
transmembrane transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                    A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                               Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                            Actinobacteridae;
                                                                                                                                                                        Streptomycetaceae;
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/organism="Streptomyces coelicolor A3(2)"
                                                                                                                       Bacteria, Firmicutes, Actinobacteria,
Actinomycetales, Streptómycineae, Stre
1 (bases 1 to 29625)
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                                   Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="cosmid H22A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCH22A.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 29625)
Murphy, L. and Harris, D.
Unpublished
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/partial
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/transl_table=11
/product="putative stress response protein"
/product="putative stress response protein"
/product="putative stress response protein"
/product="Garage stress response protein"
/product="Garage stress response stress response stress response stress response stress response stress response respo
                                                                                                                                                                                            /note="SCH22A.05, possible stress response protein, len:
194 aa; similar to TR:AAR11772 (EMBL.AE002055) Deinococcus
radiodurans tellurium resistance protein Terz, 195 aa;
fasta scores: opt: 300 z-score: 364.6 E(): 6.8e-13; 31.5%
identity in 178 aa overlap and to SW:TERz_SERMA
(EMBL:138824) Serratia marcescens tellurium resistance
protein Terz, 193 aa; fasta scores: opt: 263 z-score:
321.2 E(): 1.8e-10; 28.2% identity in 195 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MGTDGFATWTRRFEDERERRAAGGDPDWERGAVLHRAVWAGIOR
ROGGBDGGDANLVARKEESGADAVZRAVREFVREEDGNHRALLARLLARGORPALASGHW
SDTVEVRLRRLGGLFRELLULMIABEVVALRYRALROGTDDALTSEVAGRILDBERHH
VPFHCERLHHSLABELAAVTRRPVMVLWRLLLLAATVVVAADHGAGLRRLGVGRRRFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4798. .5529)
/gene="SCH22A.06c"
/note="SCH22A.06c, possible membrane protein, len: 243 aa.
Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCH22A.07c, possible regulatory protein, len: 260 aa; similar to SW:BRPA_STRHY (EMBL:M64783) Streptomyces hygroscopicus bialaphos biosynthetic pathway regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28815 ACGTCGTCACCGCCCGGCCGGCCTGCCCGCCGACGCCGACCGGGCCGCCCGGGCGC 28756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28695 GCGGCGAGACCTCGTTGCAGGGGACGGCGACCCAGGGCATCTCGGGCTCCGGCGCCGAAC 28636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 acgtecacategégecegecegaceegagagacgtteggegaggteetgateegeetgeagg 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative membrane protein"
/protein_id="CAB76975.1"
/db_xref="GI:7210995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVMASASEVAEAVLTPRPDAWSGGA"
complement(5539. 5545)
complement(5637. 6419)
/gene="SCH22A.07c"
/gene="SCH22A.07c"
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Best Local Similarity 54.9%; Pred. No. 23;
Matches 117; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tcgacgaggcgctggaccgcatcctggccgagg 391
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Job time: 13755 sec
                4088. .4672
/gene="SCH22A.05"
4088. .4677
                                                                                                                      1088. .4672
/gene="SCH22A.05"
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/transl_table=11
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gene
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                                                                                                                                                                                                                                                                                                               RILEEFIPLGITTKELADLEGVELPRGRGLLGHIJHHPEPLRVKDISRHPESAGFPPG
PPPRSELIGVATSVRGRT YGNIXLESRENGQPPEDHBEGVIRLAGFAGVATERNRLY
QOVRNSSEQPGRLLLPRLPDLRPFTAGAAY RPASAPANGGOWYDAMLLPGGACAAVI
GDVVGHDLRAAADMSQIRNMLRALYYDPGAAPSTSLARLDRIMNAALDEAPVATALLA
ELPADGGTWQLRWSSAGHPPPLVLLPDGRVRYLDMEPGLPGVAPDLRPRPDY
DSTVILFTDGLVPPPGQPLDRGLDALAVTASRLVGLAPEDLCHALVAHRPGNGHDDKA
VIALRTPPLTSYGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1435. .1917)
/gene="SCH22A.02c"
/note="SCH22A.02c"
/inite="SCH22A.02c, hypothetical protein, len: 160 aa;
/inite="SCH22A.03c, EMBL.AL049587) Streptomyces
coelicolor hypothetical 17.1 kD protein SC5F2A.32, 161 aa;
fasta scores: opt: 256 z-score: 310.3 E(): 7.3e-10; 39.4%
identity in 160 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLGPRVRGQPRTGFPCGDAMSTLLQPMPHRHVLTLPAAPPAVRL
ARETAEQALAEWGVNPGHPAVAPALLILSELVTNSVRHASPPSEGVTVTYAAGDDCLA
FAVHDRHPHQPRLHGARTTGRTGGLATVMELTGTLGGTAVVRGDGDGRGKSIWVTLPL
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GNPSWLVGRAVEATGAVGEHILDWVYQLAVAAVVVALYQLRGVAAERRFPRHHLVRT
FLLIGLLGPATYMIFPYVGPVFAXGTGARGTGGEMALADLWPHTLPPYGPPHRFTYD
GVYFRNCWPSLHTAMATVIFIHSKRGPRVLKWAGAFWLVATLTATLGFGYHYAIDLIA
GVVFAYTVAGGLRSLDRGWDRGSCLLVAHGALVFTAILASTRYLSLEWARNPWYFGPL
LLLAMASVIHGYYRTYKSWEPVTAAPPALPEREAA"
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RETITELVAAAQPGNVDALFTAAVDAGATVLKRAPASIMGYGGVVRAPDGTVWQLATSA
KRDTAPVTRDVDETVLLLGVEDVARTKRFVYEQGLTVYGKSFGGKYVREATGFGTVKLS
LYKRRALAKVAGVSADGTGSHRLVVSGGTRPFADPDGFAWQPELSH"
                                                                                                                                                                                                                                         /translation="EGPGSGPAQGSGEGPAAAPGRGGDDEPYASLLDLPLSSDLNRIG
EQLHALARAQRTLQELLQAVVNITGELELPAVLRRIVRTAMDLVGARYGAMGVLDQEG
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/gene="SCH22A.03c"
complement(1969. .3258)
/gene="SCH22A.03c"
/note="SCH22A.03c,
contains possible hydrophobic membrane protein, len: 429 aa.
Contains possible hydrophobic membrane spanning regions"
/codon_start=1
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AGLALTMVVLTWRQRLVAAAVAVGVDLTVALVRWAADATASGSHSFGNGALWVVLGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF01590 GAF, GAF domain, score 89.60, E-value 6.5e-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 .130
/gene="SCH22A.01"
/note="nominal overlap with S. coelicolor cosmid StH35"
                                                                                                                      /product="putative regulatory protein (fragment)"
/protein_id="CAB76970.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/product="hypothetical protein SCH22A.04c"
/protein_id="CAB76973.1"
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/protein_id="CaB76971.1"
/db_xref="G1:7210991"
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/gene="SCH22A.04c"
/note="SCH22A.04c, unknown, len: 206 aa"
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/product="putative membrane protein"
/protein id="CAB76972.1"
/db_xref="c1:7210992"
        at residues 48.
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complement(3337..3957)
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/gene="SCH22A.02c"
complement(1435. .1917)
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coiled-coil region
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                                                                                 /transl_table=11
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Streptomyces clavu
Pseudomonas aerugi
S. clavuligerus cl
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eryA region of S.
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Human PRO1072 (UNQ
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Nucleotide sequenc
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DNA encoding novel
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N. magadaii bacter
Platenolide syntha
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Micromonospora DNA
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Pseudomonas sp. WF
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                                                                                                                                                                      Mycobacterium
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AAI99683
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AAS88065
AAS87399
AAN70466
AAT03572
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AAD14501
AAS51470
AAQ91580
                                                                        AAV21187
AAZ32020
AAC90077
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AAQ46806
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AAA11992
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AAD17184
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AAH14184
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                                                      AAS08693
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 AAD17184
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/label= SsgA_protein
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S. spinosa DNA fra
S. spinosa DNA fra
Pseudomonas aerugi
P. aeruginosa accB
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Streptomyces netro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces golde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces grise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDDS5/gcgdata/geneseqr.embl_(NAL981.) DAT: *
| SIDDS5/gcgdata/geneseqr.embl_(NAL981.DAT: *
| SIDDS5/gcgdata/geneseqr.embl_(NAL991.DAT: *
| SIDDS5/gcgdata/geneseqr.embl_(NAL992.DAT: *
| SIDDS5/gcgdata/geneseqr.embl_(NAL992.DAT: *
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Listing first 45 summaries
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AAZ49728
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                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match
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98EP-0202148

26-JUN-1998;

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2559.8 248.6 243.8 58.8 58.8 54.4

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407

Result No.

(UYLE-) RIJKSUNIV LEIDEN

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                                                                                                                                    The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septration and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblotics, antitumor agents, immnosuppressive agents, hypocholesteroleemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters,
                                                                                                                                                                                                                                                                                                                                                                               acctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacc 120
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mycelium; antibiotic, antitumour agent; immunosuppressive agent;
hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent;
herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345;
bioinsecticide; receptor agonist; antagonist; blomass; ds.
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                                                                             enhancing fragmentation in filamentous improve their liquid culturing properties
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                                                                                                                                                                                                                              bioinsecticides, receptor agonists and antagonists and biomass
                                                                                                                                                                                                                                                                                     Length 407;
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                                                                                                                                                                                                                                                  Sequence 407 BP; 56 A; 135 C; 145 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                     100.0%; Score 407; DB 21; 100.0%; Pred. No. 2.3e-66;
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WETENSCHAPPELIJK ONDERZO
                                                                                                                                                                                                                                                                                                           0; Mismatches
                      Luiten RGM;
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                                                                                                               English.
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                                                                                                                                                                                                                                                                                                          407; Conservative
                                                                                                               60pp;
(NEWE-) NEDERLANDSE ORG
                      B,
                                                                             Reducing branching and
                                                                                         microorganisms used to
                                            2000-147269/13
                                                                                                               Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                      P-PSDB; AAY44651.
                     GP,
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                      Van Wezel
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, erzyme inhibitors, antimigraine agents, herbicides, antiparaslite agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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Pred. No. 2.2e-39;
0; Mismatches 92; Indels 0
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NEDERLANDSE ORG WETENSCHAPPELIJK
                                                                                          /*tag= a
/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     Luiten RGM;
                                               Location/Qualifiers
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77.48;
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Best Local Similarity 77.4
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Wezel GP, Kraal B,
                                                                      .405
Streptomyces griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147269/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY4649
                                                                                                                                                                   WO200000613-A1
                                                                                                                                                                                                                                                                25-JUN-1999;
                                                                                                                                                                                                                                                                                                               26-JUN-1998;
                                                                 mat_peptide
                                                                                                                                                                                                                  06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                               (UYLE-)
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gacgaggcgctggaccgcatcctggccgaggagcagaacgccggctg

us-09-749-185-6.rng

151 tggggcgttcggccgcgagctgctgctgacgggctcaacagcccgagcggcgacggcgat 210

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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesteroleamic agents, enzyme inhibitors, antimigraine agents, hebbicides, antiparasiit agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                       mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bloinsecticide; receptor agonist; antagonist; blomass; ds.
                                                                                                                                                       liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 259.8; DB 21;
Pred. No. 2.2e-39;
); Mismatches 92;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "SsgA protein"
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31..438
                                                                                                                          griseus ssgA gene-1.
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                             BP.
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ilarity 77.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-NL00395.
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                            AAZ49727 standard; DNA; 438
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                          Streptomyces
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Best Local Simi
Matches 315;
                                                                                           18-APR-2000
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                                                             AAZ49727;
m
                                                                                                                                                                                                                                                                                       Key
              AA249727
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The present sequence is a DNA (ATCC 23940) encoding S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparaslic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                           300
                                                                                                                          acggacaagatcgtgccgctgggggcaggagcgttccctcgccgacttcgacgccctgctc 360
                                                                                                                                                        331 acggacaagetegtgeegeteggeeaggageacacgetgggtgaettegaeggeaacetg 390
                                                                                                                                                                                                                                                                                                                                                                                                                                               mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                           181 gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                               211 gigoacatoggocogacocgagocogaggeoicogagatgiocacaicoggoicoaggio
                                                                                                                                                                                                                                                                                                                                                                                                                                    ssqA; liquid culture; filamentous bacteria; secondary metabolite;
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/label= SsgA_protein
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraline agents, herbicides, antiparasilic agents, tuminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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transgenic plant; insect resistance;
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.9%; Score 243.8; DB 21; 74.9%; Pred. No. 1.9e-36; Live 0; Mismatches 102;
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                                                                               Disclosure; Fig 5; 60pp; English.
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Matches 305;
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....spinosyn; polyketide synthase; biosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance; macrolide; insecticidal; ds.

Saccharopolyspora spinosa.

DE19957268-A1.

spinosa DNA fragment SEQ ID 1.

28-AUG-2001 (first entry)

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in
                                                                                                                                                                                       New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
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                                                                         (FARB ) BAYER
29-NOV-1999;
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enzymes for spinosyn biosynthesis, useful for insecticidal spinosyns and their derivatives

Claim 7; Page 14-31; 354pp; German.

New nucleic acid encoding recombinant production of

Salas JA;

Velten R,

ж,

Froede

Eberz G, Moehrle V, WPI; 2001-267102/28.

(FARB) BAYER AG.

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                                         0; Mismatches 167;
    DB 22;
Score 58.8; DB
Pred. No. 0.01;
  Query Match
Best Local Similarity 50.3%;
Matches 172; Conservative
    Query Match
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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in blosynthesis of spinosyns. (I) are used (I) to identify, inactivate or modulate genes involved in the blosynthesis of dentify, inactivate or modulate genes involved in the blosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethyltrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58.8; DB 22; Length Pred. No. 0.01; 0; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.3%;
Matches 172; Conservative
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Length 1350;

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Best Local Sin
Matches 160;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The nivention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to dentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part for the printed specification, but was obtained in electronic form the present directly from wile and the present sequence and the determined the description are sequenced to the determined the dete
                     24831 gcggacttcttgaacgacacctacgacgtggtcgaacctggtgatgaacaccggtggatg 24890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr GJ;
                                                                                                                                                                                                                                                                                                                               for cellular proliferation protein #459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1350 BP; 256 A; 468 C; 427 G; 199 T; 0 other;
                                                                                   343 gacttcgacgccctgctcgacgaggcgctggaccgcatcctg
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  AAS54328 standard; DNA; 1350 BP
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2000US-253625P.
2000US-257931P.
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2000US-207727P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
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P-PSDB; AAU36469.
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27-NOV-2000;
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26-MAY-2000;
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                                                                              824 togagitectetacgagaacggeegettetaetteategagatgaacaetegegigeagg 883
                                                                                                          104 gagatgccccggtgacctggggcgttcgggcgggagttgctcatcgacggaggtccgcggc 163
                             Gaps
                                                                                                                                     884 tggagcacccggtatctgagatggtcaccggtgtcgacatcgtcaaggagatgctgcgca
                                                                                                                                                                cgtgcggggacggacgtccacatcgcgccggccgaccggagacgttcggcgaggtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acetyl-CoA-carboxylase; accB gene; accC gene; malonyl-CoA; lipid; oilseed; transgenic plant; biotin-carboxylase; BC; biotin carboxyl carrier protein; BCCP; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing lipid levels in plants by modulating malonyl-CoA levels - partic. for ollseed crops, also nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the biotin carboxyl carrier
                             Indels
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/label= accC
/note= "encodes biotin-carboxylase"
Score 54.4; DB 23;
Pred. No. 0.087;
); Mismatches 176;
                                                                                                                                                                                                                                                                                                                                               acttcgacgccctgctcgacgaggcgctggaccgca 379
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/label= accB
  13.4%;
ilarity 47.6%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa PaO.
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                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1994;
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16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 tggccttcctggaccgcacggacaagatcgtgccgctgggggagggggggttccctcgccg 343
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                                                                                                                                                                                                                                                                                                                                                  44 tggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcatctgcccg 103
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                             The accB and accC genes of Pseudomonas aeruginosa PaO encode the biotin carboxyl carrier protein (BCCP, given in AAR66743) and biotin-carboxylase (BC, given in AAR66744) components, respectively, of acetyl-CoA-carboxylase. The genes may be used to modulate lipid accumulation in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgtgcggggacgggacgtccacatcgcgccgccgacccggaggacgttcggcgaggtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                       Length 2760;
constructs for expressing acetyl-CoA carboxylase, transgenic plants and peptide prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "NysD2 partial protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                               Sequence 2760 BP; 530 A; 962 C; 835 G; 433 T; 0 other;
                                                                                                                                                                                                                                                                       13.4%; Score 54.4; DB 16; 47.6%; Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                          0; Mismatches 176;
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2806..6906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "NysB protein"
16550..49840
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6952..16530
/*tag= d
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                                                           Disclosure; Fig. 4A-E; 48pp; English
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Matches 160; Conserv
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                                                                                                                                                                                                                                                                       Query Match
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The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme in the blosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-557614/62.
P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130,
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135, AAE10136, AAE10137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strom
                                                                                                                                                                                      protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                                     (short) protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "CDS does not include start codon" (83765..64961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E, Brautaset
Gulliksen O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIV NORGES TEKNISK NATURVITENSKAPELIGE
SINTEF STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "CDS does not include complement (62551..63615)
                                                                                                           /*tag= g
/product= "NysR1 protein"
                                                                                                                                                                                                                                                                         /product= "NysR3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "NysR5 protein"
                                              /product= "NysE protein"
51405..54305
/*tag= q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ORF2 protein"
"NysC protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= m
/product= "ORF1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 116-151; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fjaervik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sletta H,
                                                                                                                                                                                                                                                                                                                                                             "CDS does
                                                                                                                                                                                      /product= "NysR2
                                                                                                                                                                                                            "CDS does
                                                                                                                                                                                                                                                                                                                                       /product= "NysR4
                                                                                                                                            54329..57190
/*tag= h
                                                                                                                                                                                                              /note= "CDS d
57180..59963
                                                                                                                                                                                                                                                                                           60415..61047
/*tag= j
/product= "N)
50260..51015
                                                                                                                                                                                                                                                                                                                                                                                 ..62497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2001; 2001WO-GB00509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2000; 2000GB-0002840.
10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3, Sekurova ON
Ellingsen TE,
                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SINVENT AS.
DZIEGLEWSKA H.
ZOTCHEV S B.
                                                                                                                                                                                                                                                                                                                                                               'note=
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FJAERVIK E.
BRAUTASET T.
STROM A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHARMA AS.
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RESULT 12
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                                                                                                      52186 tecggeeggaegeegeegggggagegeeggeegeegaggteggeagteaegteetegeee 52245
                                                                                                                                                                                                                                                                          52246 gctcggtgcgctgcctgttggagcgccggcctgggtgcgcggcggcgtggcccgtgcca 52305
                                                                                                                                                                                                                                                                                                                                                    52306 tegeogracteggeceggagtgeacegagttgetggeggegetegeeggegteeeggeeg 52365
                                                                              98 tgcccggagatgccccggtgacctgggcgttcgggcgggagttgctcatcgacggaggtc 157
                                                                                                                                                          217
                                                                                                                                                                                                                                      218 aggtectgatecgeetgeaggtggggagegaceaggegatgtteegggteggeaeggege 277
                                                                                                                                                                                                                                                                                                              278 cgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttccc 337
                                                                                                                                                                                                                                                                                                                                                                                      Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
      Length 65140;
                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "CDS does not include start codon"
complement (59045..60241)
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                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces noursei nystatin PKS gene cluster DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= g
/product= "NysD2 complete protein<sup>|</sup>
120628..121308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "Nys1 complete protein"
34792..51099
12.8%; Score 52.2; DB 22; ilarity 48.5%; Pred. No. 0.16; Conservative 0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= h
/product= "NysR4 (long) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .ag= c /product= "NysK protein" 57503.58687 /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "NysL protein"
complement (58786..58980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "NysJ protein"
51155..57355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "NysM protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 6337..34771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD17186
ID AAD17186 standard; DNA; 125401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antifungal; antibiotic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                    Similarity
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                                        Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2001
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    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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Db 112387 igiccggcggcaatccgciggcccicgccgcctccicgacgaactccgcgcgagggcg 112446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112567, tegeegtacteggeceggagtgeacegagttgetggeggegetegeeggegteceggeeg 112626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antibidities. The present sequence is a Streptomyces noursel nystatin PKS gene cluster DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 aggiccigaticgcitgcaggigggagcgaccaggcgatgitccgggitcggcacggcgc 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 cgctggtggccttcctggaccgcacggacaagatcgtgccgctgggggagggggggttccc 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 tgcccggagatgccccggtgacctggggcgttcggggcgggagttgctcatcgacggaggtc 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-557614/62.
P-PSDB; AAE10143, AAE10144, AAE10145, AAE10146, AAE10147, AAE10148.
AAE10149, AAE10150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 tegecgaettegaegeeetgetegaegaegaegetggaeegeateetggeegaggage 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 cgcggccgtgcgggggacggggacgtccacatcgcgccgccgacccggagacgttcggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112507 gctcggtgcgctgcctgttggagcgccggccgccctgggtgcgcgggggtggccgtgcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                 Strom AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                              Brautaset T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.2; DB 22;
Pred. No. 0.15;
0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                Fjaervik E, Brautase
Jetta H, Gulliksen O;
                                                                                                     NORGES TEKNISK NATURVITENSKAPELIGE.
F STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 188-254; 266pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Ellingsen TE, Sletta H,
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Local Similarity 48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 1879
08-FEB-2000; 2000GB-0002840.
10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
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                                                                                                                                                                                                                                                                                                                                                                                                 Sekurova ON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 48.5
Matches 144; Conservative
                                                                                                                                                                                SINVENT AS.
DZIEGLEWSKA H.
DZOTCHEV S B.
SEKUROVA O N.
FJAERYLK E.
BRAUTASET T.
                                                                                                                                                             ALPHARMA AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                              STROM A R.
     08-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 SB,
                                                                                                                                                                                                                                                                                                                                                                                                                         Valla S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                             (SNTE)
(ALPH-)
(SINV-)
(DZIE/)
(ZOTC/)
(SEKU/)
                                                                                                                                                                                                                                                                                      (FJAE/)
(BRAU/)
                                                                                                                                                                                                                                                                                                                                              (STRO/)
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Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
                                                                                                Everninomicin; antibiotic; bottle-neck gene; orthomicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (14410..15363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (10232..10235)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (12108..13022)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (9463..10224)
                                                                                                                             Micromonospora carbonacea var. africana
                                                                                                                                                                                        complement (1389..1394)
                                                                                                                                                                                                            complement (1490..2611)
                                                                                                                                                                                                                                        complement (2618..2622)
                                                                                                                                                                                                                                                            complement (2622..3860)
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/note= "No start codon"
                                                                                                                                                                                                                                                                                        complement (3867..3870)
                                                                                                                                                          complement (132..1382)
                                                                                                                                                  Location/Qualifiers
         AASO8693/c
ID AASO8693 standard; DNA; 109519 BP.
                                                                                                                                                                                                                                                                                                                                                                                                            "EvdF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= q
/product= "EvdJ"
12027..12455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= s
/product= "EvdL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= u
/product= "EvrA"
                                                                                                                                                                            /product= "EvdA"
                                                                                                                                                                                                                             /product= "EvdB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            product= "EvdG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= o
/product= "EvdI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "EvdK"
                                                                                                                                                                                                                                                                                                                                                                                "EvdE"
                                                                                                                                                                                                                                                                                "EvdC"
                                                                                                                                                                                                                                                                                                                                 "EvdD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "EvdH"
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10424..11176
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/*tag= r
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/*tag= g
/product= ";
                                                                                                                                                                                                                                                                                                                                        4134..4138
/*tag= h
5309..6235
/*tag= i
                                                                                                                                                                                                                                                                                                                                                                                         6232..7275
/*tag= j
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5226..6229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3342..9364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3333..8336
                                                                                                                                                                                                                                                                                                                                                                                                                                        272,.8327
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/product=
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                                                                                                          fermentation; ds.
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                                                                                                                                                                                                                                                                                                                                                                   This sequence contains the coding information for (a) the cytochrome P450 enzyme, P450SUI; and (b) the electron donor iron sulphur protein FeS-B. It is contained in a recombinant plasmid which is used to transform host Streptomyces species which in turn are used to coot a plant seed to transform the plant. The resultant transformants are resistant to herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 cacggcgccgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcagga
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                                                                                                                                                                                                                                                                                                          DNA encoding cytochrome P450 enzymes - and electron donating iron-sulphur proteins, used to confer herbicide resistance to plants and microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 51.8; DB 12; Length 50.6%; Pred. No. 0.25; Live 0; Mismatches 122; Indels
                                                                                                                                                                                                                                                  odell JT;
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                                                                                               /*tag= c
/product= FeS-B protein
                           Location/Qualifiers
                                                                                                                                                                                                                                                          O'Keefe DP, Omer CA, Romesser JA;
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                                             /*tag= a
128..1345
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/product= P450SU1
1369..1575
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89US-0405605.
90US-0464499.
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Best Local Similarity 50.6
Matches 125; Conservative
         Streptomyces griseolus.
                                                                                                                                                                                                                                                  Harder PA,
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11-SEP-1989;
12-JAN-1990;
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222 cctgatccgcctgcaggtggggagcgaccaggcgatgttccgggtcggcacggccgct 281 282 ggtggcettcctggaccgcacggacaagatcgtgccgctgggggcaggaggttccctcgc 341 0; Gaps Length 109519; Score 51.6; DB 22; Length 1 Pred. No. 0.2; 0; Mismatches 119; Indels /product = "Evry" complement (45767..45770) /*tag = be /*tag = bf /product = "Evr2" complement (45952..45956) /*tag = bg complement (45952..45956) /rcdg-cadduct- "Evsc"
53554..54207
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/product- "EvbB"
complement (55125..55128) /*tag= ax / /product= "EvrU" complement (41679..42707) /*tag= ay / /product= "EvrV" /*tag= aw complement (40887..41576) complement (42714..42717) /*tag= az complement (42810..43799) /*tag= ba /product= "EvrW" complement (43807..43811) /*tag= bb complement (43799..44866) /*tag= bc /product="EvrX" complement (45014..45760) /*tag= bd complement (55135..56094) complement (56100..56103) complement (56184..56813) complement (40899..40902) /*tag= bh /product= "EvsA" /*tag= bi /product= "EvsB" 51629. 51622 /*tag= bj /*tag= bk /*tag= bq /product= "EvbC2" 56961..58709 /product= "EvbC" Query Match 12.7%; Best Local Similarity 50.8%; Matches 123; Conservative (p /*tag- bo /*tag= CDS CDS RBS CDS RBS CDS RBS RBS RBS CDS CDS RBS CDS CDS CDS CDS CDS CDS RBS CDS CDS QQ q g ò οy

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Iruela-Arispe L, Hastings GA,
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            The present sequence represents a Amycolatopsis mediterranei rifamycin synthesis gene cluster DNA fragment from the present invention. The DNA fragment comprises a DNA region involved directly or indirectly
cgacttcgacgccctgctcgacgaggcgctggaccgcatcctggccgaggagcagaacgc 401
                                                                                                                       Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.
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                                                                                                                                     Amycolatopsis mediterranei; rifamycin; synthesis; gene cluster; polyketide synthase; actinomycete; ansamycin; ds.
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/label= ORF_B
/product= "polyketide synthase"
30895..36060
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/product= "polyketide synthase"
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5550..30759
                                                                                                                                                                                                                                                                                                                       "polyketide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    produce rifamycin and rifamycin analogues
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Product | "polyketide
86259..41325
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1825..15543
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/label= ORF_A
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51713..5293
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the adjacent DNA regions to the right and left which, by reason of the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin biosynthesis, qualify as constituents of this rifamycin gene cluster, and functional fragments, derivatives or constituents of these. The Amycolatopsis mediterranel rifamycin synthesis gene cluster DNA fragment can be used for producing rifamycin, rifamycin analogues or precursors. It can also be used for inactivating or modifying genes involved in ansamycin or rifamycin biosynthesis. The DNA can be used for constructing mutant actinomycetes strains from which the natural rifamycin or ansamycin biosynthesis gene cluster has been partly or completely deleted. The DNA fragment can be used for assembling a library of polyketide synthases, which can be used for assembling a library of polyketides. A hybridisation probe of the invention can be used for identifying DNA fragments involved in the biosynthesis of ansamycins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 gcaggtggggagcgaccaggcgatgttccgggttcggcacggcgccgctggtggccttcct
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Pred. No. 0.27;
0; Mismatches 110; Indels 0
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51.5%;
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98US-0098539
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Matches 117; Conservative
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(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
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metalloprotease thrombospondin (METH) proteins METH1 and METH2
metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of
angiogenesis both in vitro and in vivo. They can be used for treating
cancer and other disorders related to angiogenesis including abnormal
wound healing, inflammation, rheumatoid arthritis, psoriasis,
endometrial bleeding disorders, diabetic retinopathy, some forms of
macula degeneration, haemangiomas, and arterial-venous malformations.
They may be useful in treating deficiencies or disorders of the immune
system, by activating or inhibiting the proliferation, differentiation,
or mobilisation (chemotaxis) of immune cells. The etiology of these
immune defictencies or disorders may be genetic, somatic, such as
cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
toxins), or infectious. They can also be used to treat inflammatory
conditions, both chronic and acute conditions. The products can also
tused for detection and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to
AAY49511 represent sequences given in the exemplification of the present
                                                                        New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;
                                                                                                                                                                                           Disclosure; Page 296-321; 457pp; English.
                       WPI; 1999-590684/50.
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ö 2535 eggetgacetecgaegagggegeegtegaegaetteggettegaeeeggagetgaeegae 2594 217 gaggtcctgatccgcctgcaggtgggagcgaccaggcgatgttccgggtcggcacggcg 276 Gaps 12.1%; Score 49.4; DB 20; Length 38734; 51.6%; Pred. No. 0.55; 1.4ve 0; Mismatches 106; Indels 0; Query Match
Best Local Similarity 51.6
Matches 113; Conservative q ò

2655 ggactigagaacgtgccggccgaggggggcgcactcctggtcgccaaccactccggcacc 2714 277 ccgctggtggccttcctggaccgcacggacaagatcgtgccgctgggggcaggagcgttcc Ωp οy

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Search completed: July 18, 2002, 11:37:34 Job time: 11319 sec

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STATE: California
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US-08-074-121-4
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                                                                                           (without alignments)
603.847 Million cell updates/sec
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Sequence 4, Appli
Patent No. 5212296
Patent No. 5212296
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Sequence 109, App
Sequence 109, App
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Sequence 13, Appl
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Sequence 1,
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Sequence 59,
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Sequence 2,
Sequence 1,
Sequence 9,
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Sequence 1,
Sequence 1,
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                                                                             July 18, 2002, 11:25:01; Search time 165.56 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-453-695A-109
US-08-268-161A-109
US-08-453-702A-109
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ALIGNMENTS

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UGS-004-1121-4
Sequence 4, Application US/08071121
Patent No. 5767362
GENERAL INROMATION:
PAPLICANT: Best, Elaine
APPLICANT: Real, Vic C.
TITLE OF INVENTION: Lipid Content of Plant Tissues
NUMBER OF SEQUENCES: 15
CORRESPONDERES: 15
CORRESPONDERES: 2200 Sand Hill Road, Suite 100
CITY: Mello Park
STREE: 2200 Sand Hill Road, Suite 100
CITY: Mello Park
COMPUTER: Galifornia
COUNTRY: Galifornia
COUNTRY: READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBMP C compatible
COMPUTER: REAPONERS: 32.750
ATTORNEY/AGENT INFORMATION:
FELEPRONE (415) 854-6875
TELEFRAX: (415) 854-6875
TELEFRAX: (415) 854-6875
TELEFRAX: (415) 854-6875
TELEFRAX: (415) 854-0875
TELEFRAX: (415) 864-0875
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PCT-US94-06447-4
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                                                                                                     2172 TCGAGTTCCTCTACGAGAACGCCGCTTCTACTTCATCGAGATGAACACTCGCGTGCAGG 2231
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                                               Gaps
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     13.4%; Score 54.4; DB 1; Length 3231; 47.6%; Pred. No. 0.0045; Live 0; Mismatches 176; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Calgene, Inc.
TITLE OF INVENTION: Methods and Compositions for Modulating
TITLE OF INVENTION: Lipid Content of Plant Tissues
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotshal & Manges
STREET: 2882 Sand Hill Road, Suite 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06447
FILING DATE: 06-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2472 ACAGCGTGCCGCGAACTACGACTCGCTGGTCGGCA 2507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application PC/TUS9406447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
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TYPE: nucleic acid
STRANDEDNESS: double
                                           Matches 160; Conservative
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FEATURE:
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STATE: California
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                         Best Local Similarity
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      Length 3231;
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                                                                                                                                  Indels
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Pred. No. 0.015;
0; Mismatches 122; Indels
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Patent No. 9212296
Patent No. 92
Ouery Match 13.4%; Score 54.4; DB 5; Best Local Similarity 47.6%; Pred. No. 0.0045; Matches 160; Conservative 0; Mismatches 176;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
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50.6%;
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Best Local Similarity 50.65
Matches 125; Conservative
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ORGANISM: Mycobacterium tuberculosis
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CITY: Chicago
STATE: Illinois
                                  OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-453-695A-109
                                                                                        US-09-103-840A-2
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Gaps
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-23007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATENT NOS: 2
SOFTWARE: PATENT NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1879;
                                                                                                                                          5212296-5
Patent No. 5212296
APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
                                                                                                                                                                                                :J.: O'KEEFE, DANIEL P.:OMER, CHARLES A.:ROMESSER, JAMES A.:
;TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.8; DB 6;
Pred. No. 0.015;
0; Mismatches 122;
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 465,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.7%;
50.6%;
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Matches 125; Conserv
                                     390 ggagcag 396
                                                                     432 cqacctq 438
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. LENGTH: 1879
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     positions throughout the sequence \mathfrak g
                                                                                                                                                                                                                                                                                67 gatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacctgggcg 126
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                                                                                                                                                               Length 4403765;
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TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
ADDRESSEE: Borun
                                                                                                                                                                  Score 49.2; DB 4; Length 4 Pred. No. 0.042; 0; Mismatches 178; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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t, c or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 109, Application US/08453695A Patent No. 5708143 GENERAL INFORMATION:
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NAME: No. 5708143and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32658
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474.6300
CDC 1551
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represent a, t
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CAMPUTER: IBM PC COMPATIBLE
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46.7%;
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LENGTH: 3353 base pairs
                                                                                                                                                                  Query Match 12.19
Best Local Similarity 46.79
Matches 156; Conservative
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INFORMATION FOR SEQ ID NO:
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2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2360
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                                                                                                                                                                                                                                                                186 catcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtgggag 245
                                                                                                                                                                               126 gttcgggcgggagttgctcatcgacggaggtccgcggccgtgcggggacgggacgtcca 185
                                                                                                                                                                                                                                                                                                                                                      246 cyaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacgga 305
                                                                                       Score 47.6; DB 1; Length 3353;
Pred. No. 0.096;
0; Mismatches 99; Indels 0
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TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
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Pred. No. 0.096;
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Chicago
: Illinois
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; Sequence 109, Application US/08453702A
; Patent No. 5891706
; GENERAL INFORMATION:
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NAME: No. 5891706and, Greta E.
REGISTRATION NUMBER: 35,302
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TELEPHONE: 312/474-6300
                                                                                          11.7%;
51.9%;
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51.9%;
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                                                                                     Query Match
Best Local Similarity 51.99
Matches 107; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
      763.,3123
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Best Local Similarity
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    ; LOCATION: 7
US-08-268-161A-109
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Pred. No. 0.096;
0; Mismatches 99; Indels 0
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Sequence 109, Application US/08268161A
Patent No. 5798224
GENERAL INFORMATION:
APPLICANT: SUZUKİ, Shintaro
ATILLE OF INVENTION:
NUMBER OF SEQUENCES: 115
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray,
ADDRESSEE: Borun
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,161A
FILING DATE: June 27, 1994
CLASSIFICATION: 435
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CITY: Chicago
STATE: Illinois
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NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERNCE/DOCKET NUMBER: 27866/32149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 109;
SEQUENCE CHARACTERISTICS:
LENGTH: 3353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               Query Match 11.7%;
Best Local Similarity 51.9%;
Matches 107; Conservative (
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                     NAME/KEY: CDS
LOCATION: 763..3123
                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                              ; LOCATION: 7
US-08-453-695A-109
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2421 GGCCAAGGACAACTGGCCTTGGTGTACCGGTGCAGAAGGGCTCGGGCCTGCAC 2480
2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2360
                                                                           2361 CACAGACCGCGGCTTCCCGGCGCTGAGCAGCGAGGCGCTGGTGCGGGGTGCTGGTGCTGGA 2420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                               246 cgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacgga
                                      186 catcgcgcccgacccggagacgttcggcgaggtcctgatccgcctgcaggtggggag
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                                                                                                                                                                                                                                                                                                                                                                                          Protocadherin Materials and Methods 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Sears Tower, 233 S. Wacker CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerstein,
                                                                                                                                                                                                                                                                                          RESULT 10
PCT-US95-08071-109
SCHOUGCE 109, Application PC/TUS9508071
GENERAL INFORMATION:
APPLICANT: SIZUKi, Shintaro
TITLE OF INVENTION: Protocadherin Mate;
NUMBER OF SEGUENCES: 115
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT/US95/08071
                                                                                                                                                                                                                                   2481 CGAGCTGGTGCCCCGGGCGGCGAGC 2506
                                                                                                                                                                                             306 caagatcgtgccgctggggcaggagc 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 3353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%;
milarity 51.9%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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MOLECULE TYPE: CDNA
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Best Local Similarity
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PCT-US95-08071-109
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                                                                   2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCTTCCAGGTTCCGCTGGGCCC 2360
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                                                                                                               categogecegeceggagaegtteggegaggteetgateegeetgeaggtggggag 245
                                      cgaccaggcgatgttccgggtcggcacggccgctggtggccttcctggaccgcacgga 305
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Pred. No. 0.096;
0; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEGUENCES: 115
CORRESPONDENCE ADDRESS:
99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, STREF: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/34703
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6408
TELEFX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,639
FILING DATE: 18 JUN 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/263,161
FILLING DATE: 27 JUN 1994
ATTORNEY AGENT INFORMATION:
NAME: Greta E. No. 6262237and
                                                                                                                                                                                                                                                                                                               2481 CGAGCTGGTGCCCCGGGCGGCCGAGC 2506
                                                                                                                                                                                                                                                                          306 caagatcgtgccgctggggcaggagc 331
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Patent No. 6262237
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INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.7%;
Best Local Similarity 51.9%;
Matches 107; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3353 base pairs
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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; LOCATION:
US-09-099-639-109
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US-09-099-639-109
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Matches 107;
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2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2360

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5146. CGGGCCGTCTCTTCGACGCGAAGGTGCCTGCTGCTGGTGGCCTTCCGCGGCGG 5205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 cccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtggggagcgaccag 252
                                                                                                                           313 gigocgotiggggcaggagcgitcoctcgccgacticgacgccctgctcgacgaggcgctg 372
                                          253 gegatgitteegggteggeaeggegeegetggiggeetteetggaeegeaeggaeaagate 312
                                                                                                                                                             748: GCCCATCTGTCCCAGGCGCTCGACGATGTGACCGTCGGGGTGAACTCGTCCCCGGTGAC 807
628 GTCGACGAÇCCGGGCGCGATCGCCAACGTCAAGCCGCTCTACGGGGACGCGAACGACCCG 687
                                                                                 688 TICCICGGGIACGACCGCGAGCTGCTGCCGCGGAGGACCCGCGGGCACAAGGAGGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aldoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
TITLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: JACOBSON, PRICE, HOLMAN & STERN,PPLC
; The Jenifer Buliding, 400 Seventh Street, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1418/P57452US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 13, Application US/09385028
; Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFRENCE/POCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEPHONE: (202) 39305350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
E: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 13:
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LENGTH: 11604 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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US-09-385-028-13
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US-09-385-028-13
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                                                                           2361 CACAGACCGCGGCTTCCCGGCGCTGAGCGAGCGCGTGGTGCTGCTGGTGCTGGTGCTGGA 2420
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                                     categegecegecegaeceggagaegtteggegaggteetgateegeetgeaggtggggagg
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
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49.0%; Pred. No. 0.11;
tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: D. Douglas Frice
REGISTRATION NUMBER: 24,514
REGISTRATION NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEPHONE: (202 39305350
TELERS: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   caagatcgtgccgctggggcaggagc 331
                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/09385028 Patent No. 6232106 GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 126; Conservative
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US-09-385-028-18
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US-09-385-028-18
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7178 CGGGCCCGTCTTTCGACGCGCAAGGTGCCCTGCTGCGTGGACGTGGCCTTCCGCGGGGGG 7237
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                                                                                                                                                                                                         7298' TICCICGGGIACGACCGCGAGCIGCIGGCGCCGGAGGACCCCGCGGACAAGGAGGCCGIC 7357
                                                                                                                                                            253 gcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaagatc 312
                                                                                                                                                                                                                                                     313: gtgccgctgggggcaggagcgttccctcgccgacttcgacgccctgctcgacgaggcgctg 372
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for
                                                                      193 cccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtggggagcgaccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Donadio, S
APPLICANT: Moalpine, J B
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Excombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
TURBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Edward H. Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratories D377/AP6D-2 One Abbott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING PATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OTHER INFORMATION: ,
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CITY: Abbott Park
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APPLICANT: Katz, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: NRRL 238
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ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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US-07-642-734C-3
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1266 TICCICGGGIACGACCGCGAGCIGCCGGCGCGGAGCCCCGCGGGACAAGGAGGCCGIC 5325
                                                                                                                                                                                                 5326 GCCCATCTGTCCCAGGCGCTCGACGATGTGACCGTCGGGGTGAAGCTCGTCCCCGGTGAC 5385
                                                                  253 gegatgiteegggteggeaeggegeegetggtggeetteetggaeegeaeggaeaagate 312
                                                                                                                                                         313 gtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctcgacgaggggcgctg 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
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49.0%; Pred. No. 0.1;
tive 0; Mismatches 131; Indels
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The Jenifer Buliding, 400 Seventh Street, N.W.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN 1997
FILING DATE: 29-JAN 1997
ATTORNEY AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SIGNS 666
TELERA: (202) 3930350
TELEX: RCA 24859 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09385028
Patent No. 632106
GENERL INFORMATION:
APPLICANT: Susan E. Jensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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Best Local Similarity 49.03
Matches 126; Conservative
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
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STRANDEDNESS:
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US-09-385-028-1
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LOCATION: 10831..1217.
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
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LOCATION: 4471..5847
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
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LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
FEATURE:
                                                                                                                                                                                                  LOCATION: 97..1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module
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LOCATION: 1723..20235
LOCATION: 1723..20235
OTHER INFORMATION: /codom_start= 10723
OTHER INFORMATION: /function= "gene =erya"
OTHER INFORMATION: /product= "orf3 encoding modules
OTHER INFORMATION: /codouct= "orf3 encoding modules
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
FEATURE:
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LOCATION: 9433..9984
COTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: /function= approximate span
OTHER INFORMATION: /function= approximate span of
OTHER INFORMATION: /function= approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
NAME/KEY: misc_feature
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LOCATION: 4171.4428
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
                                              NAME/KEY: misc_feature
LOCATION: 19..4470
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 3"
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LOCATION: 4471_10722
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: module 4"
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LOCATION: 10723.15165
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: module 5"
OTHER INFORMATION: 6-deoxyerythronolide
                                                                                                                                                                          NAME/KEY: misc_feature
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6644 CCCCGGAGGTGGCGCGCATCGAGGACCGGCTCGCGGCCGAGCTGGGCACCATCACCGCCG 6703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 aggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaaga 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 ggcgggagttgctcatcgacggaggtccgcggccgtgcggggacgggacgtgcacatcg 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 egecegeegaceegagaegtteggegaggteetgateegeetgeaggtggggagegace 250
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LOCATTON: 15172..16569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
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LOCATION: 18379.18921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
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                           LOCATION: 12379..13350
OTHER INFORMATION: /function= "approximatr span of
OTHER INFORMATION: acyltransferase domain of module
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) CCCATION: 19492..20235

COCATION: J/40nction approximate span of

OTHER INFORMATION: thloesterase domain of module 6"

US-07-642-734C-3
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LOCATION: 1857...15114
OCCATION: 7 function= "approximate span of OTHER INFORMATION: Afluction acyl carrier domain of module 5"
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COCATION: 19149..19398
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
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LCGATCON: 15166..20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 6"
                                                                                                                                                                                    5 to
                                                                                                                                                       LOCATION: 14062..14610
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47.4; DB 1;
Pred. No. 0.1;
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Best Local Similarity 47.2%;
Matches 144; Conservative
misc_feature
12379..13350
                                                                                                                                    misc_feature
  NAME/KEY:
LOCATION:
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NAME/KEY: misc_feature
LOCATION: 4471..5847
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
FEATURE:
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LOCATION: 10831..12174
OCHER INFORMATION: /function= "approximate span of
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LOCATION: 7165..9216
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NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
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/function= "gene =eryA"
/product= "orf3 encoding modules 5 &
6-deoxyerythronolide B formatio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
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LOCATION: 10225..10483
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OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
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LOCATION: 14857..15114
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
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LOCATTON: 9433..9984
OTHER INFORMATION: __function= "approximate span
OTHER INFORMATION: __beta-ketoreductase of module 4"
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LOCATUON: 10723.15165
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 5"
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LOCATION: 14062..14610
COCHER INFORMATION: /tunction= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
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LOCATION: 4471..10722
OTHER INFORMATION: /function= "approximate span oTHER INFORMATION: module 4"
FEATURE:
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LOCATION: 12379..13350
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
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LOCATION: 19.10722
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OTHER INFORMATION: /function= "gene eryA"
OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for OTHER INFORMATION: 6-deoxyerythronolide B"
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COGATION: 97..1482
COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
                                                                                                                                                                                                                                           APPLICANT: Donadio, S
APPLICANT: Donadio, S
APPLICANT: Katz, L
APPLICANT: Mcalpine, J
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 27
CORRESPEET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Abbott Laboratories D377/AP6D-2 IL
STREET: Abbott Park
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STREET: Abbott Park
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LOCATION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
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OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 3"
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40.943
REFERENCE/DOCKET NUMBER: 4952.US.DI
TELEPHONE: 847-938-3137
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LEMOTH: 20235 base pairs
TYPE: uncleic acid
STRANDEDNESS: double
TYPE: UNCLEIC acid
STRANDEDNESS: double
TOPOCLOGY: UNKNOWN
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STRAIN: NRRL 238
                                                                                                                                                              Sequence 3, Application US/08439009A Patent No. 6004787 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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  US-08-439-009A-3
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172..16569
CTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
COCATION: 18379-.18921
COTHER INFORMATION: /Lunction= "approximate span of
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LOCATION: 16768..17721
OTHER INFORMATION: /function- "approximate span of
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NAME/KEY: misc_feature
LOCATION: 19149..i9398
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NAME/KEY: misc_feature

LOCATION: 19492..20235

O'THER INFORMATION: /function= "approximate span of OTHER INFORMATION: thioesterase domain of module 6" US-08-439-009A-3
                          OTHER INFORMATION: /function- "approximate span of OTHER INFORMATION: module 6"
LOCATION: 15166..20235
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                                                                         71 cctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacctgggcgttcg 130
                                                                                                                                            131 ggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacgggacgtccacatcg 190
                                     0; Gaps
Query Match 11.6%; Score 47.4; DB 3; Length 20235; Best Local Similarity 47.2%; Pred. No. 0.1; Matches 144; Conservative 0; Mismatches 161; Indels 0;
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Search completed: July 18, 2002, 11:34:02 Job time: 11432 sec

us-09-749-185-6.rst

18 49.8 12.2 1203 12 CNS015f4 AL106054 Drosophil 20 49.6 12.2 568 9 AW231567 AW233567 687067004 20 49.4 12.1 440 12 AA852321 AA234356 AA234352 AA234332 AA234323 AA234332 AA2343323 AA234332 AA234332 AA234332 AA234332 AA234332 AA234332 AA234332 AA234332	48.8 12.0 454 9 AV698167 48.8 12.0 522 12 AQ848096 48.8 12.0 584 10 BT79714 48.8 12.0 720 10 BF037954 48.8 12.0 720 10 BF037954 48.8 12.0 1039 9 AL543130 48.6 11.9 327 9 AL52193 48.4 11.9 327 9 AJ282193 48.4 11.9 327 9 AJ282193	RESULT 1 CNSO06XK/C LOCUS LOCUS LOCUS LOCUS LOCUS DEFINITION DOSOPPHIA melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit f1y), genomic survey sequence. ALO66051.1 GI:4945019 ALO66051.1 GI:4945019 VERSION GSS. SOURCE CNGANISM Drosophila melanogaster ELAMOROS Fruit f1y, CNGANISM Drosophila melanogaster ELAMOROS Fromorpha; Ephydroidea; Drosophila. REFERENCE AUTHORS JOURNAL JOURNAL SUBMITTE JOURNAL	The BLOS is the constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Goosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST library is now detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. FEATURES John Street
sic - nucl	Scoring table: IDENTITY_NUC Gapor 10.0 , Gapext 1.0 Searched: 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: 27472414 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 0% Listing first 45 summaries	Database: EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estin:* 10: qb_est1:* 11: qb_htc:* 12: qb_gss:* 11: qb_htc:* 12: qb_gss:* 13: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_hum:* 15: em_gss_hum:* 16: em_gss_hum:* 16: em_gss_hum:* 18: em_gss_hum:* 18: em_gss_hum:* 19: em_gss_hum:* 10: qb_ass_hum:* 11: qb_htc:* 12: qb_ass.* 13: em_gss_hum:* 14: qb_ass_hum:* 15: em_gss_hum:* 16: em_gss_hum:* 16: em_gss_hum:* 16: em_gss_hum:* 17: qb_ass_hum:* 18: em_gss_hum:* 18: em_gss_hum:* 19: em_gss_hum:* 10: qb_ass_hum:* 10: em_gss_hum:* 11: qb_ass_hum:* 12: em_gss_hum:* 13: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_hum:* 16: em_gss_hum:* 16: em_gss_hum:* 17: em_gss_hum:* 18: em_gss_hum:* 18: em_gss_hum:* 19: em_gss_hum:* 10: em_gss_hum:*	C 1 64.2 15.8 935 12 CNSOO6XK ALO56051 Drosophil ALO53013 Drosophil CNSOO91P ALO53013 Drosophil CNSOO91P ALO53013 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66051 Drosophil CNSOO91P ALO66052 Drosophil CNSOO91P ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 Drosophil CNSOO91P AND ALO66052 DROSOPHIL CNSOO91P AND ALO66052 DROSOPHIL CNSOO91P ADD ALO66052 DROSOPHIL CNSOOPHIL CN

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KEYWORDS
SOURCE
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- Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ibrary was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                 159 geggeegtgeggggaegggaegteeacategegeeeggeeggaggagaegtteggega 218
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                                                                                                                                                                                            915 GSGCGSGSGCCCCSGSCCCSCSCGCCSSCSSSSCCCSSCSCGCSCGGSSCC
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                                                                                                             Query Match 15.8%; Score 64.2; DB 12; Best Local Similarity 33.0%; Pred. No. 0.16; Matches 102; Conservative 72; Mismatches 135;
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/clone="BACR14N09"
/note="end : T7"
170 c 162 g
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Liber Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammeoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoral digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
                                                                 melanogaster"
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/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="S20147"
                                                             /organism="Drosophila m
/db_xref="taxon:727"
/clone_lib="kpc1-98"
/clone="taxcR19116"
/note="end : TET3"
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Fax: 81-298-38-7468
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Listed (102-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |

- Web : www.genoscope.cns.fr |

- Web : www.genoscope.cns.fr |

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Cancer Genetics at the Roswell Park Cancer Constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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b; Pred. No. 1.7;
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/organism="Drosophila me/db_rref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
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723 bp mRNA linear EST 31-MAR-2000 Rice mature leaf Oryza sativa cDNA clone S20147, mRNA
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1 (bases 1 to 723)
Sasaki, T. and Yamamoto.K.
Rice CDNA from mature leaf (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                               249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tsassaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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/db_xref="taxon:4530"
/clone="c60023_11A"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_l: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. # 4 others
                                                                                                                                                                                                                                                                                                                                                                         83 CCGCGCGCCCATGGCGTGGTGGTGATCGCGGTCGCCCGGGACCACGACGACGACGACGGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 AAGAAGGGTGGGGTCTCGCCGCCGCCGCCCCCCCCTTCGGGGACGAGGCGGGGTTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttcc 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                   37 attocggtggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcat 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 ctcgccgacttcgacgccctgctcgacgaggcgctggacgcatcctggccgaggag 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558 bp mRNA linear EST 19-0 sativa cDNA clone C60023_11A, mRNA
                                                                                                                                                                                                                                                                                                                          23 ACTTCGTCGGAGTCGGAGTCCGAGTCCACCGCCTCGCCGGAGATGGAGCACGCCTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaggteetgateegeetgeaggtggggagegaceaggegatgtteegggteggeaeggeg
                                                                                                                                                                                                                 ó
                                                                                                                                                             Length 723
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 0; Mismatches 188;
                                                                                                                                                       Score 56.2; DB 9;
Pred. No. 3.1;
/clone_lib="Rice mature leaf"
/tissue_type="mature leaf"
197 c 270 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .558
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGF'.
Location/Qualifiers
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                                                                                                                                                          Query Match 13.8%;
Best Local Similarity 47.3%;
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C97336.1 GI:3760078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -' RGP'
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                                                       127
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TITLE
JOURNAL
COMMENT
                                                         BASE COUNT
ORIGIN
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VERSION
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Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, TT-1:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG146122
AG146122.1 GI:16675800
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-007K01.TJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                            167 geggggaegggaegtecaeategegeeegaeeeggaggagaegtteggegaggteetga 226
                                                                                                                        294 GCGAGGGCGTGGTTCGCCACGGCGAGGGTCCGGCACTACGCGCTCGACGACGTGATGG 353
                                                                                                                                                                                               227 tecgeetgeaggtggggagegaceaggegatgtteegggteggeaeggegeetggtgg 286
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                        287 ccttcctggaccgcacggacaagatcgtgccgctgggggaggggttccctcgccgact
                                                                                                                                                                                                                                                                                                                                          414 GAGCTGCTGCCCGCGCGCGCGCGCACTTGTTGCTGGTGCAGGTCACGTACCTGNGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG146122 1002 bp DNA linear GSS 08
Pan troglodytes DNA, clone: RP43-007K01.TJ, genomic survey
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1002)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
404 c 455 g 25 t 61 others
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  Length 558;
                                              Indels
13.1%; Score 53.2; DB 10; 51.1%; Pred. No. 9.4; ative 0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
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No. 9.4;
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/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9598"
/clone="RP43-007K01.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score Pred.
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing: TJ
Query Match 13.19
Best Local Similarity 51.19
Matches 121; Conservative
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Best Local Similarity
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194 747

S

Matches

148 338

δ a

218 268

g δ q δλ

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328

g

DEFINITION

RESULT. CNS00720

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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AW564221 633 bp mRNA linear EST 19-JUL-2000 LG1_289_A06.bl_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 706 542 1805
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref=branish Grown 1 (LG1)"
/note=lib="Light Grown 1 (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Ecof; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                            255 gatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaagatcgt 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 tcggggggggggttgctcatcgacggaggtccgcggggcgtgcgggggacggggacgtccaca 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 tegegecegecegacecegagagacgtteggegaggteetgateegeetgeaggtggggageg 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 033)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
  ggagttgctcatcgacggaggtccgcgggccgtgcggggacggggacgtgccacatcgcgcc
                                          195 egecgaeceggagaegtteggegaggteetgateegeetgeaggtggggagegaecagge
                                                                                                                        808 - SSGSSGGGSGGGSSGCSSGSGCCSSGCGCGSSGCGCGCGCGSG
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                                                                                                                                                                                                                                                                                         315 geogetggggcaggagcgttccctcgccgacttcgacgccctgctcg 361
                                                                                                                                                                                                                                                                                                                       0; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by mass excision."
184 c 226 g 108 t
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cordonnier-Pratt MM
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POLYA=No.
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49.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW564221
AW564221.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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KEYWORDS
SOURCE
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Direct Submission

Submitted (02-10N-1999) Genoscope - Centre National de Sequencage:

Bp 191 91006 EVRY cedex - FRRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For futther information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo,

NY. The library is named RPCI 98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 03-JUN-1999
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                                                                                            ggcacggcgccgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcag 327
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  Gaps
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/clone="BACR14B09"
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/strain="Friedlin strain V1"
/db.ref="taxon:5664"
/clone="LMAJFV1_m15c01"
/clone="LMAJFV1_m15c01"
/clone="LMAJFV1_m15c01"
/clone="Nector: pZero-2 (Invitrogen); Site_1: EcoRV;
/deb_nost="TCP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
/denomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's EcoRV site."
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DNA Sequencing by: Washington University Genome Sequencing Center

If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major

Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining

clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.

Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania.

1 (bases 1 to 390)

Akopyants,N.S., Clifton,S.W., Martin,J., Pape,D., Wylie,T., Li,L.,
Kissinger,J., Roos,D.S., Marra,M., Hillier,L., Chinwalla,A.,
Blistain,A., Schmitt,A., Person,B., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cole,R., Underwood,K., Cardenas,M., Gibbons,M.,
Harvey,N., McCann,R., Tsagareishvili,R., Williams,T., Jackson,Y.,
Bowers,Y., Swaller,T., Waterston,Wilson,R. and Beverley,S.M.
A survey of the Leishmania major Friedlin strain v1 genome by shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                   AQ846145
LMAJFV1_Im15c01.y1 Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_lm15c01 5' similar to
contains element 212bp.2 leishmania repetitive element ; DNA
248 accaggogatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggaca 307
                                                                                        agategtgeegetgggggagggtteectegeegaettegaegeeetgetegaegagg 367
                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                            Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Biochem. Parasitol. 113 (2), 337-340 (2001) 21192569
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                                                                                                                                                                                          cgctggaccgcatcctggccgaggagcagaa 398
                                                                                                                                                                                                                     254 GCGCGGACGCCGCCGAGGCGGAGGA 284
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Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Elilopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 440)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudle, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D. F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Uppublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 bp mRNA linear EST 26-SEP-200 EBT007_SQ002_B16_R IGF Barley EBr007_SQ002_B16_R IGF Barley EBro07 library Hordeum vulgare cDNA clone EBr07_SQ002_B16 5', mRNA sequence.
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                                                                                                         72 ctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacctgggcgttcgg 131
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  Length 390;
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/tissue_type="Etiolated root and shoot"
/lab_host="DH10B"
Score 51.4; DB 12;
Pred. No. 18;
0; Mismatches 166;
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Invergowite, Dudee, DD2 5DA, Scotland,
110.04 11382 562731
Fax: 00 44 1382 562426
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All sequence has a Phred quality score of primer: Ml3 reverse
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  Query Match
Best Local Similarity 47.6%;
Matches 151; Conservative
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Unit of Genomics
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/clone_lib="Leibmania major FVI random genomic library"
/lab.host="TOP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_l: ECGRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size polymerase, dephosphorylated with Sirimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECGRV site."
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1 (bases 1 to 616)
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Tetraodon nigroviridis.
Tetracdon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 ttcatctgcccggagatgccccggtgacctggggcgttcggggcgggagttgctcatcgacg 151
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                                                                                                                                              /strain="Friedlin strain V1"
/db_xref="taxon:5664"
/clone="LMAJFV1_lm29c04"
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204 g
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Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
If using this information please cite:
N.S. Akopyants and S.M. Bewerley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(hatalia@borcim.wustl.edu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMAJFV1_lm29c04.y1 Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm29c04 5' similar to contains element V1-chl_type_II.2 V1-chl_type_I leishmania repetitiive element ;, DNA sequence.
                                                                                                                                                                                                                                                                                                                                               133 cgggagttgctcatcgacggaggtccgcgggccgtgcggggacgggacgtccacatcgcg 192
                                                                                                                                                                                                                                                                      113 CGGATGGTGGCCGATGCCGTGGTGCAGGCGTCGTCGGTGTTCGCCGCCTTCGACAAGGAC 172
                                                                                                                                                                                                                                                                                                                                                                                                                     gcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaagatc 312
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 GAGGIGICCGAGGAGGAGGCCGCGGCGATCCTGGCCACGGTGGACGCCGACGCGACGGG
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Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                          Length 440;
       Gene Function) project."
34 q 59 t 3 others
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21192569
                                                                                                                                              Pred. No. 25;
0; Mismatches 137;
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
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Cordonnier-Pratt, M. -M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE125039 397 bp mRNA linear EST 19-JUL-20 DG1_14_C09.b1_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA sequence.
BE125039 GI:8547726
 Bouneau, L., Fisher, C.,
                                                      using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                Human gene number estimate provided by genome wide analysis
Tetraodon nigroviridis DNA sequence
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fishe
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                  : C0BG037AD04SP1~end
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                                                                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="037G07"
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                                                                                                                                                                                                                                                                           Email: mmpratt@ug.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/db_cref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Corgan: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
174 c 99 g 62 t
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pred. No. 33;
); Mismatches 147;
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High quality sequence stop: 382
POLYA-No.
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Contact: Cordonnier-Pratt MM
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Contact: Cordonnier-Pratt MM
                                                                                                The University of Georgia plant Sciences Building, Frel: 706 542 1860 Fax: 706 542 1805
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                                                          Department of Botany
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Sorghum bicolor
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Tel: 706 542 1860
Fax: 706 542 1805
Fax: 706 542 1805
Famil: muprattenga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 472
POLXA=NO.
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12.2%; Score 49.8; DB 10;
Best Local Similarity 48.4%; Pred. No. 33;
Matches 138; Conservative 0; Mismatches 147;
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Search completed: July 18, 2002, 10:12:53 Job time: 9973 sec

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Streptomyces grise
Streptomyces netro
Streptomyces albus
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                     - protein search, using sw model
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                                                                  The present sequence is S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents,
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                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                   hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                   Length 135;
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                                                                                                                                                                                                                                                Score 701; DB 21;
Pred. No. 3.4e-75;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY44649 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces griseus SsgA protein.
                                           English.
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100.0%;
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                                                                                                                                                                                                                                                                            Conservative
                                          60pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147269/13
                                          Disclosure; Fig 5;
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                          135 AA;
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                                                                                                                                                                                                           Sequence
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The present sequence is S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                              1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD
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                                                                                                                                                                                                                                                                        79.3%; Score 556; DB 21; Length 135; 78.5%; Pred. No. 5.6e-58;
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                                                                                                                                                                                                                                                                                                                 12; Mismatches
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                                                                                                                                                                                                                                                                                                                 106; Conservative
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AAU56775;
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Best Local 9
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                                                                                                                                                                                                                                                                                                   61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                     Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SsgA: liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
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                                                                                                                                                                                       ;
                                                                                                                                                          Length 135;
                                                                                                                                                                                         18; Indels
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                                                                                                                                                          Score 544; DB 21;
Pred. No. 1.5e-56;
                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                       12;
                                                                                                                                                     77.6%;
77.8%;
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-147269/13.
                                                                                                                                                                         Similarity
                                                                                                            135 AA;
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                                                                                                                                                                                       105;
                                                                                                                                                        Query Match
Best Local S
Matches 105
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint, central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                      61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                Gaps
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                                                                                                                                                                                 1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60
                                                                                                                                                                                                    ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                               Length 135;
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                                                                                                                                                Indels
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                                                                                                             68.6%; Score 481; DB 21;
71.1%; Pred. No. 4.5e-49;
ive 14; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang S
Jen S, Carter D;
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02:JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                              Best Local Similarity 71.1
Matches, 96; Conservative
                                                                                                                                                                                                                                                                                                                                               121, DEALDRILAEEQNAG 135
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                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used a diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; protein tyrosine phosphatase; PTPase; vulnerary; cytostatic; antlinflammatory; antidiabetic; viral infection; inflammation; cancer; receptor-type protein tyrosine phosphatase beta; RPTPbeta; carbonic anhydrase; CAH; diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                   72 GEVLIRLOVGSDQAMFRVGTAPLVA---FLDRTDKIVP-----LGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                                      12 RIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPETF 71
                                                                                                                                                                                                                                              Length 400;
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                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                           10.8%; Score 76; DB 2
ilarity 25.2%; Pred. No. 2.2;
Conservative 20; Mismatches
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91US-0654188.
92US-0961235.
93US-0015973.
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Best Local Similarity
Matches 32; Conserv
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15-OCT-1992;
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                                                                                                                                                                                              Sequence
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receptor-type protein typosine in a signature of the protein typosine prospection of glycoprotein. The receptor and its ligands are useful for developing compounds and strategies for modifying cellular processes (e.g. normal cellular processes such as differentiation, metabolism, cell cycle control, wound healing and neuronal function, cellular behaviour such as motility, migration, and contact inhibition, in addition to abnormal or potentially deleterious processes such as virus-receptor interactions, inflammation, cellular transformation to a cancerous state, and the development of Type 2, insulin independent, diabetes mellitus, under the control of the receptor protein tyrosine phosphatases. The receptors of the receptor protein tyrosine phosphatases. The receptors of the receptor molecules for available ligands, thus reducing transmembrane receptor molecules for available ligands, thus reducing to ribibiting ligand binding to endogenous RPTPasses. RPTPasses and/or their ligands, may also be used to screen for additional molecules that can act to modulate the activity of cellular processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is given in a specification relating to a novel
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 6642; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 6642.
                                                                                                                                                                                                                                                                                                                                                                                                          1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 75.5; 28.2%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB59950 standard; Protein; 736 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   259 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yenes from Dr
Interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB59950;
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09-APR-1999; 99US-0128697.
20-JAN-2000; 2000US-0176929.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                    38; Conservative
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                            222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                          Best Local
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                                                           (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
    and
                                                                                                                                                                                                                           272 fttsngsvfriglgngvev-dpeeinvtfedvkgcdeakgelkevvef1kspekfsnlgg 330
                                                                                                                                                                                                                                                                        331 klp-----kgvllvgpp---gtgktllaravageakvpffhaagpe-fdevlvgqgarr 380
                                                                                                                                                                              60; Gaps
                                                                                                                                                                                                                                                  DAPVTWAFGRELLIDGGPRPCGDGDVHIA------PADPETFGEVLIRLQVGS 82
                                                                                                                                                                                                                                                                                              83 DQAMFRV--GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE----EQNAG 135
                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL16176-ABL30511).
                                                                                                                                                       DB 22; Length 736;
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                                                                                                                                                                              53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #16446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                     Score 74; DB 2
Pred. No. 8.6;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID No 16745; 1069pp; English.
                                                                                                                                                                                                     FLVSEELSFRIPVELRYETCDPYAVRLTF-
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                                                                                                                                                       10.6%; 22.9%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                         Query Match
Best Local Similarity 22....
Best Local 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Persing
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                                                                                                                     736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS59569.
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07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                      AAU55550;
                                                                                                                      Sequence
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AAU55550
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the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to down; acres infections. The antibodies may also be used a diagnostic agents for determining P. acnes proteins by acres proteins acres infections. The antibodies may also be used a diagnostic agents for determining P. acnes prosence, for example, by note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidererial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----vqvapadmgsasygdiltrmapgaaliprggvgsyalrrwlaagalavclddv 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 lvddkvsfalpvaanrevld--alrqagipaapdalt---pnevraawgagada---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 RPCGDGDVHIAPAD--PETFGEVLIRLQ------VGSDQAMFRVGTAPLVAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein BLAST search protein SEQ ID NO: 154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 71.5; DB 22; 25.3%; Pred. No. 3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DKIVPLGQERS-----LADFDA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis G;
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The invention relates to the isolation of genes AAC81710-C81758 encoding the human secreted proteins AAB45386-B5434. This sequence represents a fragment of the protein encoded by the gene given in the descriptor inc. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins are susful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclenosis, rheumatoid arthritis and ulcerative colitis; (c) wound halling; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and infectious diseases such as wiral, bacterial, fungal and parasitic infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . 4
New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 PADPETFGEVLIRLQVGS------DQAMFRVGTAPLVAFLDRTDKIVPLGQERSLA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 plgpldfgnvvatldpgaarhltlachydsklfpsgstp---fvgatdsavpcalllela 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71; DB 21; Length 16
Pred. No. 2.6;
7; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological; osteopathic; neuroprotectant
                                                                               Disclosure; Page 513-514; 521pp; English.
                      diagnosing, preventing, treating or amel
used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Persing DH, Mitcham JL,
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32.9%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nfections
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Sequences AA039105-AA068017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by content and acceptance of the treatment, prevention and diagnosis of medical conditions caused by purposes. The disorders include SAPHO syndrome (synovitis, acne, content and solve in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and cherefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contact in the sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fip.wipo.int/pub/published_pct_sequences.
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                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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99US-0155139.
99US-0155486.
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990S-0156458.
990S-0156596.
990S-0157117.
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04-OCT-1999;
05-OCT-1999;
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57 GDG--DVHIAPADPETFG----EVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis; pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae type 4 protein sequence #144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ERSLADFDAL-----LDEALDRIL ...----AEEQNAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 70; DB 30.7%; Pred. No. 6.4; ive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY81644 standard; Protein; 386 AA
990S-0158029
990S-0158232
990S-0158238
990S-0159294
990S-0159294
990S-0159329
990S-0159330
990S-0159330
990S-0159637
990S-0159638
990S-0160740
990S-0160767
990S-0160767
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990S-0160768
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99US-0161993.
99US-0162142.
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99US-0125164.
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99US-0161404.
99US-0161405.
99US-0161406.
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99US-0161360.
99US-0161361.
99US-0161920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 10.0
Best Local Similarity 30.7
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200006737-A2.
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sequences from the Coryneform bacterium Corynebacterium glutuamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, considerable assign amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium, coryneform bacterium coryneform bacterium or are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                      mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotied; lipid; saturated fatty acid; unsaturated fatty acid; diacusobyydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 LIDGGPRPCGDG------DVHIA--PADPETFGEVLIRLQVGSDQAMFRVGTAPLV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 mvtggaggigrgiseklaadgfdiavadlpqqeeqaaetiklieaaggkavf-vg---- 59
                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum SMP protein sequence SEQ ID NO:238.
                                                                                                                                                                Claim 17; SEQ'ID NO: 6436; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 69; DB 22; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 AFLDRTDKIVPLGQERSLADFDALLDEALDRI 127
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99DE-1031413.
99DE-1031419.
99DE-1031420.
99DE-1031424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        European Patent Office.
                    2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AA;
                                   N-PSDB; AAH67901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200100844-A2.
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                           AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antilifiammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and/or antigens. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                     New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 lpgtmiedylvefngkrfeavdggmkpnepvevvirpedlritlpeeg-----klqvkvd 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 QAMFRVGTAPLVAF------LDRTDKIVPLGQERSL-------ADFDAL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C glutamicum protein fragment SEQ ID NO: 6436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.0%; Score 70; DB Best Local Similarity 27.2%; Pred. No. 11; Matches 37; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG92682 standard; Protein; 258 AA.
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                                                                                                                                             Claim 1; Page 87; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizoguchi H, Ando
Senoh A, Ikeda M,
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2000JP-0159162.
2000JP-0280988.
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 Hansbro PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium;
                                  WPI; 2000-195300/17.
Gilbert CFG,
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03-AUG-2000;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Mismatches

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metabolism and oxidative prospectivation (SMP) proteins given in metabolism and oxidative prospectivation (SMP) proteins given in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corprehacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to c. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 479-480; 1246pp; English.
                                                                                                                                                                                                                        99DE-1040765.
99US-0151572.
99DE-1042076.
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99DE-1031634
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99US-0143208
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N-PSDB; AAF71478.
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03-SEP-1999
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Search completed: July 18, 2002, 14:15:03 Job time: 10333 sec

5; 22; Indels 30; Gaps DB 22; Length 258; 9.8%; Score 69; DB 26.1%; Pred. No. 8.5; iive 16; Mismatches Query Match 9.8% Best Local Similarity 26.1% Matches 24; Conservative

48 LIDGGPRPCGDG------DVHIA--PADPETFGEVLIRLQVGSDQAMFRVGTAPLV 95 ò g

96 AFLDRTDKIVPLGQERSLADFDALLDEALDRI 127

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OM protein - protein search, using sw model

July 18, 2002, 14:16:07; Search time 51.31 Seconds (without alignments) 64.265 Million cell updates/sec Run on:

US-09-749-185-7

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

231628 seqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Database :

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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 10, Appl	Sequence 6, Appli	10,	9	9	٦	11,	2, A	4,	4	12,	12,	11	4, Ar	23	11	11,	11,	6, A	9	Sequence 2, Appli	'n	7	122	118,	75,	75,
SUMMAKIES	ID	US-08-015-986A-10	US-08-015-973-6	US-08-446-363-10	US-08-448-164-6	US-08-081-929-6	US-08-309-512-11	PCT-US92-08756A-11	US-09-040-774-2	US-08-701-240-4	US-09-138-236-4	US-09-012-710-12	US-09-556-273-12	US-09-228-986-119	US-08-924-345-4	US-09-056-556-234	US-08-357-598-11	US-09-003-289-11	PCT-US95-16435-11	US-09-036-987A-6	us-09-370-700-6	US-08-777-405A-2	US-08-977-871A-2	US-09-225-951-2	-09	US-09-228-986-118	-08-484	US-08-481-985B-75
	BB :	-	-	7	7	4	-	S	4	~	4	٣	4	4	4	4	7	7	S	4	4	~	~	~	4	4	7	m
	Length DB	259	259	259	259	259	493	493	1241	692	695	837	837	190	158	182	1100	1100	1100	5588	5588	1044	1044	1044	142	153	306	306
æ	Query	10.8	10.8	10.8	10.8	10.8	9.6	9.6	9.5	9.5	9.5	9.5	9.5	9.1	9.0	0.6	0.6	9.0	9.0	0.6	0.6	8.9	8.9	8.9	8.8	8.8	8.8	8.8
	Score	75.5	75.5	75.5	75.5	5.	69	69	66.5	•		64.5	64.5	64	63	63.	63	63	63	63	63	62.5	62.5	62.5	61.5	61.5	61.5	61.5
	Result No.	-	7	m	7	Ŋ	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

7;

Gaps

33;

Length 259; Indels

Query Match 10.8%; Score 75.5; DB 1; Best Local Similarity 28.2%; Pred. No. 0.23; Matches 31; Conservative 13; Mismatches 33;

24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75

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61.5 8.8 306 4 US-08-370-476-75 61.5 8.8 694 2 US-08-370-476-75 61.5 8.8 694 4 US-09-138-256-2 61.5 8.8 1379 3 US-09-138-226-2 61.5 8.8 1379 4 US-09-138-226-2 61.5 8.8 11877 4 US-09-105-537-3 61.5 8.8 11877 4 US-09-105-537-3 61.6 8.7 106 2 US-08-531-13-3 61.8 7 236 1 US-08-56-570-6 61 8.7 236 1 US-08-56-570-6 60 8.7 236 1 US-08-56-570-8 60 8.6 290 3 US-08-449-99-8 60.5 8.6 290 3 US-08-448-96 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-995B-80 60.5 8.6 290 3 US-08-481-99 60.5 8.6	Sequence 75, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 80, Appli Sequence 236, Appli Sequence 236, Appli Sequence 236, Appli		Ga Ga			
61.5 8.8 306 4 61.5 8.8 694 2 61.5 8.8 694 2 61.5 8.8 694 4 61.5 8.8 79 4 61.5 8.8 3739 4 61.5 8.8 3739 4 61.5 8.8 3739 4 61.5 8.8 3739 4 61.5 8.8 3739 4 61.8 7 106 2 61 8.7 106 2 61 8.7 236 1 61 8.7 236 1 60.5 8.6 290 3 60.5 8.6 20.0 9 60.6 8.6 20.0 9 60.6 8.6 9.0 9 60.6 8.6 9 60.6 8.6 9 60.6 8.6 9 60.6 8.6 9 60.6 8.6 9 60.6 8.6 9 60.6 8.6 9 60.6 8	m 0 0 +	C NA EN L	ph EPTOR-TYPE PHOSPHOTYROSINE SE-GAMMA Americas	-bos #1.0, Version #1.2	986	
28 61.5 8.8 8.8 33 61.5 8.8 8.8 61.5 8.8 8.8 8.3 61.5 8.8 8.8 8.3 61.5 8.8 8.8 8.3 61.5 8.8 8.8 61.5 8.8 8.8 61.5 8.8 8.8 61.5 8.8 8.6 61.5 8.8 8.6 61.5 8.8 61.5 8.8 61.5 8.8 61.5 8.8 61.5 8.6 61.5 8.8 61.5 8.8 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 9.6 61.5 8.8 61.5 9.6 9.6 9.6	404644001010106440	tion US/08015	ssinger, Jose N: NOVEL REC N: PHOSPHATA ES: 14 DRESS: Venue of the	k FOR lopp PC c M: ntin	ON DATA: BER: US/08/0 0-FEB-1993 435 FORMATION: S. Leslie MER: 18,872 MER: 18,872 MER: 7 INFORMATION:	-790-9090 69-8864/9741 EDNUE ID NO: 10: RISTICS: ino acids ind single own
28 61.2 29 61.3 31 61.3 33 61.3 34 61.3 34 61.3 35 61.3 36 61.3 37 61.3 38 61.3 38 61.3 38 61.3 39 61.		4-10 Applica 5532123 FORMATION	r: Schle INVENTIO INVENTIO F SEQUENC NDENCE AD SEE: PEN 1155 A	New Yor (: U.S.A 10036 READABLE TYPE: F TYPE: F ER: IBM	APPLICATI ATION NUM DATE: 1 FICATION: AGENT IN MISTOCK, RATION NU NCE/DOCKE	X: 212-8 X: 212-8 X: 66141 P X: FOR SEQ CHARACTE CHARACT CHARACTE CHARACTE CHARACTE CHARACTE CHARACTE CHARACTE CHARACTE
	661 61 61 60 60	RESULT 1 US-08-015-9866 ; Sequence 10, ; Patent No. : ; GENERAL IN A PATENT NO SEPRERAL NO	APPLICANT TITLE OF TOTLE OF NUMBER OF CORRESPON ADDRESS STREET: CITY:	STATE: COUNTRY ZIP: COMPUTER MEDIUM COMPUTE OPERATI	CURRENT APPLICY APPLICY FILING CLASSIN ATTORNEY, NAME: REGISTI REFEREN TELECOMM	TELEPH TELEXI TELEXI INFORMATION SEQUENCE LENGTH: TYPE: STRANDE MOLECULE MOLECULE

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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 7683
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%;
28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.24
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-446-363-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                    New York
: U.S.A.
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                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                       10036
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                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-448-164-6
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                   CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%; Score 75.5; DB 1; Length 259; 28.2%; Pred. No. 0.23; tive 13; Mismatches 33; Indels 3
                                      76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 RDGIAVIGIFLKIGHENGEFQI-----FLDALDKIKTKGKEAPFTKFD 178
                                                                                                                                          Sequence 6, Application US/08015973
Patent No. 5604094
GENERAL INFORMATION:
APPLICANT: SCHIESSINGET, JOSEPH
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF SEQUENCES: 9
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASE-GAMMA NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Nata:
APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
FILLING DATE: 10-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 7683-021
TELCOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-8864/9741
TELEEX: (6141 PENTE
TELEX: 6614 PENTE
TELEX: 6514 PENTE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08446363; Patent No. 5891700; GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 28.29
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-015-973-6
                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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                                                                                                           RESULT 2
US-08-015-973-6
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86 PYRLR-OFHL-----HWGSSDDHGSEHTVDGVKYA---AELHLVHWNPKYNTFKEALKQ 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08448164
Patent No. 592536
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Indels
                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/446,363 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
.SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,164
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 75.5; DB 2;
; Pred. No. 0.23;
13; Mismatches 33;
                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,986
FILING DATE: 10-FEB-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: PENNIE & EDMONDS
1155 Avenue of the Americas
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Gaps

33;

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24' PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                            10.8%; Score 75.5; DB 4; Length 259; 28.2%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                       76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Gelfand, David H.
APPLICANT: Calhoon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,512
                                                                                                                                                                                      33;
                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILLING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BOTTNEY, SCOTE R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08309512 Patent No. 5759828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENT INCOME. Bortner, Scott R. Scott R. WINNER: 34,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds STREET: 2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECISTRATION NUMBER: 34,291
REFERENCE/DOCKET NUMBER: 8
TELECHONE: (415) 854-360
TELEFAX: (415) 854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 Best Local Similarity 28.2
Matches; 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                     SS: single
unknown
                                        TOPOLOGY: unknown;
MOLECULE TYPE: protein
US-08-081-929-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
      amino acid
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APPLICANT: Tal, R
                         STRANDEDNESS:
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US-08-309-512-11
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                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 RDGIAVIGIFLKIGHENGEFQI-----FLDALDKIKTKGKEAPFTKFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlessinger, Joseph
APPLICANT: Barnea, Gilad
APPLICANT: Grumet, Martin H.
APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: A NEW CLASS OF RPTPASSS: THEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%; Score 75.5; 28.2%; Pred. No. 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7683-041-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                              NAME: Misrock, S. Leslie
RECISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1993
23-JUN-1993
23-JUN-1993
                       US 08/015,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08081929
Patent No. 6160090
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COTUZZİ, LAUTA A. REGIGSTRATION NUMBER: 30742 REFERENCE/DOCKET WUMBER: 76 TELECOMMUNICATION INFORMATION: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212 866-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                       APPLICATION NUMBER: US 06
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-448-164-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-081-929-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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GENERAL INFORMATION:
APPLICANT: Wong, Albert J.
APPLICANT: Wong, Albert J.
APPLICANT: Wong, Albert J.
APPLICANT: Wong, Albert J.
TITLE OF INVENTION: GAB1, A GRB2 BINDING PROTEIN, AND
TITLE OF INVENTION: COMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NDIHGHHAGDEVLKVIGQRLIEL- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 VTWAFGRELLIDGGPRPCGDGDVHIAP----ADPETFGEVLIRLQVGSDQAMFRVGTAP 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1241;
                                            80. VGSDQAMFRVGTAPLVAFLDRTDKIVP----LGQERSLADFDALLDEALDRI 127
                                                                 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                   E: McDonnell Boehnen Hulbert & Berghoff
300 S. Wacker Drive, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TY99940SON, Karl
APPLICANT: Kestila, Marjo
APPLICANT: Lenkkeri, Ulla
APPLICANT: Mannikko, Minna
TITLE OF INVENTION: Nephrin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESSONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Bergho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66.5;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 LVAFLDRTDKIVPLGQERSLADFDALLDEA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/CDCKET NUMBER: 97,8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
                                                                                                                                                             US-09-040-774-2; Sequence 2, Application US/09040774; Patent No. 6207811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1241 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (312)913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.6%
Matches 23; Conservative
      173 EPQAL-VMFDLDGFKPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-040-774-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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STREET: 30c.
-mv: Chicago
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COUNTRY:
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                                                                                                                 23 DPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE---TFGEVLIRLQ 79
                                                                                        23 DPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE---TFGEVLIRLQ 79
                                                                                                                                                                                               80 VGSDQAMFRVGTAPLVAFLDRTDKIVP----LGQERSLADFDALLDEALDRI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.8%; Score 69; DB 5; Length 493; Best Local Similarity 27.7%; Pred. No. 3.5; Matches 31; Conservative 16; Mismatches 37; Indels
        9.8%; Score 69; DB 1; Length 493; 27.7%; Pred. No. 3.5;
                                                  37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BOTTOR, SCOLT R.
REGISTRATION NUMBER: 34,298
REGISTRATION NUMBER: 34,298
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                16; Mismatches
                                                                                                                                                                                                                                                                                                          Sequence 11, Application PC/TUS9208756A
GENERAL INFORMATION:
APPLICANT: Tal, Ronny
APPLICANT: Gelfand, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Calhon, Roger D.
APPLICANT: Calhon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08756A
FILLING DATE: 19921014
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/800,218
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, SOFTWARE: Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Limbach and Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), ORGANISM: Acetobacter xylinum PCT-US92-08756A-11
                                                                                                                                  173 EPQAL-VMFDLDGFKPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 493 amino acids
AMINO ACID
                                                    31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111
COMPUTER READABLE FORM:
                             Best_Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            RESULT 7
PCT-US92-08756A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C. COUNTRY:
          Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
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STATE: New Jersey
COUNTRY: USA
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        999 ÖÖGAAAA 099
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                         FILING DATE:
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Sequence 4, Application US/09138236

Sequence 4, Application US/09138236

Sequence 4, Application Sequence 4, Application US/09138236

Sequence 4, Application Sequence 4, Sequence 4, Sequence 4, Sequence 5, Sequence 6, Sequence 6, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9, Sequence 9
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                                                 Woodcock Washburn Kurtz Mackiewicz & No. 5912160ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 695;
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 64.5; 21.3%; Pred. No. 19
                                                                                            STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TJU-2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,641
FILING DATE: US 60/002,641
CLASSIFICATION:
AFTONEY/AGGIV INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TJI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       695 amino acids
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Best Local Similarity 21.38
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215-568-3439
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19103
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                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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Patent No. 6087478

GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Ruriyan, John
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 64.5; DB 4; Length 69
21.3%; Pred. No. 19;
Live 23; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                  PatentIn Release #1.0, Version #1.30
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STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/09/012,710
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MAIK
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: TJU-?
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 amino acids
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Best Local Similarity 21.38
Warches 27; Conservative
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APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-138-236-4
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SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                                                       MOLECULE TYPE:
HYPOTHETICAL: 1
US-09-556-273-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-228-986-119
                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 119
LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-924-345-4
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                        59 ----GDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAP----LVAFLDRTDKIV---- 105
                                                                                                                                                                                                                                                                                                                                                                                                             7 EELSFRIPV-ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLID---GGPRPCGD---- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-TERMINAL DOMAIN OF A METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                9.2%; Score 64.5; DB 3; Length 837;
25.3%; Pred. No. 25;
tive 17; Mismatches 59; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 PLGOE-----RSLADFDALLDEAL-----DRILAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
   REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                            LENGTH: 837 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 25.3%
Matches 41; Conservative
                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                             TYPE: amino a STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New COUNTRY: US. ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-556-273-12
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 PRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLD---RTDKIVPLGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 ----GDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAP----LVAFLDRTDKIV---- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 EELKFTTPLGRLHHRVRETRLLRESLHL---GPKTGQVSLONLIDPPLNGPGPSEDLPTI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 PSPCGSEDVHVLAVDDSLVDRKVI------BHLLKISSCKVTA-VDSGIRALQFLGLDE 83
                                                                                                                                                                                                                                                                                                                                                                    7 · EELSFRIPV - ELRY ETCDPY AVRLIFHLPGDAPVTWAFGRELLID - · · · GGPRPCGD - · · · 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                            Indels 45;
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APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree
APPLICANT: AUDONNET Jean-Christophe, Francis
APPLICANT: RIVIERE Michel, Emile, Albert
TITLE OF INVENTION: Mutants and vaccines of the Infectious
TITLE OF INVENTION: Bovine Rhinotracheitis virus
                                                                                                                                                                                                                                                          Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.1%; Score 64; DB 4; Length 190;
Best Local Similarity 23.5%; Pred. No. 3.9;
Matches 19; Conservative 18; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 QLHQEIGAASGELEPKTRASLISRLDEVLRTLVTSSFLVEKQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106' PLGQE-----RSLADFDALLDEAL-----DRILAEEQ 132
                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                       9.2%; Score 64.5; D: 25.3%; Pred. No. 25; tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 119, Application US/09228986
Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/08924345; Patent No. 6224878; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110. ERSLADFDALLDEALDRILAE 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Eucalyptus grandis
US-09-228-986-119
LENGTH: 837 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          Best Local Similarity 25.3%
Matches 41; Conservative
                                                                                                    . protein
NO
                                                                                        linear
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47 PHRGRADQHLGLDARLCAAACNVLLVDGVQHRPQRHGPGPRFGFPRVVVACG---IRQAR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PYAVRLTFHLPGDAPVTWAFGRELLIDG------GPRP------CGDGDVHIAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVP----LGQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.0%; Score 63; DB 4; Length 182; Best Local Similarity 30.3%; Pred. No. 4.9; Matches 33; Conservative 7; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 VEVERFGGVLPERAHGVGORNNRVAT-----DRLTDRMPIDRGLGRE 145
                  NAME: Maki, David J.
REGISTRATION NUMBER: 210121.457
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 234:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: July 18, 2002, 14:16:08
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: protein US-09-056-556-234
                                                                                                                                                                                                                                                                                                    linear
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Patent No. 6350456

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                OPERATING SYSTEM: CONTROL OF SOFTWARD SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO) SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO) GURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/924,345 CLASSIFICATION 424 PRIOR PAPLICATION DATA: PLING DATE: 09-AUG-1994 APPLICATION NUMBER: FR 92 07930 FILING DATE: 26-JUN-1992 APPLICATION NUMBER: FR 92 O7930 FILING DATE: 26-JUN-1992 APTONNEY-AGENT INFORMATION: NAME: SARRO, THOMAS P. REGISTRATION NUMBER: 19396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 4; Length 158;
Pred. No. 4.1;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APPL
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LARSON AND TAYLOR
STREET: 727 SOUTH TWENTY-THIRD STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GGYVPVPAADADCYYSESDSETAGEFLIRM 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 GG--PRPCGDGDVHIAPADPETFGEVLIRL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               STATE: VIRGINIA
COUNTY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: XI
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) 920-7200
TELEFA: (703) 892-8428
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.0°
Best Local Similarity 46.7°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-924-345-4
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98104-7092
                                                                                             CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 0
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-09-056-556-234
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein July 18, 2002, 14:17:35; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec .. 0

US-09-749-185-7 Perfect score:

701 1 MSFLVSEELSFRIPVELRYE......FDALLDEALDRILAEEQNAG 135 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			probable requiator			probable regulator		hypothetical prote	carbonate dehydrat	probable transcrip		cytochrome c-type	carbonate dehydrat	MHC class I RT1.C-	purine-binding che	probable peroxidas	mixed-lineage prot	hypothetical prote	carbonate dehydrat	peptidylprolyj iso	deoxyribonuclease	probable secreted	choline monooxygen	probable peroxin-6	probable basal-bod	penicillin-binding	penicillin binding	hypothetical prote	probable alcohol d	conserved hypothet	medium-chain acyl-
		ΙD	73.	T36147	T35247	T35319	A53121	H70678	A43641	T29420	S71090	D83460	CRHU3	169009	B82380	T09164	S68178	T16511	A22612	S55383	JC1483	T44873	T08550	T37816	AD0089	G97472	AC2691	G87687	н69789	0	н84176
		DB	7	7	7	7	7	7	7	7	~	7	-	7	~	7	Н	7	7		7				7	~	7	7	-	~	7
		Match Length DB	136	142	138	142	1025	291	260	892	980	407	260	343	175	323	954	1387	259	559	230	387	426	948	218	757	757	966	346	289	9
æ	Query	Match	84.0	30.7	24.0	18.7	12.0	11.6	11.2	11.2	11.1	11.1	10.8	10.7	10.6	10.6	10.6	10.6			10.3			10.3	10.3	10.2	10.2	10.2	10.1	10.1	10.1
		Score	589	215	168	131	84	81.5	78.5	78.5	78	77.5	75.5	75	74	74	74	74	73.5	73	72.5	72.5	72.5	72.5	72	71.5	71.5	71.5	71	70.5	70.5
	Result	No.	-	7	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote	late expression fa molybdenum cofacto	conserved hypother naringenin-chalcon peroxisomal assemb	quinone oxidoreduc hypothetical prote	hypothetical prote hypothetical prote	DnaA-related prote probable ATPase -	hypothetical prote probable sensor/re	nodulation control
F95161 E98027	T10360 G84292	SYZMCC A48667	G83766 E89958	T05873 E70980	C87461 S42826	T01461 H83132	A39017
77	0 0 0	7 2	2 2	7 7	77	7 7	Н
385 385	163	400 1165	322	398 143	230 662	859 1417	237
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70 70	. 69.5	2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	69	69	68.5	68.5 68.5	89
30	333	3 3 4	37	39,:	41.42	4 4 4	45

ALIGNMENTS

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probable regulator - Streptomyces coelicolor (Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor (Species: O3-Dec-1999) #sequence_revision O3-Dec-1999 #text_change O3-Dec-1999 (Species: O3-Dec-1999) (Species: O3-Dec-1999) (Species: O3-Dec-1999) (Species: O3-Dec-1999) (Species: O4-Dec-1999) (Species:

ö Gaps ; Length 136; Indels 13; Score 589; DB 2; Pred. No. 5.1e-52; 7; Mismatches Query Match 84.0%; Best Local Similarity 85.2%; Matches 115; Conservative

61 1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60 2 MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGD g 61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120 δy g

121 DEALDRILAEEQNAG 135 δy

g

probable regulator - Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.5pecies: Orabec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 (5.5cession: T36147)

R.Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, July 1999 A.Reference number: 221598 A.Reference number: 221598 A.Reference number: 221598 A.Reference number: 22159 A.Residues: T36147 A.Molecule type: DNA A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE> A.Residues: 1-142 <SEE>

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12.0%;
27.8%;
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Best, Local Similarity 27.8%
Matches 25; Conservative
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    C; Genetics
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R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-138 <OLI>
A; Cross-references: EMBL:AL049587; PIDN:CAB40672.1; GSPDB:GN00070; SCOEDB:SC5F2A.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-142 - COLI>
A.Residues: 1-142 - COLI>
A.Residues: BMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
A.Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, May 1999
A;Reference number: 221575
A;Accession: T35319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T35319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                          48 LIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIAGMQEPNGHGDVRVR---PYAYDRTVLEFHAPEGTAVIHVRSGELRRFLQAAGELVPV 117
                                                                                                                                   Gaps
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFLVSEELSFR-----IPVELRYETCDPYAVRLTFHLPG---DAPVTWAFGREL 47
                                                                                                                                 ;
0
A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: SCOEDB:SC5F2A.05c
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                        Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 138;
                                                                                                                                 Indels
                                                                                                                                 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                 Query Match 30.7%; Score 215; DB 2; Best Local Similarity 38.1%; Pred. No. 2.1e-14; Matches 48; Conservative 18; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.0%; Score 168; DB 2; allarity 31.4%; Pred. No. 1.1e-09; Conservative 17; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable regulator - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 GQERSLADFDALLDEAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 GLEHLQLDLDHDLAELM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z21573
A; Accession: T35247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                     121 DEALDR 126
                                                                                                                                                                                                                                                                                                                                                                                                137 AELLAR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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peroxisome assembly protein PAY4 - yeast (Yarrowia lipolytica)
C;Species: Yarrowia lipolytica, Candida lipolytica
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 02-Feb-2001
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 02-Feb-2001
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 02-Feb-2001
C;Date: 02-Jun-1995 #sequence_revision 03-Jun-1995 #text_change 02-Feb-2001
R;Nuttley, W.M.; Brade, A.M.; Eitzen, G.A.; Veenhuis, M.; Aitchison, J.D.; Szilard, R
J; Biol. Chem. 269, 585-586, 1994
A;Title: PAY4, a gene required for peroxisome assembly in the yeast Yarrowia lipolyti
A;Reference number: A53121; MUID:94103271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , D.; Golucian, N.; Holroyd,
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go;
R;Cole, S.T.; Brosch, R.; Davlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:99295997
A;Accession: H70678
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 MWDELRIEL-LGDGRADGERHRAVVFVWAAAVEAFLRETHAVVRPGRE-----EVRVDD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 TFGEVLIRLQVGS-----DQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALLDE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 PCGDGDVHIAPADPETF-----GEVLIRLQVGSDQAMFR-----VGTAPLVAFLDR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761 PPGTGKTLLAKAIATTFSLNFFSVKGPELLNMYIGESEANVRRVFQKARDAKPCVVFFDE 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <VATP>
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      12 RIPV--ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                           16;
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A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                       Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 84; DB 2; Length 1025;
; Pred. No. 3.2;
12; Mismatches 37; Indels
                                                                                                                                                                   Query Match 18.7%; Score 131; DB 2; Length 14 Best Local Similarity 30.5%; Pred. No. 5.8e-06; Matches: 39; Conservative 20; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: A53121
A, Status: preliminary
A, Molecule type: DNA
A, Reconstructions (NUT)
A, Cross-references: GB.L23858; NID:q393290; PID:q393291
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101"TDKIVPLGQERSLADFDALLDEALDRILAE 130
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Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
                  Cyaccesion: T29420
Ryparkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A; Reference number: 220619
A; Accession: T29420
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-892 < PAR>
A; Cross-references: EMBL:AL031155; PIDN:CAA20065.1
C; Genefics:
A; Note: SC3A7.02c
C; Superfamily: regulatory protein malT
                                                                                                                                                                                                                                                                                                                                                                                     33; Conservative
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Query Match
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                                              GB:AL123456; NID:g3261662; PIDN:CAB03770.1; PID:g1666159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: 11-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 22-Jun-1999
C.Species: A.Still A4400
Biochem. Genet. 27, 17-30, 1989
A.Filte: Mouse carbonic anhydrase III: nucleotide sequence and expression studies.
A.Reference number: A43641; MUID:89227981
                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                            PYRLR-QFHL-----HWGSSDDHGSEHTVDGVKYA---AELHLVHWNPRYNTFGEALKQ 136
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                    24 TGYLPDTATATAVFLADRLGKPLLVEG---PAGVGKTELARAVAQATGSGLVRLQCYEGV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADP--ETFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:9309127
as Leu
                                                                                                                                                                                                                                                                                             30 TFHLPGDAPVTWAF----GRELLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQV--GS
                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: carbonate dehydratase; carbonic anhydrase homology Keywords: carbon-oxygen lyase; hydro-lyase; zinc 5-259/Domain: carbonic anhydrase homology <CAH>
                                                                                                                                                                                                       Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-260 < TWE>
A; Cross-references: 0B:M27796; NID:g192331; PIDN:AAA37355.1; 1
A; Note: the authors translated the codon TAC for residue 114 & Stanton, L.W.; Ponte, P.A.; Coleman, R.T.; Snyder, M.A.
Mol. Endocrinol. 5, 860-866, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 79-85,'G',87-93,'X',95-96 <STA>
A;Note: sequence extracted from NCBI backbone (NCBIP:57846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Expression of CA III in rodent models of obesity. A;Reference number: A45400; MUID:92017893 A;Accession: A45400
                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                       DB 2;
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; Pred. No. 2.3;
13; Mismatches
                                                                                                                                                                                                     Score 81.5; DI
Pred. No. 1.3;
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - mouse
                                                                                                                                    Superfamily: hypothetical protein MTH1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbonate dehydratase (EC 4.2.1.1) III
                                                                                                                                                                                                                                                 14;
                A, Residues: 1-291 <COL>
A, Cross-references: GB:281451; GB:AI
A, Experimental source: strain H37Rv
C, Genetics: RV2426C
C, Superfamily: hypothetical protein
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28.2%;
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ilarity 27.4%;
Conservative 14
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Best Local Similarity 28.2%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 SLAD--FDALLDEAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 DKADIEIEGLLLEVL 155
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 37; Conserv
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C: Species: Homo sapiens (man)
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C: Species: Homo sapiens (man)
C: Species: Homo sapiens (man)
C: Species: Homo sapiens (man)
C: Species: Homo sapiens (man)
C: Saccession: S71090
R: Yahraus, T.; Braverman, N.; Dodt, G.; Kalish, J.E.; Morrell, J.C.; Moser, H.W.; Val
EMBO J. 15, 2314-2923, 1996
A; Title: The peroxisome biogenesis disorder group 4 gene, PXAA1, encodes a cytoplasm
A; Reference number: S71090; MUD: 96272151
A; Accession: S71090
A; Stefus: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Corsos-references: EMBL: U56602; NID: 91354752; PIDN: AAC50655.1; PID: 91354753
C; Superfamily: FteH/SEC18/CDC48-type ATP-binding domain homology
C; Keywords: ATP; nucleotide-binding motif A (P-loop)
F; 719-928/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>
F; 744-751/Region: nucleotide-binding motif A (P-loop)
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83460
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yann, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lature, 406, 959-964, 2000
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                                                                                                                                                                                                              720 TIQLPLEHPELLSLGLRRSGLLLHGPP---GTGKTLLAKAVATECSLTFLSVKGPELINM 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 TFHLPGDAPVTWAFGRE----LLIDGGPRPCGDGDVHIAPADPE----TF----GEVLIRL 78
                                                                                                                                                       12 RIPVE-LRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCG--DGDVHIAPADP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79. QVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 980;
12;
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11.2%; Score 78.5; DB 2; 34.4%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                              69 ETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                             |: |: | | | :: | | | | :: | SGVGQRLL----ASLAAELNALDSPVVLVLDEYDRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 11.1%; Score 78; Best Local Similarity 28.8%; Pred. No. Matches 34; Conservative 14; Mismatch
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275 LGKEQSYTCLVEHEGLPEPLTQR 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC class I RT1.C-type protein - rat
                                                                                                                                                                                                                                 ch 10.8%;
il Similarity 28.2%;
31; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.79
Best Local Similarity 24.55
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 DMELVETRPAGDG----
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-175 <HEI>
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B82380
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A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathd A;Reference number: A82950; MUID:20437337
A;Accession: D83460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <STO>
A;Cross references: GB:AE004577; GB:AE004091; NID:g9947430; PIDN:AAG04872.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: cycH; PA1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wade, R.; Gunning, P.; Eddy, R.; Shows, T.; Kedes, L. Proc. Natl. Acad. Sci. U.S.A. 83, 9571-9575, 1986
A;Title: Nucleotide sequence, tissue-specific expression, and chromosome location of hum CAII genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-260 cWADD.
A:Residues: 1-260 cWADD.
A:Cross-references: GB:M29458; GB:M22658; NID:g179787; PIDN:AAA52293.1; PID:g179789
A:Cross-references: CB:M29458; GB:M25658; NID:g179787; PIDN:AAA52293.1; PID:g179789
B:Lloyd, J: Brownson, C.; Tweedle, S.; Charlton, J.; Edwards, Y.H.
Genes Dev. 1, 594-602, 1987
A:Title: Human muscle carbonic anhydrase: gene structure and DNA methylation patterns in A:Reference number: A26690; MUID:88056301
A:Reference number: A26690
A:Status: not compared with conceptual translation
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A;Introns: 12/1; 78/1; 117/3; 148/3; 169/3; 221/3
C;Function:
A;Description: catalyzes the reversible dissociation of carbonic acid to carbon dioxide A;Note: this form is predominantly expressed in slow-twitch, aerobic, type I muscle fibe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ē
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A; Residues: 1.15;74-81;113-121;144-152;165-173;217-225 <LL2>
A; Coss-references: GB:M27974
A; Cross-references: GB:M27974
A; Note: the complete sequence is not given
B; Lloyd, J; MMM1lan, S.; Hopkinson, D.; Edwards, Y.H.
Gene 41, 233-239, 1986
A; Title: Nucleotide sequence and derived amino acid sequence of a cDNA encoding human rA; Reference number: A25850; MUD:86221704
A; Reference number: A25850; MUD:86221704
A; Residues: 1-30, 1', 32-260 <LLO>
A; Molecule type: mRNA
A; Residues: 1-30, 1', 32-260 <LLO>
A; Note: allelic variant sequence with 31-11e; parts of this sequence were determined by C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c;Date: U5-Feb-1988 #sequence_revision 05-May-1995 #text_change 18-Jun-1999
C;Accession: A26658; A26690; A25850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFGEVL------IRLOVGSDQAMF----RVGTAPLVAFLDRTDKIVPLGQERSLADF 116
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ELRYETCDPYAVRLTFHLPGDAPVTWAF-----GRELLIDGGPRPCGDGDVHIAPADPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N:Alternate names: carbonic anhydrase III; muscle carbonic anhydrase C:Species: Homo sapiens (man)
C:Date: 05-Feb-1988 #sequence_revision 05-May-1995 #text_change 18-Ju
                                                                                                                                                                                                                                                                                                                                                                Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                             2;
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16; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Score 77.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbonate dehydratase (EC 4.2.1.1) III - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:119740; OMIM:114750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A26658; MUID:87092290
A; Accession: A26658
                                                                                                                                                                                                                                                                                                                                                                11.18;
27.08;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.08
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 DALLDE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 DAMMPQ 351
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C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; metalloprotein;
F;2-250/Product: carbonate dehydratase III #status predicted <MAT>
F;5-259/Domain: carbonic anhydrase homology <CAH>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;94,96,119/Binding site: zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT1.Eu and RT1.Aw31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Cispecies: Rattus norvegicus (Norway rat)
Cispacesion: 169009
Risalgar, S.K.; Kunz, H.W.; Gill, T.J.
Immunogenetics 42, 244-253, 1995
A;Title: Nucleotide sequence and structural analysis of the rat RT1.Eu and R A; Reference number: 154554; MUID:95402978
A; Accession: 169009
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-343 <RES>
A; Residues: 1-343 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 D---GGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVP 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87. PYRLR-QFHL-----HWGSSDDHGSEHTVDGVKYA---AELHLVHWNPKYNTFKEALKQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24. PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 4.5; 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 75.5;
Pred. No. 4.
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Query Match
Best Local Similarity
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A;Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; PIDN:AAE96986.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
C; Date: 28-Oct-1996 #sequence, G; Nicholl, J.K.; Sutherland, G.R.; Simps Eur. J. Blochem. 234, 492-500, 1995
A; Title: Complete nucleotide sequence, expression, and chromosomal localisation of human
                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable peroxidase (EC 1.11.1.7) (clone PC44) - spinach
C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| :| || |:
-----:GESMVVPFL---SGILN 149
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                                                                                                                                                                                                                                            47 LLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                        Gaps
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S. Superfamily: peroxidase
C; Superfamily: peroxidase
C; Superfamily: peroxidase
C; Superfamily: peroxidase
C; Superfamily: peroxidase
F; 37-118/Disulfide bonds: #status predicted
F; 64/Active site: Arg #status predicted
F; 68.196/Esinding site: heme iron (His) (axial ligands) #status predicted
F; 70-75/Disulfide bonds: #status predicted
F; 124-319/Disulfide bonds: #status predicted
F; 203-228/Disulfide bonds: #status predicted
                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                           Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 323;
                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mixed-lineage protein kinase 2 (EC 2.7.1.-) - human
                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, January 1997
A;Reference number: 216599
A;Accession: T09164
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 74; DB; Pred. No. 8.3; 12; Mismatches
                                                                                                                                                           Score 74;
                                                                                                                                                                               Pred. No.
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                                                                                                                                                                                                                                                                                                                                                        115 LVVDSVSDVIGQGDMPLHPA------
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                                                                                                                                                                                                    10;
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24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Residues: 1-323 <SIM>
A:Cross-references: EMBL:Y10465
A:Experimental source: subspecie
C;Genetics:
                                                                                                                                                                                                    28; Conservative
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R; Simon, P.
                                                                   A; Gene: VCA1094
A; Map position:
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Best Local
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A; Accession: 138044
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-461, 'A', 'V', 465-470, 'S', 472-806, 'R', 808-817, 'A', 819-954 <RES>
A; Residues: 1-461, 'A', 'V', 465-470, 'S', 472-806, 'R', 808-817, 'A', 819-954 <RES>
A; Cross-references: EMBL: 248615; NID: 9758592; PIDN: CAA88531.1; PID: 9758593
R; Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur. J. Biochem. 213, 701-710, 1993
A; Title: identification of a new family of human epithelial protein kinases containin A; Reference number: $32467; MUID: 93238756
A;Reference number: $68178; MUID:96128179
A;Accession: $68178
A;Accession: $68178
A;Accession: $68178
A;Accession: $68178
A;Accession: $68178
A;Cross-references: EMBL:X90846; NID:g971419; PIDN:CAA62351.1; PID:g971420
B;Katch, M.; Hirai, M.; Sugimura, T.; Terada, M.
Oncogene 10, 1477-1451, 1995
A;Title: Cloning and characterization of MST, a novel (putative) serine/threonine kin
A;Reference number: 138044; MUID:95249256
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C,Superfamily: mixed'lineage protein kinase 2; protein kinase homology; SH3 homology
C,Superfamily: mixed'lineage protein kinase 2; protein kinase homology; SH3 homology
C,Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
F;23-76/Domain: SH3 homology <SH3>
F;96-364/Domain: protein kinase homology <KIN>
F;104-112/Region: protein kinase ATP-binding motif
F;384-405/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:419-440/Region: leucine zipper motif
F:449-463/Region: basic
F:125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:362654; GDB:624810; OMIM:600137
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31.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 244-464,'AQAAGRRQPHQPALWL' <DO2>
C;Genetics:
A;Gene: GDB:MLK2; GDB:MST
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Job time: 9547 sec
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July 18, 2002, 14:31:54; Search time 45.63 Seconds (without alignments) 114.555 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-749-185-7 701 1 MSFLVSEELSFRIPVELRYE......FDALLDEALDRILAEEQNAG 135 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Poeu 1 t		ا ما مو			SUMMARIES		
NO.	Score	Match	Length	DB	ΔΙ	Description	
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~	78.5	11.2	259	Н	CAH3_MOUSE	mus	musculu
m	78	ä	978	٦	PEX6_RAT	P54777 rattus	us norv
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9	δ.	ö	259	Н	CAH3_HUMAN	P07451 homo	sapien
7	74	10.6	256	Н	GLO2_RHOCA		
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σ	73.5	Ö.	259	-	CAH3_HORSE	_	s cabal
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13	72.5		230	Н	DRNE_AERHY		aeromonas h
12	ċ	。	948	-	PEX6_SCHPO		schizosacch
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14	70	10.0	419	Н	IRF3_MOUSE		mus musculu
15	7	٠	457	٦	LEF4_NPVOP	_	orgyia pseu
16	6	9.9	400	г	CHS2_MAIZE	zea	mays (m
17	68.5		143	7	YW84_MYCTU	myc	mycobacteri
18	ω.	٠.	662	П	YME1_SCHMA		schistosoma
19	68	9.7	237	7	NOLA_BRAJA		bradyrhizob
20	68	9.7	318	П	BCHC_RHOSH		rhodobacter
21	99		413	П	FTZ2_PYRAB	Q9uz61 pyro	pyrococcus
22	68	9.7	549	Н	SRYA_DROPS	-	drosophila
23	9	•	607	7	YJKO_YEAST		saccharomyc
24	67.5	•	291	7	ISPE_TREPA		treponema p
25	7		382	7	DXR_BACHD	6	bacillus ha
56	7	•	1159	٦	DP3A_VIBCH		vibrio chol
27	67		414	-	FTZ2_PYRHO		pyrococcus
28	67	•	450	-	HEMN_BRAJA	-	bradyrhizob
29	67	•	484	-	HXK1_SCHPO		schizosacch
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	ALIGNMENTS					
P11654 rattus norv	GP21_RAT	, 	1886	9.5	. 64.5	45.
	STA6_MOUSE	1	837	9.2	. 64.5	44
	TRI1_STRCO	7	1067	6.6	65	43
026944 methanobact	Y856_METTH	Н	454	9.3	65	42
P40373 schizosacch	HIS1_SCHPO	Н	310	9.3	65	41
P38932 saccharomyc	VP45_YEAST		577	9.3	65.5	40
P22541 butyrivibri	GUNA_BUTFI	Н	429	9.3	. 65.5	39
P32860 saccharomyc	YKE0_YEAST	-	256	9.3	65.5	38
Q44064 aeromonas h	DRNF_AERHY	1	237	9.3	65.5	37
O35904 mus musculu	P11D_MOUSE	т	1043	4.6	99	36
P94188 alcaligenes	MERA_ALCSP	1	559	9.4	99	35
P31800 bos taurus	UCR1_BOVIN	1	480	9.4	99	34

1D PETÉ_TABLI STANDARD; PRT; 1025 AA. P10 101N-1994 (Rel. 29, Created) DT 01-10N-1994 (Rel. 29, Created) DT 01-10N-1994 (Rel. 29, Last sequence update) DT 01-10N-1994 (Rel. 26, Last sequence update) DT 01-10N-1994 (Rel. 27, Last sequence update) DT 01-10N-1994 (Rel. 27, Last sequence update) DT 01-10N-1994 (Rel. 27, Last sequence update) DT 01-10N-1994 (Rel. 27, Last sequence update) DT 01-10N-1994 (Rel. 27, Last sequence update) DT 01-10N-1994 (Rel. 27, Last sequence update) DE Peroxisome bloomy cape and sequence update) DE Peroxisome bloomy cape and sequence update) DE Peroxisome bloomy cape and and and and and and and and and and	RESULT PEX6_Y	RESULT 1 PEX6_YARLI						
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PERCAKISONE biosynthesis protein PAV4 (Peroxin-6). PEXG OR PAV4. Yarrowia lipolytica (Candida lipolytica). Sucharowycetales, Dipodascaceae; Yarrowia. Sucharowycetales, Dipodascaceae; Yarrowia. NUBL_TAXID-4922; (1) SEQUENCE FROM N.A. MEDIINB-9410371; PubMed-8276851; Nuttley W.M., Brade A.M., Eitzen G.A., Veenhuis M., FAV4, a gene required for peroxisome assembly in the yeast Yarrowia lipolytica. encodes a novel member of a family of putative ArPases."; PAV4, a gene required for peroxisome assembly in the yeast Yarrowia lipolytica. encodes a novel member of a family of putative ArPases."; FAVATION: INVOLVED IN PEROXISOME BIOSYNTHESIS.	DŢ	01-NOV-1997 ((Rel. 35, Last	annotatic	on update			
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Sacchanounycettales; Dipodascaceae; Yarrowia. NUBL_TaxID=4952; SEQUENCE FROM N.A. MEDLINE-94103271; PubMed-8276851; NUBLITE W.M., Earde A.M., Elzen G.A., Veenhulis M., Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Szliard R.K., Glover J.R., Rachubinski R.A.; Inpolytica, encodes a novel member of a family of putative ArPases."; I. BOLO, Chem. 269:556-566(1994). I. SUBCELLUAR LOCATION: Cytoplasmic (Probable). Instruction: INVOLVED IN PEROXISONE BLOSKYTHESIS. Instruction: INVOLVED IN PEROXISONE BLOSKYTHESIS. Instruction: Interprofit institute of Bioinformatics and the EMBL outstatton between the Swiss Institution Sas long as its content is in no modified and this statement is not removed. Usage by and for commercentifies requires a license agreement (See http://www.isb-sb.ch/announ or send an email to license@isb-sib.ch). EMBL: LOSSES; AAALSSSS, AAA_Subfam. EMBL: LOSSES; AAALSSSS, AAA_Subfam. PROSTIE: PROMOSTS, AAA. 1. PROSTIE: PROSTIE: PROMOSTS, AAA	ပ္ပ	Eukaryota; Fu	ıngi, Ascomyco	ta; Sacchi	romycoti	na; Saccharo	mycetes;	
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SEQUENCE FROM N.A. MUSLINE-94103271; PubMed-8276851; Nuttley W.M., Brade A.M., Silzen G.A., Veenhuis M., Altchison J.D., Sailard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Sailard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Sailard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Sailard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Sailard R.K., Glover J.R., Rachubinski R.A.; Altchison J.D., Sailard R.K., Glover J.R., Rachubinski R.A.; Inpolytica, encodes a novel member of a family of putative Arpases."; J. Biol. Chem. 209:556-566(1994). I.: SUBCELUIAR LOCATION: Cytoplasmic (Probable). I.: SUBCELUIAR LOCATION: Cytoplasmic (Probable). Interproton: Involved In PREDINGEMENT OF THE AAR FAMILY OF AFPASES. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the Emble outstations on the Entry Institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announcentities requires a license agreement (See http://www.isb-sib.ch/announcentities requires a license@isb-sib.ch). EMBL: Lasses, AAAA; 1. EMBL: Lasses, AAAA; 1. EMBL: AAAA; 1. EPROSITE: PSO0674; AAA, 1. EPROSITE: PSO0674; AAA, 1. EPROSITE: PSO0674; AAA, 1. EPROSITE: PSO0674; AAA, 1. ERCORDER 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88ABJA6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88AB	ŏ	NCBI_TaxID=4	952;					
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Altchison D.D., Sallard R.K., Glover J.R., Rachubinaki R.A., Tapara, agene required for peroxisome assembly in the yeast Yarrowia lipolytica, encodes a novel member of a family of putative Arpases."; J. Biol. Chem. 269:556-566(1994). J. Biol. Chem. 269:556-566(1994). J. Biol. Chem. 269:556-566(1994). J. Biol. Chem. 269:556-566(1994). J. SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES. J. SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES. This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to licenseéisb-sib.ch). EMBL; L2368; AAA16622.1; InterPro; IPR003959; AAA_sub. InterPro; IPR003959; AAA_sub. InterPro; IPR003959; AAA_sub. InterPro; IPR003959; AAA_sub. InterPro; IPR003959; AAA_sub. InterPro; IPR003959; AAA_sub. InterPro; IPR003959; AAA_sub. InterPro; IPR003960; AAA_sub. InterPro; IPR003960; AAA_sub. InterPro; IPR003960; AAA_sub. InterPro; IPR003969; AAA_sub. InterPro; I	RA	Nuttley W.M.	, Brade A.M.,	Eitzen G.	Veer	uis M.,		
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NP_BIND 760 767 ATP (POTENTIAL). SEQUENCE 1025 AA; 112258 MW; C41229CAE88AB7A6 CRC64; SEQUENCE 1025 AA; 112258 MW; C41229CAE88AB7A6 CRC64; C41229CAE88AB7A6 CRC64; C41229CAE88AB7A6 CRC64; C41239CAE84 C41239CAE84 C51239CAE84	ΚW	Peroxisome; 1	ATP-binding.					
SEQUENCE 1025 AA; 112258 MW; C41229CAE88AB7A6 CRC64; Suery Match 12.0%; Score 84; DB 1; Length 1025; Best Local Similarity 27.8%; Pred. No. 0.94; 4atches 25; Conservative 12; Mismatches 37; Indels 16; Gaps 55 PCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDR 100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	FE	NP BIND	767 097		OTENTIAL)			
Duery Match 12.0%; Score 84; DB 1; Length 1025; Best Local Similarity 27.8%; Pred. No. 0.94; Matches 25; Conservative 12; Mismatches 37; Indels 16; Gaps 55 PCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDR 100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	So	SEQUENCE 1(025 AA; 11225		1229CAE88	AB7A6 CRC64;		
July Match 12.0%; Score 84; DB 1; Length 1025; Jest Local Similarity 27.8%; Pred. No. 0.94; Adtches 25; Conservative 12; Mismatches 37; Indels 16; Gaps 55 PCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDR 100 101 TDKIVPLOGRESLAPFSNFSVKGPELLNWYIGESEANVRNVFQKARDAKPCVVFFDE 820 101 TDKIVPLOGRESLAPFDALLDEALDRILAE 130 11		:						
dest local Similarity 27.8%; Fred. No. 0.94; Matches 25; Conservative 12; Mismatches 37; Indels 16; Gaps 55 PCGDGDVHIAPADPETFGEVLIKLQVGSDQAMFRVGTAPLVAFLDR 100 1	no	ery Match		Score	80		25;	
55 PCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDR	Ве Ма	Local Similes 25;	vat	; Pred. I 12; Mism	No. U.94; natches		16;	
	ò		TAPADPETE	GEVI,TE	PLOVGSDOAL	4FRVGT)		100
761. PPGTGKTLLAKAIATTFSLNFFSVKGPELLNMYIGESEANVRNFGKARDAKPCVVFFDE 101 TDKIVPLGQERSLADFDALLDEALDRILAE 130	7			-		: :-) }
101 TDKIVPLGQERSLADFDALLDEALDRILAE	QQ	761. PPGTGKTI	CLAKAIATTFSLNF	FSVKGPELL	MYIGESEA	nvrrveqkardai		820
: : : : 821 LDSVAPQRRNQGDSGGWMDRIVSQLLAE	Οy		SQERSLADFDALLD	EALDRILAE				
821 LDSVAPQRRNQGDSGGVMDRIVSQLLAE		- -	:: - ::	= :: ::				
	음	821 LDSVAP-	- QRRNQGDSGGVMD	RIVSQLLAE		-		,

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16-OCT-2001 (Rel. 40, Last annotation update)
Peroxisome assembly factor-2 (PAF-2) (Peroxisomal-type ATPase 1)
16-0CT-2001 (Rel.
                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476
748
299
                      (Peroxin-6)
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MUTAGEN
CONFLICT
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 PYAVRLIFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADP--ETFGEVL-- 75
                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                         Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                             Tweedie S., Edwards Y.; {\tt ^{\rm 1}}{\tt ^{\rm 1}}{\tt ^{\rm 1}} {\tt ^{\rm 1}}{\tt ^{\rm 1}}{\tt ^{\rm 1}} incleotide sequence and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
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ZINC (CATALYTIC).
ZINC (CATALYTIC).
E35B5CDDC4A54A93 CRC64;
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                                        259 AA.
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28.2%; Pred. No. 0.69;
tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEX6_RAT STANDARD; PRT; 978 AA. P54777; 055097; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88270; Car3.
InterPro; IPR001148; Carb_anhydrase.
Pfam: PF00194; carb_anhydrase; 1.
Probom: P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase: Zinc.
                                        PRT;
                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-89227981; Pubmed-2496681;
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HSSP; P00918; 1CIM.
SWISS-2DPAGE; P16015; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
29397
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Best Local Similarity 28.28
Matches 31; Conservative
                                        STANDARD;
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93
95
118
259 AA;
                                                                                                              OR CAR3.
                                        CAH3_MOUSE
                                                                                                                                                                                                                                                                             FAMILY
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SEQUENCE
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                    RESULT 2
CAH3_MOUSE
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CA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                      "Peroxisome assembly factor-2, a putative ArPase cloned by functional complementation on a peroxisome-deficient mammalian cell mutant."; Nat. Genet. 11:395-401(1995).
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718 TIOLPLEHPELLSLGLRRSGLLLHGPP---GTGKTLLAKAVATECSLTFLSVKGPELINM 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 QVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                            Tsukamoto T., Miura S., Nakai T., Yokota S., Shimozawa N.,
Suzuki Y., Orii T., Fujiki Y., Sakai F., Bogaki A., Yasumo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K->A: NO LOSS OF FUNCTION.
K->A: LOSS OF FUNCTION.
D -> G (IN REF. 2).
V -> A (IN REF. 2).
O -> R (IN REF. 2).
R -> C (IN REF. 2).
R -> C (IN REF. 2).
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3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78;
Pred. No. 3
                                                                                                                               SEQUENCE FROM N.A.
STRAIN-FISCHER 344; TISSUE-Liver;
MEDLINE-96083586; Pubmed-7493019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART: SMUJOS, proc., PROSITE: PS00674; AAA; 1.
Peroxisome; ATP-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D89660; BAA24931.1; -. D89657; BAA24931.1; JOINED. D89658; BAA24931.1; JOINED. D89659; BAA24931.1; JOINED.
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Interpro; IPR003960; AAA_sub.
Interpro; IPR003959; AAA_subfam.
Pfam; PP00004; AAA; 2.
SWART; SM00382; AAA; 1.
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28.8%;
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Rattus norvegicus (Rat).
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476
748
299
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     978 AA;
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AF108097; AAF62564.1; JOINED

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DR ADD BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AND BANK MAN AN
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C -1- SUBCELLULAR LOCATION: CYLOPIASSMIC.

C -1- SUBCELLULAR LOCATION: CYLOPIASSMIC.

C -1- DISCASE BEFECTS IN PEXG ARE THE CAUSE OF PEROXISOME BIOGENESIS DISCASES: DEFECTS IN PEXG ARE THE CAUSE OF PEROXISOME BIOGENESIS.

C -1- DISCASE GROUP 4 (PBD GROUP 4). PBD ARE A GROUP OF LETHAL BIOGENESIS DISCASES. THEY ARE CLINICALLY DIVIDED INTO FOUR GROUPS: CELMEGER SYNDROME (2S), NEONATAL ADRENOLEUKODYSTROPHY (NALD), INFANTILE REFSUM DISCASE (TRD), AND CLASSICAL RHIZOMELIC CHONDRODYSPLASIA PUNCTATA (RCDP). ZS IS THE MOST SYVERE PHENOTYPE OF THE PBD AND IS CHARACTERIZED BY THE ABSENCE OF PEROXISOMES AND BY MULTIPLE METABOLIC DEFECTS: PATIENTS WITH ZS HAVE SEVERE NEUROLGICAL ABNORMALITIES, DYSMORPHIC FACIAL FEATURES, HERDALOMES, HERDALOMES, MOST IND THEN AND AND IRD ARE SIMILAR TO 2S, BUT PROGRESSIVELY MILDER, WITH SOME IRD PATIENTS SURVIVING BEYOND THE THIRD DECADE OF LIFF. CLASSICAL RCDP, DISTINCT FROM THE ZS SPECTRUM, IS ASSOCIATED WITH A CHARACTERISTIC FACIAL APPEARANCE, RHIZOMELIA, CHITANDELIA, AND SEVERE NEUROLGGICAL IMPAIRMENT.

C ASSOCIATED WITH A CHARACTERISTIC FACIAL APPEARANCE, RHIZOMELIA, CHITANDELIA, CHITANDELIA, AND SEVERE NEUROLGGICAL IMPAIRMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANTS 2S GLN-812 AND TRP-812.
MEDLINE-9932564; PubMed-10408779;
Zhang 2., Suzuki Y., Shiancawa N., Fukuda S., Imamura A.,
Tsukamoto T., Osumi T., Fujiki Y., Orii T., Wanders R.J.A.,
Barth P.G., Moser H.W., Paton B.C., Besley G.T., Kondo N.;
"Genomic structure and Genefitication of 11 novel mutations of the
PEX6 'peroxisome assembly factor-2' gene in patients with peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=97094178; PubMed=8940266; Anang Z., Tomatsu S., Fukuda S., Shimozawa N., Suzuki Y., Zhang Z., Tomatsu S., Fukamoto T., Hashiguchi N., Osumi T., Masuno M., Imalaumi K., Kuroki Y., Fujiki Y., Orii T., Kondo N.; "Human peroxisome assembly factor-2 (PAF-2): a gene responsible for Agroup C peroxisome blogenesis disorder in humans."; Am. J. Hum. Genet. 59:1210-1220(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96272151; PubMed-8670792;
Yahraus T., Braverman N., Dodt G., Kalish J.E., Morrell J.C.,
Moser H.W., Valle D., Gould S.J.;
"The peroxisome biogenesis disorder group 4 gene, PXAAA1, encodes
cytoplasmic APPase required for stability of the PIS1 receptor.";
EMBO J. 15:2914-2923(1996).
                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  PEX6_HUMAN STANDARD; PRT; 980 AA.
131608; 099476;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peroxisome assembly factor-2 (PAF-2) (Peroxisomal-type ATPase 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hum. Mutat. 13:487-496(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                        PEX6 OR PXAAA1.
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EMBL; EMBL; EMBL;

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720 TIQLPLEHPELLSLGLRRSGLLLHGPP---GTGKTLLAKAVATECSLTFLSVKGPELINM 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAH3_RAT STANDARD, PRT; 259 AA.
P14141; 054961;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             30 TFHLPGDAPVTWAFGRE---LLIDGGPRPCGDGDVHIAPADPE----TF----GEVLIRL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79. QVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A.;
"cDNA sequence of rat liver carbonic anhydrase III.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89166882; PubMed-2852973;
Kelly C.D., Carter N.D., Jeffery S., Edwards Y.H.;
"Characterisation of cDNA clones for rat muscle carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Wistar; TISSUE-Liver;
MEDLINE-20361776; PubMed-10900145;
MEDLINE-20361776; PubMed-10900145;
Makausue K., Yamada H., Oguri K.;
Maksusue K., Yamada H., Oguri K.;
"Suppression of carbonic anhydrase III in rat liver by a dioxin-related toxic compound, coplanar polychlorinated biphenyl, 3,3',4,4',5-pentachlorobiphenyl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                   11.1%; .Score 78; DB 1; Length 980; 28.8%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                        48; Indels
                                                                                                                                                                                                812 812 K -> W (IN ZS; ATYPICAL).

/FTIG=VAR_007918.

/FTIG=VAR_007919.

77 77 S -> N (IN REF. 1).

980 AA; 104060 MW; 0ECIC2A75CE0038F CRC64;
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PROSITE; PS00674; AAA; 1.
Peroxisome; ATP-binding; Repeat; Disease mutation.
NP_BIND 470 477 ATP (POTENTIAL).
7.44 751 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
           InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA_sub.
InterPro; IPR003959; AAA_subfam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biosci. Rep. 8:401-406(1988).
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.8%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                   Pfam; PF00004; AAA; 2.
SMART; SM00382; AAA; 1.
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MIM; 214100;
                                                                                                                                                                                                                                                                             SEQUENCE
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93
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29440 MW;
            PARTIAL SEQUENCE FROM N.A.
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259 AA;
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SEQUENCE FROM N.A.
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P96981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter
                                                                                                                                   FAMILY.
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METAL
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           PYAVRLIFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87092290; PubMed-3099285; Wade R., Gunning P., Eddy R., Shows T., Kedes L.; Wale R., Gunning P., Eddy R., Shows T., Kedes L.; Mucleotide sequence, tissue-specific expression, and chromosome location of human carbonic anhydrase III: the human CAIII gene is located on the same chromosome as the closely linked CAII and CAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liloyd J., McMillan S., Hopkinson D., Edwards Y.H.;
"Nuclectide sequence and derived amino acid sequence of a cDNA
encoding human muscle carbonic anhydrase.";
Gene 41:233-239(1986).
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                  136 PDGIAVVGIFLKIGREKGEFQI-----LLDALDKIKTKGKEAPFNHFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                     -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
A -> G (IN REF. 1).
FG -> SE (IN REF. 1).
KL -> NV (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes.";
Proc. Natl. Acad. Sci. U.S.A. 83:9571-9575(1986).
                                                                                                                                                                                                                                                                                                                                 10.9%; Score 76.5; DE 28.2%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AA
                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                           InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
ProDom; P0000865; Carb_anhydrase; 1.
PROSITE: PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase: Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                    EMBL; M22413; AAA40846.1; -.
EMBL; AF037072; AAB92558.1; -.
EMBL; AB030829; BAB08111.1; -.
                                                                                                                                                                                                                                                                                    224 KI
29300 MW;
                                                                                                                                                                                                                                                                                                                                                      Conservative
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95
118
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                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                      HSSP; P00918; 1CIM.
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Best Local Similarity
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223
259 #
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95
118
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P07451;
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INIT_MET
METAL
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CONFLICT
CONFLICT
SEQUENCE
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                         Lloyd J., Brownson C., Tweedie S., Charlton J., Edwards Y.H.;
"Human muscle carbonic anhydrase: gene structure and DNA methylation
patterns in fetal and adult tissues.";
Genes Dev. 1:594-602(1987).
-!- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
-!- TISSUE SPECIFICITY: OF THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Probable hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase
II) (Glx II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDGIAVIGIFLKIGHENGEFQI-----FLDALDKIKTKGKEAPFTKFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
I -> V (IN REF. 2).
W; EFBC56CF721E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 75.5; DB 1; 28.2%; Pred. No. 1.4; Live 13; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001148; Carb_anhydrase. Profile, carb_anhydrase; 1. Propom: PP00194; carb_anhydrase; 1. PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M29452; -; NOT_ANNOTATED_CDS. PIR; A25850; A25850. PIR; A26658; A26658. PIR; A26690; A26690. HSSP; P00918; 1CIM. HSC-2PPAGE; P07451; HUMAN.
MEDLINE-88056301; PubMed-2824285;
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SMART; SM00326; SH3; 1.
SMART; SM00221; STYKC; 1.
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Matches 28; Conservative
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463
464
480
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954 AA;
   SEQUENCE FROM N.A.
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104
125
222
384
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
MEDLINE-98101484; PubMed-9440534;
Borghese R., Crimi M., Fava L., Melandri B.A.;
"The APP Synthase atpHAGDC (F1) operon from Rhodobacter capsulatus.";
J. Bacteriol. 180:416-421(1998).
-!- FUNCTION: THIOLESTERASE THAT CATALYSES THE HYDROLYSIS OF S-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 IAWYLPGAGLLFSGDSLMSWGCGR--LFEGTPAQMFDTLTRLAALPPETRVCSGHEYTAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIFHLP-----GDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPET----- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 FGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADF----DALLDEAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 NGRFALSLEPGNGRLHDRMDRVTALRLAGEPSLPVTLGEERATNPFLRADDAALRAAL 234
                                                                           LACTOYL-GLUTATHIONE TO FORM GLUTATHIONE AND D-LACTIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                       -!- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M3KA_HUWAN STANDARD; PRT; 954 AA.
002779; 012761; 014871;
001-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
(Mixed lineage kinase 2) (Protein kinase MST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                            ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-Brain;
MEDLINE-96128179; PubMed-8536694;
DOTOW D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
Sutherland G.R., Simpson R.J.;
"Complete nucleotide sequence, expression, and chromosomal
"Complation of human mixed-lineage kinase 2.";
Eur. J. Biochem. 234:492-500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glutathione + a 2-hydroxy acid anion.
-!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
-!- PATHWAY: GLYOXAL PATHWAY.
-!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
                                                                                                                                                                                                                                                                                                                                             InterPro: IPR001279; Beta_lactam_met. Pfam; PF00753; lactamase_B; 1. Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27342 MW;
                                                                                                                                                                                                                                                                                                                     EMBL; X99599; CAA67905.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAP3K10 OR MLK2 OR MST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                           SIMILARITY)
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Best Local S
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50002; SH3: 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
ATP-binding; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARG/LYS-RICH (BASIC).
SRL -> AV (IN REF. 2).
LKLREGGSHISLPSGF -> AQAAGRROPHQPALWL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
LEUCINE-ZIPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEUCINE-ZIPPER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 74; DB 1; Length 954; 31.5%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                       Katoh M., Hirai M., Sugimura T., Terada M.;
"Cloning and characterization of MST, a novel (putative)
serine/threonine kinase with SH3 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REF. 3).

G -> S (IN REF. 2).

G -> R (IN REF. 2).

V -> A (IN REF. 2).

W -> A (IN REF. 2).

MW; 538F4AAA559B0ABA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSTIE: PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Euk_pkinase. InterPro; IPR001452; SH3. InterPro; IPR00440; STY_pkinase. InterPro; IPR00290; Ser_thr_pkinase. InterPro; IPR001245; Tyr_pkinase. Pfam; PF00069; pkinase; 1.
MEDLINE=95249256; PubMed=7731697;
                                                                                                                                               SEQUENCE OF 244-480 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X90846; CAA62351.1; -. EMBL, 248615; CAA88531.1; -. PIR, S32468, S32468.
                                                                                              Oncogene 10:1447-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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P39658;
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Best Local S
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DRNE_AERHY
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
70 Kba peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans isomerase) (Cyclophilin) (Ppiase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                             01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annoctation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                   Wendorff K.M., Nishita T., Jabusch J.R., Deutsch H.F.;
"The sequence of equine muscle carbonic anhydrase.";
J. Biol. Chem. 260:6129-6132(1985).
-i- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-i- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum (Wheat).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                       EVPYREIDALAVAYGVAMNKLTLPIPSTCPEPFA---RLL----EECWDPDPHGRP---
   ELRYETCDPYAV-----RLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADP
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 PDGIAVVGVFLKIGREKGEFQL-----FLDALDKIKTKGKEAPFTNFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
B3EECDFF89BFED02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                        259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 73.5; DI
Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P00918; 1BV3.
InterPro; IPR001148; Carb_anhydrase.
Pfan; PF00194; carb_anhydrase; 1.
ProDom; PD000865; carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc; Acetylation.
                                                          - DFGSILKRLEVIEQSALFQM---PLESF 373
                                             69 ETFGEVLIRLQVGSDQAMFRVGTAPLVAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                            MEDLINE=85207593; PubMed=3922970;
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                                                                                                                        STANDARD;
                                                                                                                                                                                                              Eguus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                            PIR; A22612; A22612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 AA;
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Best Local Similarity
Matches 29; Conserv
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Q43207;
                                                                                                                        CAH3_HORSE
P07450;
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SEQUENCE
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MOD_RES
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                                                                                                   RESULT 9
CAH3_HORSE
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FKB7_WHEAT
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   16
                       300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 IAPADP-ETFGEVLIRLQVG----SDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLA 114
                                                                                                                                                                                                                                                    BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
                                                            STRAIN-CY. ATIR; TISSUE-Root tip;
Oshra B., Breiman A.;
Sobnitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASE THAT BINDS CALMODULIN.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PERTIDES IN OLIGOPEPTIDES.
-!- INDUCTION: BY HEAT SHOCK.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-ocT-1994 (Rel. 30, Created)
01-ocT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Extracellular deoxyribonuclease precursor (EC 3.1.21.-) (DNase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73; DB 1; Length 559;
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5C5DAE70D716B541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001179; FKBP_PPHase.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
InterPro; IPR00154; FKBP; 3.
SMART; SM00028; TPR; 3.
PROSITE; PS00453; FKBP_PPHASE_1; 1.
PROSITE; PS50054; FKBP_PPHASE_2; 3.
ISOMERASE; ROTAMASE; 13.
ISOMERASE; ROTAMASE; 14.
ISOMERASE; ROTAMASE; 14.
ISOMERASE; ROTAMASE; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.
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                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPIASE,
PPIASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPR 1.
TPR 2.
TPR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62056 MW;
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29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X86903; CAA60505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483
                                                                                                                                                                                                                                                                                FKBP-LIKE DOMAINS
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401
450
484
559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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NCBI_TaxID=4565;
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PEX6 OR PAS5
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                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                        Chang M.C., Chang S.Y., Chen S.L., Chuang S.M.;
"Cloning and expression in Escherichia coli of the gene encoding an extracellular deoxyribonuclease (DNase) from Aeromonas hydrophila.";
Gene 122:175-180(1992).
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE ENDA/NUCM FAMILY OF NUCLEASES.
                                                                                                                                                                                                                                                                                                                                                                                 41 WAFGRELLI--DGGPRPCG------DGDVH-IAPADPETFGEVLIRLQVGSDQAMFRV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deviin K., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                             POTENTIAL.
EXTRACELLULAR DEOXYRIBONUCLEASE.
D6C60274CFAE7E29 CRC64;
                                                                                                                                                                                                                                                                                                                                Score 72.5; DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 948 AA.
                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.5;
8; Mismatches
                                                                                                                                                                                                                                                Hydrolase; Endonuclease; Nuclease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                     90 GTAPLVAFLDRTDKIVPLGQERSLADF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 -----FSDWNGKPNOYGKCOMLVDF 155
            MEDLINE=93083980; PubMed=1452026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA_sub.
InterPro; IPR003959; AAA_subfam.
                                                                                                                                                                                                                                                                                        SEQUENCE 230 AA; 26699 MW;
                                                                                                                                                                                                                                                                                                                              10.3%;
                                                                                                                                                                                                                        EMBL; M99491; AAA21942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z98849; CAB11501.1; -.
                                                                                                                                                                                                                                                                                                                                                        28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable peroxin-6. SPAC17A5.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                     PIR; JC1483; JC1483
                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEX6_SCHPO
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              013764;
                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHPO
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
PEX6_SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spong A.P., Subramania S.;
"Cloning and characterization of PAS5: a gene required for peroxisome biogenesis in the methylotrophic yeast pichia pastoris.";
J. Cell Biol. 128:535-548(1933)
-!- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. NECESSARY FOR MATRIX PEROXISOMAL PROTEINS IMPORT. ESSENTIAL FOR GROWTH ON OLEIC ACID AND METHANOL AS SOLE CARBON SOURCE.
-!- SUBCELLULAR LOCATION: IT MAY BE ASSOCIATED WITH THE CYTOSKELETON OR IT MAY BE CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   667 LRDTLQLPLQFPELFSQGLKPRSGVLLYGPP---GTGKTLLAKAVATELSLEFVSIKGPE 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 LIRLQVGSDQAMFR-----VGTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRIL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 VRLTFHLPGDAPVTWAFGRE----LLIDGGPRPCGDGDVHIAPADPETF------GEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pichia pastoris (Yeast).
Bukaryota; Mugdi, Ascomycota; Saccharomycetes; Saccharomycetales;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    859 866 ATP (POTENTIAL).
1165 AA; 129137 MW; DEA192C1D5CA46EA CRC64;
                                                                                                                                                                                                                                                                                                                     F41DFD7DE6D391B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Peroxisome biosynthesis protein PAS5 (Peroxin-6).
                                                                                                                                                                                                                                                                  ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%; Score 72.5; DB 25.4%; Pred. No. 13; cive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA_sub.
InterPro; IPR003959; AAA_subfam.
Pran; Pr00004; AAA; 2.
SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS0674; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-NRRL 11430;
MEDLINE-94043437; Pubmed-8227124;
Pfam; PF00004; AAA; 2.
SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; FALSE_NEG.
PECTXISOME; ATP-binding.
NP_BIND
SEQUENCE 948 AA; 106505 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 222556; CAA80278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches: 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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(Rel. 35, Created) (Rel. 35, Last sequence update) (Rel. 35, Last annotation update)

457 AA.

PRT;

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Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                 Late, expression factor 4.
                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=164623;
                                                                                                        01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                  LEF4_NPVOP
                       RESULT
                                                                                         a
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                                            5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                       TFHLPGDAPVTWAFGRE----LLIDGGPRPCGDGDVHIAPADPETF-----GEVLIR 77
                                                                                                                                                                               78 LQVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                           26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSTIE: PS00601; IRF; 1.

Transcription regulation; DNA-binding; Nuclear protein; Activator.

DNA_BIND 7 107 TRYPTOPHAN PENTAD REPEAT.

TABLE 19 AA: 46852 MW; IFF67C4E0FC7F027 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                               23;
  DB 1; Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9;
7; Mismatches 19; Indels
                                            Indels
                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interferon regulatory factor 3 (IRF-3).
                                                                                                                                                                                                                                                                                                                                           419 AA
                                            Mismatches
10.3%; Score 72.5; 1
23.5%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70;
                                                                                                                                                                                                                                                                                                                                           PRT;
                                            19;
                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0267; INTERNREGECT PRODOM; PD002355; IRF; 1. SMART; SMO0348; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%;
32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U75839; AAB36924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| | | |:||311 AVFDLRPFVADLIAFME 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSF; K23700, 21....
MGD; MGI:1859179; Irf3.
INTERPRO; IPR001346; IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.0%
Best Local Similarity 32.5%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AMF -- RVGTAPLVAFLD 99
                                            Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P23906; 2IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
                       Best Local Sim
Matches 28;
                                                                                                                                                                                                                                                                                                                                           [RF3_MOUSE
  Query Match
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                                                                                     30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 LQVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLAD------FDALLD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
SEQUENCE FROM N.A. MEDIAGE-9126251; Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rhrans C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.; The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear
                                                                                                                                                      polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- FUNCTION: REQUIRED FOR LATE AND VERY LATE GENE EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 1; Length 457; Pred. No. 9.9; 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51151 MW; E21E06E50BAC8390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: July 18, 2002, 14:31:56
Job time: 945 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U75930; AAC59090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%;
35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 35.2 nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 EALDRILAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220. SATPRRFTREQ 230
                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription
SEQUENCE 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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OM protein

Run on:

Sequence:

Title:

Searched:

Database

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Q9KK10 vibrio chol
P99548 spinacia ol
077949 rattus norv
0941y0 drosophila
Q21029 caenorhabdi
Q9K20 streptomyce
0914y1 streptomyce
06499 mycobacteri
Q931w2 streptomyce
Q95zr0 arabidopsis
Q9ewy7 streptomyce
                                                                                                                                                                                                        09a2m0 caulobacter
03a788 bacillus su
092k21 rhizobium m
09a400 caulobacter
092py5 rhizobium m
09kh05 bradyrhizob
032384 synechococc
09hsm3 halobacteri
09hsm3 halobacteri
                                       Q94fg5 acopirillu
Q94ki0 avicennia m
Q31271 rattus norv
O87043 vibrio chol
                    Q991c9 mus musculu
Q9i3m9 pseudomonas
          086603 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195770: AAG28481.1; -
SEQUENCE 135 AA; 14843 MW; 32006CC86EDE4ED6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=121022;
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100.0%; Pred. No. 3.3e-62;
ive 0; Mismatches 0;
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Q99LC9
Q913M9
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Q21029
Q9KZ00
Q9L4Y1
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Q9SZR0
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Best Local Similarity 100.
Matches 135; Conservative
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09rx0 streptomyce
09rx1 streptomyce
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09rx2 amycolatops
P71922 mycolatops
P71922 mycolatops
091639 glomerella
09c109 glomerella
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166.638 Million cell updates/sec
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                                                                      July 18, 2002, 14:30:55; Search time 140.15 Seconds
                     Compugen Ltd
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                      562222 seqs, 172994929 residues
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Q9FZO2
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    sp_rodent:*
    sp_virus:*
    sp_vertebrate:*
    sp_unclassified:*
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sp_mammal:*
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Maximum Match 100%
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Kawamoto S., Ensign J.C.;
"Isolation of mutants of Streptomyces griseus that sporulate in
nutrient rich media.";
                                                         Nippon Hosenkin Gakkaishi 9:124-135(1995)
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Matches 105; Conservative
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Kinsahi H., Hopwood D.A.;
Masch of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microblol. 21:77-96(1996).
EMBL; A0196823; CAB46964119-5
SEQUENCE A136 AA: 14920 MW; 4B67CIFIEOBECC88 CRC64;
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                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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                                                                                                                                                                                         Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                   James K.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                         Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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MEDLINE=97000351; Pubmed=8843436;
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                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
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                       PRELIMINARY;
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Matches 115; Conserv
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van Wezel G.P., Rousseau C., Kraal B.;

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195772: AAG28483.1; -

SEQUENCE 145 AA; 15838 MW; 92AC0F30DF3D2620 CRC64;
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Kawamoto S., Ensign J.C.; "Loning and characterization of a gene involved in regulation of sporulation and cell division of Streptomyces griseus."; Nippon Hosenkin Gakkaishi 9:136-151(1995).
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                                                                                                                                                                                                                                                        MEDLINE-97286526; PubMed-9141673; Rawamoto S., Watanabe H., Hesketh A., Ensign J.C., ochi K.; Rawamoto S., Watanabe H., Hesketh A., Ensign J.C., ochi K.; Expression analysis of a ssgA gene product associated with sporulation and cell division in Streptomyces griseus."; Microbiology 143:1077-1086(1997).

EMBL; D50051; BAA21558 I., C6A28A7823AD7C8B CRC64;
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RESULT **09F9B6**

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL137778; CAB70943.1;
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MEDLINE=97000351; PubMed=8843436;
     MEDLINE=97000351; PubMed=8843436;
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Best Local Similarity
Matches: 55; Conserv
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Seeger K., Harris
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces albus ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF195771; AS264821.; -
SEQUENCE 135 AA; 14735 MW; OFCBF4BDBBA201B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.6%; Score 481; DB 2; Length 135; llarity 71.1%; Pred. No. 2.5e-40; Conservative 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                         135 AA
                                                                                                                                                                                                                                Created)
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131 EAALGKILAEEONAG 145
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121 DDALNRSLAEEQSAG 135
                                                         121 DEALDRILAEEQNAG 135
                                                                                                                                                                                         PRELIMINARY;
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STRAIN=A3(2);
Seeger K.J., Harris D.
Submitted (JAN-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 96; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1888
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                                                                                                                                                                                                         Q9F9B6;
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Q9L268

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61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
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                                                                                                                                       Gaps
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Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
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the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; ALO96852; CASIOS5.1; -
SEQUENCE 142 AA; 15364 MW; 857862390AA5ICCB CRC64;
                                                                                                                                                                                        1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 142;
                                                                                  Length 159;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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17472 MW; BA41013F940D7315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                            33.4%; Score 234; DB 2; I ilarity 42.3%; Pred. No. 1.1e-15; Conservative 13; Mismatches 58;
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Best Local Similarity 38.1%; Pred. No. 7.4e-14;
Matches 48; Conservative 18; Mismatches 60;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL391041; CAC01575.1;
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EMBL; AL049863; CAB42228.1; -SEQUENCE 142.AA, 15741 MW; E24AA52C00AF40F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 IPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHI---APADPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE REGULATOR.
SC5H1.03.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomyces.
NCBL_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70. TFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 97. T---AWLQVNAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 156;
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                                                                                                                                                                                            Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55; Indels
                                               STRAIN=A3(2);
Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J., Barrell B.G., Rajandream M.A.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oliver K., Harris D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1041; CAC01575.1; -.
156 AA; 17188 MW; 7181972EE7F33FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.1%; Score 155; DB 2; 35.3%; Pred. No. 7.7e-08; tive 14; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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MEDLINE=97000351; PubMed=8843436;
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MEDLINE=97000351; PubMed=8843436;
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Oliver K., Ha
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Q9X7R1
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MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLGIDDGL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 LIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPL 107
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                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL, AL049587; CAB40672.1; -
SEQUENCE 138 AA; 15261 MW; F531BA29514ABA5 CRC64;
                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                       138 AA.
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                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 СЕНГОГОГОНОГАЕТМ 134
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                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 43; Conserv
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                                             121 DEALDR 126
                                                                                            137 AELLAR 142
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RESULT **Q9FC07**

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Local Similarity 25.29
nes 33; Conservative
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Chem. Biol. 5:0-0(1998).
                                Penicillium chrysogenum.
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August P.R., Tang L.,
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                                                                    NCBI_TaxID=5076;
                                                                                                                                                                                                                                ATP-binding.
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          PEROXIN-6.
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL: AL132674; CAB59654.1; -.
SEQUENCE 126 AA; 13742 MW; D54A8574D28B4D69 CRC64;
                                                                                             70 TFGEVLIRLQVGS-----DQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALLDE 122
                                                                                                            Gaps
                                              RIPV--ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE 69
                                                                    21 RFPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRPESRG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 IPVELRYE-TCDPYAVRLTFHLPG-----DAPVTWAFGRELLIDGGPRPCGDGDVHIAPA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
                     Indels
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Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 13.7 KDA PROTEIN.
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         Pred. No. 1.7e-05;
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34.0%; Pred. No. 0.12
ative 10; Mismatches
                       Mismatches
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MEDLINE-97000351; PubMed-8843436;
30.5%; P1.
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                     Conservative
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                                                                                                                                                                                                                                                                                                           SCE87.09C.
Streptomyces coelicolor.
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Best Local Similarity
          Best Local Similarity
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01-MAR-2001 (
01-DEC-2001 (
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Q9HG03
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Q9RKC9
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1045 TIQLPLERPELFAKGMKKRSGILFYGPP---GTGKTLLAKAIATEFSLNFFSVKGPELLN 1101
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
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Eukaryota; Fungī; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                MEDINE-20421849; PubMed=10968639;
Kiel J.A., Hilbrands R.E., Bovenberg R.A., Veenhuis M.;
Kiel J.A., Hilbrands R.E., Bovenberg R.A., Veenhuis M.;
Isolation of Penicillium chrysogenum PEX1 and PEX6 encoding AAA proteins involved in peroxisome biogenesis.";
Appl. Microbiol. Biotechnol. 54:238-242(2000).
EMBL; AF233277; AAG09749.1; -..
InterPro: IPR003595; AAA.
Efam; PF00004; AAA:
Ffam; PF00004; AAA: 1.
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August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Yu T.W.,
Taylor M., Hoffmann D., Kim C.G., Zhang X., Hutchinson C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%; Score 85; DB 3; Length 1459; 25.2%; Pred. No. 10; Live 19; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AFC40570; AAC01740.1; -.
HSSP; Q00441; 10XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C5219F4DBA6E49B9 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE CYTOCHROME P450 MONOXYGENASE.
CYP105G1.
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                                                                                                                                                                                                                                                                                                                     39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VSEELSFRIP------WELRYETCDPYAVRLTFHLPGDAPVT------WAFGRELL 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Goborne J., Quail M.A., Rajandream M.A., Rogers J., Stuter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
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                                                                                                                                                                                                                                              11.8%; Score 82.5; DB 2; Length 351; 24.3%; Pred. No. 3.3;
InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Hypotherical protein; Monooxygenase; Oxidoreductase.
SEQUENCE 351 AA; 38512 MW; 2C390B56A60D5571 CRC64;
                                                                                                                                                                                                                                                                                                                     Indels
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Pfam. PF00004; AAA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 291 AA; 31950 WW; FA611423E14B4DCF CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 31.9 KDA PROTEIN.
RV2426C OR MTCX428.21.
                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                     23; Mismatches
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Nature 393:537-544(1998).
EMBL; Z81451; CAB03770.1; -.
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Matches 37; Conservative
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1062 ELLNMYIGESEANVRVFQRARDARPCVVFFDELDSVAP--KRGNQGDSGGVMDRIVSQL 1119
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MEDLINE-21380423; PubMed-11487704;
MEDLINE-21380423; PubMed-11487704;
MEDLINE-21380423; PubMed-11487704;
Mimura A., Takano Y., Furusawa I., Okuno T.;
Peroxisomal Metabolic Function Is Required for Appressorium-Mediated Plant Infection by Colletotritchum lagenarium.";
Plant Call 13:1945-1957(2001).
EMBL; AF343063; AANLS11; -.
InterPro; IPR003369; AAALsubfam.
InterPro; IPR003959; AAALsubfam.
Pfam; PF00004; AAA.
SWART; SW00382; AAA: 1.
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Last annotation update)
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25.2%; Pred. No. 34;
tive 18; Mismatches
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Best Local Similarity 25.25
Matches 31; Conservative
141 DKADIEIEGLLEVL 155
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BARRND (NL); LUITEN RUDOLE GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
                                             AL096823 Streptomy
AX007222 Sequence
AX007220 Sequence
AX195771 Streptomy
AL137778 Streptomy
AL056852 Streptomy
A28303 S.albus bet
AL391041 Streptomy
AX089419 Sequence
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AX089416 Sequence
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AL021529 Streptomy
AX196078 Sequence
AX195929 Sequence
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AP003825 Oryza sat
U41300 Blastocladi
AL355832 Streptomy
AL139298 Streptomy
       AF195772 Streptomy
AX007218 Sequence
AX007216 Sequence
D50051 Streptomyce
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AL583944 Streptomy
AL359779 Streptomy
AR099281 Sequence
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Scoring table:

PAT 06-SEP-2000

Score

Result No.

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1 (bases 1 to 438)
van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces netropsis ssgA gene
Unpublished
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Submitted (18-OCT-1999) Biochemistry, University of Leiden, PO
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
1.438
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                         /gene="ssgA"
/note="strain ATCC of Streptomyces netropsis"
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                 /gene="ssgA"
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van Wezel, G.P.
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 407; DB 1; Length 438; Best Local Similarity 100.0%; Pred. No. 2e-38; Matches 407; Conservative 0; Mismatches 0; Indels
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Sequence 3 from Patent WO0000613.
AX007218
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1. .407
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/note="similar to
division protein"
                                                                                                                  /codon_start=1
/transl_table=11
/product="SsgA"
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GDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTA
PLVAFLDRTKLVPLGQEHTGDFDGNLEDALGR"
145 c 153 g 72 t
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Streptomyces griseus
Streptomyces griseus
Bacteria: Firmicutes; Actinobacteria; Actinobacteriae; Actinobacteriaes; Actinobacteriaes; Actinomycetales; Streptomycineae; Streptomyces.
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Isolation of mutants of Streptomyces griseus that sporulate in
nutrient rich media
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Kawamoto, S. and Ensign, J.C.
Cloning and characterization of a gene involved in regulation sporulation and cell division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
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complete cds.
                                                                                                                         /gene="ssgA"
/note="strain ATTC of Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 298.2; DB 6;
Pred. No. 6.3e-26;
0; Mismatches 68;
    /organism="Streptomyces griseus"
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                                                                                                                                                                        /codon_start=1
                                                                                /gene="ssgA"
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Best Local Similarity 83.3%;
Matches 339; Conservative
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                                                                                                                                                                                                   /trans.t.co.--
/product="Ssga"
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/db_xref="GI:9995085"
/db_xref="GI:9995085"
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Reducting branching and enhancing fragmentation in culturing
filamentous microorganisms
Patent: WO 0000613-A 1 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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Streptomyces griseus
Bacteria; Firmicutes; Actinobacteriae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 407;
                                                                                                                                               Streptomyces griseus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 298.2; DB 6;
Pred. No. 6.5e-26;
0; Mismatches 68;
/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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Sequence 1 from Patent W00000613.
AX007216 GI:9995082
                                                                                               1. .>405
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                                                                                                                                                                        /codon_start=1
                                                                           /gene="ssgA"
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.3'
Best Local Similarity 83.3'
Matches 339; Conservative
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330

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Gaps 9 90

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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(23):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nin.go.jp/

hutp://www.nin.go.jp/
hutp://www.nin.go.jp/
hutpi-language of (alt) where possible we choose an initiation codon (atg, etg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most uppstream initiation codon.
                                                                                                                                         abaB; bldA regulation; cysA; cystathionine/methionine
gamma-synthase/lyase; gntR-family; integrated element; korSA;
lysR-family; membrane protein; phosphotyrosine protein phosphatase;
pra; pSAM2; ptpA; ssgA; thiamine biosynthesis; thIC;
transcriptional regulator; traSA.
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomyclneae; Streptomycesoe;
Actinomycetales; Streptomyclneae; Streptomycesoe;
Klassi, L. (bases I to 15441)
S Redenbach, M. Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
Klashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
L. Mcroblol. 21 (1), 77-96 (1996)
                                               BCT 08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-JUL-1999) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrellgeanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the AseI-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
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                                                  linear
                                                  DNA
                                       Streptomyces coelicolor cosmid Q11.
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/clone-"cosmid 011"
complement(1, .289)
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Seeger, K. and Harris, D.
Unpublished
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abaB; bldA r
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RESULT
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GRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRT
DKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG"
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Shinichi,K. and Ensign,J.
Shinichi,K. and Ensign,J.
Cloning and characterization of a gene involved in sporulation and
cell division of Streptomyces griseus
Unpublished (1995)
5 (bases 1 to 1513)
Shinichi,K.
Direct Submission
Submitted (06-APR-1995) Kawamoto Shinichi, National Food Research
Institute, Blomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac 180
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Pred. No. 4.5e-26;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces griseus"
/strain="B2682"
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/db_xref="GI:2281004"
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385. .389
392. .802
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Best Local Similarity 83.3%;
Matches 339; Conservative
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                                                                                        795 aa; unknown function, previously sequenced as TR:053870 (EMBL:U37580), S.coelicolor hypothetical protein ORF5 downstream of phosphotyrosine protein phosphatase (159 aa). Weak similarity to the N-terminus of TR:069888 (EMBL:AL023797) Streptomyces coelicolor hypothetical protein (172 aa), fasta scores; opt: 158 z-score: 206.4 E(): 0.00036, 46.2% identity in 65 aa overlap. Continues as SCH24.40c in cosmid H24 (EMBL:AL049826)"
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/gene="SCO11.03c"
/forte="SCO11.03c, rotal probable cystathionine/methionine
gamma-synthase, len: 392 aa; previously sequenced as SW:CYSA_STRCO (EMBL:U37580), cysA, S.coelicolor putative cystathionine gamma-lyase (392 aa). Similar to many e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MTVRPVVKRTARAVLLDGDHLILIKRTKPGVDPYWVTPGGGVEP
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RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIABTGLEDDSTLRTLHLAGPPBEFTA
ERALPALGELTGEDGQAFALRASFGNAEETLEGLAAGHHDLAIGTTRPRGALHTATPL
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SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
RTGTLAMPHTARAHEWLLRAAADWN"
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/protein_id="CAB46957.1"
/db_xref="G1:5457269"
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complement(1. .4279)
/note="sequence corresponding to EMBL:U37580 from 1 to
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//note="overlap with Streptomyces coelicolor cosmid H24 (GMGL-AL049826) from 41528 to 41625"
//gene="SCQ11.02c"
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/gene="SCQ11.02c"
/note="Match to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"
/gene="SCQ11.02c"
                                                                  partial
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/gene="SCQ11.02c"
/note="SCQ11.02c, abaB, probable lysR-family
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/db_xref="GI:5457268"
complement(<1. .289)
/gene="SCQ11.01c"
/note="SCQ11.01c, hypothetical
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/gene="SCQ11.03c"
/note="cysA"
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/transl_table=11
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methionine gamma lyase (398 aa), fasta scores; opt: 608 z-score: 653.6 E(): 4.5e-29, 36.98 identity in 404 aa overlap. Highly similar to TR:Q53668 (EMBL:X91393) streptomyces antibioticus hypothetical protein found upstream of the abaB gene (232 aa) (87.1% identity in 232 aa overlap). Contains Pfam match to PF01053 ac overlap. Cys_Met_metabolism plb-dependent enzyme and PS00868 Cys_Met_metabolism enzymes pyridoxal-phosphate attachment site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGVETLVFASGMAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTYRVCFVCTGNICRSPWAEAVFRARVEDAGLGHLVEADSAGTG GWHEGEGADPRTEAVLADHGYCLDHAARQFQQSWFSRLDLVVALDAGHLRALRRLAPT ERDAAKVRLLRSYDPAVAGGDLDVPDPYYGGRDGFEECLEMVEAASTGLLAAVREQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IETPSNPGLDVCDVRRLVEAAHAGGALVAVDNTLATPLGQRPLELGÄDFSVASGTKQL
TGHGDVLLGYVAGRDAGAMAAVRRWRKIVGAIPGPMEAMLAHRSIATLQLRVDRQDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALKVAEALRTRPEITGLRYPGLPDDPSHKVASQQMLRYGCVVSFTLPSRARADRFLDA
LRLVEGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine-phosphatase (164 aa). Contains Pfam me
to PF01451 LMWPc, Low molecular weight phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5475 AIGAGCTITCTCGTGTCCGAGGAGCTCTCTTTCCGCATCCCGGTGGAGCTGCGCTACGAG 5534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2693. .3187)
/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
protein-tyrosine-phosphatase, len: 164 aa; previously
sequenced as SW:PTPA_STRCO (EMBI.U37580), ptpA,
S.coelicolor low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 acccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgacc 120
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/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PS00868 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
complement(2693, .3187)
/gene="SCQ11.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine-phosphatase"//protein_id="CAB46959.1"
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/protein_id="CAB46958.1"
/db_xref="GI:5457270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2031. . 2075)
/gene="SCQ11.03c"
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/transl_table=11
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/transl_table=11
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/protein_id="AAC28481.1"
/db_xref="G1:11066159"
/tb_xref="G1:11066159"
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RYVPLGGGRSLADDALLDBALDRILAEEQNAG"
135 c 145 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ssgA"
/note="sinilar to Streptomyces griseus SsgA; possible cell
division protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                              01-NOV-2000
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van Wezel,G.P.
Direct Submission
Submitted (18-0cr-1999) Biochemistry, University of Leiden, PO Box 9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces goldeniensis.
Streptomyces goldeniensis
Streptomyces goldeniensis
Bacteria: firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 408)
van Wazel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces goldeniensis ssgA gene uppublished
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                                                                    301; acggacaagtcggtcgctcggtcaggaacagactctgggtgacttcgaggacagcctg
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181 gtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccggctccaggtg
                                                                                                                                                                                                                                                                                                                                   AF195770 408 bp DNA linear BCT (
Streptomyces goldeniensis SsgA (ssgA) gene, complete cds.
AF195770
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                                                                                                                                                                                                                                                   361 GACGAGGCGCTGGACCGCATCCTGGCCGAGGAGCAGAACGCCGGCTG 407

    .408
/organism="Streptomyces goldeniensis"
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/db_xref="taxon:121022"

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Best Local Similarity 75.7%; Pred. No. 3.3e-20;
Matches 308; Conservative 0; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                   AF195770.1 GI:11066158
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Kradlen, R.G. and Van Wezel, G.P.
Feducing branching and enhancing fragmentation in culturing
filamentous microorganisms
Patent: WO 0000613-A 7 06-JAN-2000;
UNLY LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MSFLVSEELSFRIPVELRXETCDPYAVRLFFHLPGDAPVTWAFG
RELLIDGGPRPCGDGDVHIAPADPEFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPLGQERSLADFDALLDEALDRILAEEQNAG"
135 c 145 g 77 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycetaceae; Streptomyces
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                                   5655 GTGGGCATCGCGCCGGTGGAGCCGGAGCCGCTGGCCGAGGTGCTGATCCGACTTCAGGTC
                                                                         ggcgcggaccgcgccctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgc
                                                                                          1 atgagettectegtetecgaggagetetectteaagateceagtegaactgegatacgag
 181 giccacategeceegacegaecegagggeetgieggaegieteeateeggeieegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ssgA"
/note="strain ATCC of Streptomyces goldeniensis"
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Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
1 (bases 1 to 407)
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                                                                                                                                                                                                                     gaggccgcgctcggcaagatcctcgccgaggagcagaacgccggctg 407
                                                                                                                                                                                                                                                                                                                                                    linear

    .407
    /organism="Streptomyces goldeniensis"
    /db_xref="taxon:121022"

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Pred. No. 3.3e-20;
0; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                    DNA
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/protein_id="CAC07387.1"
/db_xref="G1:9995089"
                                                                                                                                                                                                                                                                                                                                                Sequence 7 from Patent WO0000613.
AX007222
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/transl_table=11
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75.78;
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Matches 308;
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/translation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
RELLVEGVLDAAGDGDVRVCPVGQTATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
QGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
219 c 180 g 80 t
                                                                                                                                                                                                                                                                                                                                               BCT 01-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycesor.

1 (bases 1 to 566)

van Wezel, G. P., Rousseau, C. and Kraal, B.

Cloning and sequencing of the Streptomyces albus ssgA gene
Unpublished

2 (bases 1 to 566)

van Wezel, G. P.
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241 ggcgcggaccgcgccttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc
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                                                                           Greeggrereceggreggecagaegecaccaccaggaggrecaccarcaccaeggre
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Submitted (18-OCT-1999) Biochemistry, University
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
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/organism="Streptomyces albus"
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/note="similar to
division protein"
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1 (bases 1 to 407)

Kraal, B., Luiten, R.G. and Wazel, G.P.

Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms

Patent: WO 0000613-A 5 06-JAN-2000,

UNIV LEIDEN (NL); RRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA

(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
RELLVEGVLDAAGDGDVRVCPVGQPATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
RGLLGSERANDFDSHLDDALNRSLAEEQSAG"
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Pred. No. 1.9e-17;
0; Mismatches .114;
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Sequence 5 from Patent WO0000613.
AX007220
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/note="strain ATCC of Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 29-JAN-2000
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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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phosphoribosiltransferase; DNA helicase; DNA polymerase III;
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Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac
                                                                                                               146 TGGGTCTTCGGGCGTGAACTGCTGGTCGAGGCAGGCCTGGACGCCGGGCGACG
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Colney, Norwich, Norfolk NR4 7UH, UK
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Seeger, K.J. and Harris, D.
Unpublished
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SVNERWEALGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGGFTPRHARVPRA"
1010. 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identical to previously sequenced SW.RELA_STRCO (EMBL:X87267) Streptomyces coelicolor GTP syrophosphokinase (EC 2.7.6.5) RelA 847 as and highly similar to SW:RELA_STRAT (EMBL:RF072829) Streptomyces antibioticus RelA protein, 841 as; fasta scores: opt: 4969 and to SW:RELA_CORGI. (EMBL:AF038651) Corynebacterium glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA, 760
                                                                                                                                                                                             jun/cg1-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg. grg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be the entire insert of the sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          len:
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where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Blube et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pore="SCI2.01"
/note="SCI2.01, hypothetical protein, len: >328 aa;
/note="SCI2.01, hypothetical protein, len: >328 aa;
similar to TR:033236 (EMBI:298209) Mycobacterium
tuberculoais hypothetical 49.8 kD protein MTCY174.11,
450 aa; fasta scores: opt: 843 z-score: 874.7 E.16; 0,
45.9% identity in 296 aa overlap. Contains possible
coiled-coils region"
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/note="previously sequenced region SW:SCAPTRELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptomyces coelicolor A3(2)"
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/protein_id="CAB70914.1"
/db_xref="G1:6822208"
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/gene="SCL2.02"
/gene="SCL2.02"
/note="SCL2.02" unknown, len: 46 aa"
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/clone="cosmid L2"
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/transl_table=11
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/partial
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Best Local Similarity
Matches 218; Conserv
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/note="SCL2.04c, apt, adenine phosphoribosiltransferase,
len: 182 aa; identical to previously sequenced
len: 182 aa; identical to previously sequenced
swa.pr_STRCO (EMBL:X87267) Streptomyces coelicolor adenine
phosphoribosyltransferase (EC 2.4.2.7) Apt, 182 aa and
highly smilar to SW.APT_ECOLI (EMBL:M14040) Escherichia
coli adenine phosphoribosyltransferase (EC 2.4.2.7) Apt,
183 aa; fasta scores: opt: 600 z-score: 682 8 E():
1.2e-30; 54.8% identity in 168 aa overlap. Contains Pfam
match to entry PF00156 Pribosyltran, phosphoribosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3273. .7460)
/note="previously sequenced region SW:SCSECAPT EMBL:X85969
S.coelicolor secb, secF & apt genes"
complement(378 .3781)
complement(3704 .4568)
aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.7% identity in 774 aa overlap. Contains Pfam match to entry PF01842 ACT, ACT domain and match to Prosite entry PS00017 ATP/GTP binding site motif A (P-loop)"
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DRVLVVDDVLATGGTAEASLELIRRAGAEVAGLAVLMELGFLGGFRRNLEPALAGAPLE
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ETVRKMVVAMAKDPRVLVIKLADRLHNMRTMRYLKREKQEKKARETLEIYAPLAHRLG
                                                                                                                                                                                                                                                                                                                                                          MNTIKWELEDLAFAILYPKMYDEIVRLYAERAPKRDEYLAVYTDEVOODLRAARIKAT
YARRKHYYSYVKMIVRRDPAEIYDLYGIRKLYDTVRDCYAALGYYHARWNPYDGR
FKDYIAMPKDNWYQELHTYUIGGGRPVELOIRTFDMHRAEYGIAAHWKYKOEAVAG
ASKVRTDAPKSSGKSKDDHLNDMAWLRQLLDMOKETEDPGEFLESLRPDLSRRDFYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPKGDVIALPAGATPVDFAYAVHTEVGHRTIGARVNGRLVPLESTLDNGDLVEVFTSK
AAGAGPSRDWLGFVKSPRARNKIRAWFSKERRDEAIEQGKDAIVRAMRKQNLPIQRIL
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SRGRGRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIIGFVTRGSGVSVHRSDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVDSLSREPERILEVEWAPTQSSVFLVAIQVEALDRSRLLSDVTRVLSDQHVNILLSAA
VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
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                                                                                                                                                                                                                                /translation-"MPDEAQPLTAAKPESASASAAKPAPSAPQAKNDTHGPIQHAPAA
PVDKPAEQQPRPKPLPAERPQNAPVVRAPAGQPARSGSSNRVRARLAKLGVQRANPYN
                                                                                                                                                                                                                                                                                        PVLEPLLRIVRGNDPKIETSTLRQIERAYQVAERWHRGQKRKSGDPYITHPLAVTTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15" complement(2378. .2401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00156 Pribosyltran,
domain, score 150.30, E-value
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Purine/pyrimidine phosphoribosyl transferases signature"
/codon_start=1
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EMBL:X87267 S.coelicolor apt & relA genes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="adenine phosphoribosiltransferase"
/protein_id="CAB70916.1"
/db_xref="GI:6822210"
                                                                                                                                                    /product="GTP pyrophosphokinase"
/protein_id="CAB70915.1"
/db_xref="G1:6822209"
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/note="Pfam match to entry
Phosphoribosyl transferase
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/gene="relA"
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                                                                                                                                    /transl_table=11
                                                                                                            /codon_start=1
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Submitted (16-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCT 16-JUL-1999
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1 (bases 1 to 35284)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                              /gene="sec;"
/note="SCL2.05c, secf, protein-export membrane protein,
len: 373 aa; identical to previously sequenced
SW.SECF.STRC0 (EMBL.X85969) Streptomyces coelicolor
protein-export membrane protein Secf, 373 aa and similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinashi, H. and Hopwood, D.A. set of cordered cosmids and a detailed genetic and physical map has to for ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                             35030 TGGCCTCGTTGTGTCGAGCGAGTCCTCCTGCCTGTCCCCGCAGGCCTGCGGGTACGACA 35089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35090 CGCCCGACCCCTACGCGTGCCACCTTCCACACCGGAGCCGAGGAGACCGTCGAGT 35149
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                                                                                                                                                                                                                                                                                                                                                     2 tgagettectegtetecgaggagetetectteaagateceagtegaaetgegataegaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tecacategeceegacegaeceegagggeetgteggaegteteeateeggeteeaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 gegeggacegegeectetteegtgeaggegeecegeegetggtegeetteetegaeegea
                                                                                                                                                                                                                         Length 38640;
                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                         28.2%; Score 114.8; DB 1; 55.9%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                         0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor cosmid E19A. AL096852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35390 CGCACATCCTGGCGGAAAGCTAGGGCGGGG 35419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 aggccgcgctcggcaagatcctcgccgagg 391
complement(4501. .5622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 35284)
Seeger, K. and Harris, D.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL096852.1 GI:5531349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 35284)
                                                                                                                                                                                                                                                                                         Conservative
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COMMENT

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aa overlap)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):478-4778(1994) as implemented at http://www.nih.go.jp/

Nucleic Acids Research, 22(22):478-4778(1994) as implemented at http://www.nih.go.jp/

Nucleic Acids Research, 12(22):478-478 as implemented at http://www.nih.go.jp/

Jun/cgl-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. Tif this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most imposured clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapp between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the Asel-E genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCE19A.01"
/note="SCE19A.01, hypothetical protein, partial CDS, len:
/al asi unknown function, similar to members of the alkyl
hydroperoxide reductase C/thiol-specific antioxidant
family e.g. TR:053226 (EMBL:AL021185), bcp, Mycobacterium
tuberculosis bacterioferritin comigratory protein (157
aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06,
/codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 aa; unknown function, similar to many e.g.
SW:Y03Q_MYCTU (EMBL:273902) Mycobacterium tuberculosis
SW:Y03Q_MYCTU (EMBL:273902) Mycobacterium tuberculosis
sw:Y03Q_MYCTU (EMBL:0.2000) Mycobacterium tuberculosis
z-score: 743.6 E(): 0, 52.0% identity in 200 aa overlap.
Similar to SW:YGGV_ECOLI (EMBL:028377), yggv, Escherichia
coli hypothetical protein (197 aa) (49.5% identity in 198
                                                                                                                                                                                                                                                                      (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                 sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(243. .845)
/gene="SCE19A.02c"
/note="SCE19A.02c, conserved hypothetical protein, len:
.
Innes Centre, Norwich Research Park,
                                                                                                                         Streptomyces coelicolor sequencing at The Sanger Centre is fu
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="tRNA Leu anticodon TAG, Cove score 69.78"
/product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="IVVDEQGKVERALYNVRATGHVAKIIKDLGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .35284 /organism="Streptomyces coelicolor A3(2)" /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SCE19A.01
/product="hypothetical protein"
/protein.id="CAB50982.1"
/db_xref="GI:5531350"
       David A. Hopwood, [3] John Lunes Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(243. .845)
/gene="SCE19A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="cosmid E19A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCE19A.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <1. .97
                                                                                                                                                                                                                                                                                                                                                                                               strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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FEATURES

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/product="hypothetical protein"
/protein_id="cab50983.1"
/db_xref="G1:5531351"
/translation="WTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                           TGVTFAENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARWAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGOLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=SCE19A.03c
/product="putative secreted protein"
/product="putative secreted protein"
/protein_id="CAB50984.1"
/db_xxef="c01:5AB1352"
/translation="WAASRHRERRTVTAVATVATTALTAGLTTGCDAVDKALDCVRT
ADAIADSVTELOQAVENADDFTQWEESLNSIDKNLDRIGDGTDNTDVNKAVDDLGKAV
DNVRTSVARGDETPBLESPVTDAAGELTKVCTP"
complement(1201. 1233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1454. .2191)
/gene="SCE19A.04c"
/note="SCE19A.04c"
/note="S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein, len: 134 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCE19A.05c, hypothetical protein, len: 77 aa;
windnown function, similar to parts of many sugar permeases
e.g. TR:P96159 (EMB:1065013), malX, vibrio Lurnissii PTS
(phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSRIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEGVPRWRKGSGEGWVTAEYAMLPRATNTRGDRESVKGRIGGRTHEISRLIGRSLRAV
IDYKALGENTVVLDCDVLQADGGTRTAAITGAYVALADAVAWAQGRKLIKANRKPLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown function, probable CDS suggested by GC frameplot, positional base preference and amino acid composition. Contains probable Vierminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSAVSVGIVDGTPLLDLRYEEDVRADTDMNVVCTGDGRFVEVQGTAEAEPFARDELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF01138 RNase_PH, 3'
exoribonuclease family, score 266.70, E-value 3.1e-76"
complement(1805 .1843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS01277 Ribonuclease PH signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SCE19A.03c, possible secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative ribonuclease PH" /protein_id="CAB50985.1" /db_xref="GI:5531353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLLDLATAGCTELAELQRKALDATLER"
complement(1511. .2185)
/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCE19A.05c"
/note="sce10a.05c"
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/gene="SCE19A.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(892. .1296)
/gene="SCE19A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(892. .1296)
/gene="SCE19A.03c"
/codon_start=1
/transl_table=11
/label=SCE19A.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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Eur. J. B
87275916
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                                                                                                                                                                                                                                                                                                                                                                                                               repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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VERSION
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                                                                                                                                              gene
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                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SC8A11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                       /translation="MASKAEKIVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK AAGAHGVVKMGTAIQVVIGTDADPIAAEIEDDM"
complement(2385. 2489)
/gene="SCE1994.05"
/note="Pfam match to entry PF00367 PTS_EIIB,
phosphotransferase system, EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 26-APR-1993
     scores; opt:
ty in 77 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1410)
Dehottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J.,
Erpicum, T., Frere, J.-M. and Ghuysen, J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                                                                                                                                                                                                                                                                                                                                                             (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system) permease for glucose (523 aa), fasta scores; op 217 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 a overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2660. .3955
//gene="SCE19A.06"
//note="SCE19A.06, possible PTS transmembrane component,
len: 431 at, similar to many PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20322 rGCGGGTGTGGCCGTCGAAGACGGAGGCCGCAGCGTCGTACTCGTCGTCGTGAGCAGCC 20381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tecacategeceegacegacecgagggeetgteggacgtetecateeggetecaggtgg 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cccgggatccctacgcggtgcggatgaccttccacctccccggagacgcctgtgacct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tgagottcctcgtctccgaggagctctccttcaagatcccagtcgaactgcgatacgaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10202 CGGACGATCCCTACGCGTGCACTCCACATCGACTCGGCCACCGGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcgcggaccgcgcctttccgtgcaggcgccccgccgccgctggtcgccttcctcgaccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 35284;
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Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STMLACBG 1410 bp DNA S.albus beta-lactamase gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 108.2; DB 1;
Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 168;
                                                                                                                        /product="hypothetical protein"
/protein_id="CaB50986.1"
/db_xref="GI:5531354"
                                                                                                                                                                                                                                                                                       2660. 3955
/gene="SCE19A.06"
2660. 3a55
                                                                                       /transl_table=11
/label=SCE19A.05c
                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20502 CCGAGCTGCTCGCCAGG 20518
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.6%;
Best Local Similarity 55.4%;
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 aggccgcgctcggcaag 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M28303.1 GI:153338
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SOURCE
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/traislation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
SVSDAERRLAGLERASGARLGVYAVDTGSGRTVAVRADELEPPMCSVRTLSSAAVLRD
LIDNGEFLSRRILYTQDDVGQAGGAGPETGKPQNLANAQLTVEELCEVSITASDNCAA
NLMLRELGGPAAVTREVRSLGDRVTRLDRWEPELNGAEPGRYTDTTSGRAITRYGRL
VLGDALNPRDRRLLTSWLLANTTSGDRFRAGLPDDWTLGDKYTGAGRYGTNNDAGVTWP
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Streptcomyces coelicolor cosmid BAI1.
AL391041.
AL391041.
AL391041.
AL391041.
AL391041.
AL391041.
AL391041.
AL391041.
Anison acid transport integral membran protein; branched amino acid transport system binding secreted protein; branched amino acid transport system permease; integral membrane protein; ion transport integral membrane protein; polysaccharide blosynthesis protein; regulator; regulatory protein; polysaccharide blosynthesis protein; regulator; protein; secreted amidase; secreted peptidase; secreted peptidase; secreted protein; sigma factor; transcriptional regulator; transcriptional regulatory
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Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A. A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95.4; DB 1;
Pred. No. 0.0095;
0; Mismatches 26;
                                                                                                                                /organism="Streptomyces albus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų
beta-lactamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
                                                                                                                                                                                                                                                                                                                                                                          /product="beta-lactamase"
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/db_xref="GI:153339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1204. 1216
/gene="beta-lactamase"
/note="inverted repeat"
1230. 1242
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540 c 496 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="beta-lactamase"
                                                                                                                                                                                                                            /gene="beta-lactamase"
243. .1187
                                                                                                                                                                                                                                                                                            /gene="beta-lactamase"
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                                                                                                                                                                            /db_xref="taxon:1888"
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.4%;
81.0%;
                                                                                                                                                              /strain="G"
                                                                                                                                                                                                                 243. .1242
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Matches 111; Conservative
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon at the sequence MAY NOT be the entire insert of the sequenced clone. If may be shorter because we only sequence coverlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                      3 (bases 1 to 32704)
Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note" nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial regulatory proteins, luxR family and match to Prosite entry PS00622 Bacterial regulatory proteins, luxR family signature. Also contains a possible helix-turn-helix motif at residues 699. ,720 (+3.25 SD)"
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/note="SCBAll.01, possible transcriptional regulator
/note="SCBAll.01, possible transcriptional regulator
/Exagment), len: >750 as; similar to TR:095124
(EMBL.ALl09747) Streptomyces coelicolor probable
transcriptional regulator ScJ21.13, 919 as; fasta scores:
opt: 818 z-score: 913.7 E(): 0; 32.6% identity in 775 as
overlap. Contains Pfam match to entry PF00196 gerE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor),
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative transcriptional regulator (fragment)" /protein_id="CAC01573.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrellésanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
Mol. Microbiol. 21 (1), 77-96 (1996)
97000351
                                                                                                                                                                                                                                                                                                                                                                                                                           Colney, Norwich, Norfolk NR4 7UH, UK
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                                                                                                   Saunders, D.C. and Harris, D.
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/gene="SCBA11.01"
<1. .2254
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/gene="SC8A11.01"
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/transl_table=11
                                                                          (bases 1 to 32704)
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                                                                                                                                          Unpublished
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   JOURNAL
MEDLINE
                                                                                                      AUTHORS
JOURNAL
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                                                                          REFERENCE
                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                 AUTHORS
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complement(3297. 7058)

complement(3297. 7058)

/gane="SC8A11.04c, probable secreted peptidase, len: 1253

/gane="SC8A11.04c, probable secreted peptidase, len: 1253

aa: similar to TR:09KL54 (EMBL:AL121566) Streptomyces

coelicolor probable secreted peptidase SCF51A.10, 1245

fasta scores: opt: 1827 z-score: 1848.13 (F): 0: 37.24

identity in 1300 aa overlap, to TR:P95684 (EMBL:B8367)

Streptomyces albogriseolus subtilisin-like protease, 1102

aa; fasta scores: opt: 1365 z-score: 1380.6 E(): 0; 33.44

identity in 1268 aa overlap and to Streptomyces coelicolor probable secreted peptidase SC8A11.16c, 1239 aa; fasta scores: opt: 1835 z-score: 1467.4 E(): 0; 46.94 identity in 1279 aa overlap. Contains Pfam matches to entries PROMO82 peptidase_288, Subtilase family and PF02225 PA, Adomain and matches to Prosite entries PSO0136 Serine proteases, subtilase family, histidine active site and PS00138 Serine proteases, subtilase
                                  VRARI LQRAAGNPLALVELPRAAQGI SPPLDDLPLTQRLETAFASRTDSLTRECRTFL
LVLAAEPTAPLNQLLDVASRLAGSEVTVYALQEAVDAGLVVLTGRTPEFRHPLMRSAI
                                                                                                                                                                                  ARIMLVSDKAAFEPDEPQRRIQDMIDAAAGAFDVGSTSVÄENLLWRAAARCFFQDGDA
RVRAQAAAELDRWKPDPDAPHVLTVRAYTEPYRRGTDLIARLEKLRPDREDGRLLHYL
                                                                                                                                                                                                                                                            GSGSMAIGDVGRATRYLAQAASVWRSQGRLGLLARSLAGSWPRLYLGQLAQAREESAE
GIAALAERTGRAIVWLGLRATSALTAYLEGBREBAARSYNELARHSLEPPWPFASYWAQ
GIVGGLIAALFDSRAVBACARAFDRTDPHYHSTSRWLLVPDIVDAAAAARAKBCARE
LLVELPELADRIPSEWMIVARTYSTAVLAPDDTAEDCYDSALSALPDTWPLARARLHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SCBAll.03"
/gene="SCBAll.03"
/note="SCBAll.03, possible regulator, len: 156 aa; similar
to TR:095277 (EMBL:AL096852) Streptomyces coelloolor
putative regulator SCE19A.24, 142 aa; fasta scores: opt:
272 z-score: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                                                                                                                   LAAAVPALRQAGELVHDPRRQTGLLVRAAELASEINDRVQAQILLNRADLAEPGPTER
                                                                                                                                                                                                                                                                                                                                                                                                               QHGRRLRRQRRNVDARKPLRLARDEFDRVGAQPWADMAREQLRAAGESDGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDHPLLVTIRFAPEGAPPVTWHVGRDLLHEGLRTTSGLGDVQVWADTPTDRETAWLQV
NAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
complement(3297. .7058)
                                                                                                            YTRATVADRLSTHRALAETLEGSPGRRLVHLAAATLGPDDELAGQLERFADDAQKRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MASAAATAGTAGALPVMSGQAHADTRGLPSLWDVDRSVVNPENA
YTVTVDQVRAEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
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/translation-"IGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2093. .2176
/gene-"SC8A11.01"
/note-"PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2042. .2239
/gene="SC8A11.01"
//note="Pfam match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 49.10, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical protein SCBA11.02c"
/protein_id-"CAC01574.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2184. .2453)
/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
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/protein_id="CAC01575.1"
/db_xref="GI:9716214"
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complement(2184.
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/gene="SC8A11.03"
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/transl_table=11
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/db_xref="G1:9716215"
/translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAGĀROLLINDGYGKFDPWADLPEAAPLPVASLGTDDSARLLARFRGAGTTĪRVVS
HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSOGRAVEYRQDISLLGO
PLGIVPTQVRAQGELTSWYTADDDVRWVSFASRPDLGORGVARSYEPRSTTRETWFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IOHPRILISDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGE
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                                                                                                                                                                                                                                                                                                                      GPTRVLTLITGDRVTVTGEDGAETVLSVTDPHGRSGGAHVMTVGSDTYVYPDAAVPYL
                                                                                                                                                                                                                                                                                                                                                           GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
IRGAAISAEHSRAADFWTSLTGTGDAAAGGSAARSATSGGRLAGGIAKVWLDGKVRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLGEDVNERIVMVGGLSPGPKPYRLVLEGSRNLPDRPYSTRTRTVWDFTSATTDPTRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCBAII.04c"
/note="Pfam match to entry PF02225 PA, PA domain, score
19.00, E-value 0.058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2896 TTCCGGCGGAGTTCCGTTACGATCCCGACCACCCCTCCTCGTCACGATCCGCTTCGCCC 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 teceeggagaegeetetgtgaeetgggeegtteggeeggggagetgetegaegggatea 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 cgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggtcaggaacagactc 337
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tamily, serine active site. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGVGQTLIRAFGLR"
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Pred. No. 0.025;
0; Mismatches 146; Indels 0;
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                                                                                                                                                               /product="putative secreted peptidase"
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                                                                                                                          /transl_table=11
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54.78;
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KEYWORDS
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codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
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The length in codons is given for each CDS.

CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot http://www.nih.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bentley.S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A. Bentley.S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A. Direct Submitssion
Submitted (07-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; Streptomycineae; S
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finethylaminohydrolase, len: 258 as; hydrolyses
asymmetrically methylated arginine with preference
dimethylated arginine over monomethylated arginine
regulator; thiolase; transferase.
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//note="Nominal overlap with cosmid 4C6"
complement(83. .859)
/gene="SC5F2A.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces
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                                                 Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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/gene="SC5F2A.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="A3(2)"
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Oliver, K. and Harris, D.
Unpublished
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gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to many egs. TR:086699 (EMBL:AL001515) UvrA-like protein from Streptomyces coelicolor (796 aa) fasta scores; opt: 2047, z-scores 12164.0, E(): 0, (51.9% excinuclease ABC subunit A from Escherichia coli (940 aa) fasta scores; opt: 634, z-score: 669.2, E(): 5.8e-30, (33.9% identity in 938 aa overlap). Contains two Pfam matches to entry PF00005 ABC_tran, ABC transporter and two. Prosite matches to $800017 ARP/GTP-binding site motif A process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"UvrA-like ABC transporter"
/protein_ld-"CAB40669.1"
/db_xref="GI:484466"
/db_xref="SPTREMBL:09X7M5"
/db_xref-"SPTREMBL:09X7M5"
/translation-"MSEFISTIGARENNLODVTLRIPKGRLTVFTGVSGSGKSSVVFD
/Lranslation-"MSEFISTIGARENNLODVTLRIPKGRLTVFTGVSGSGKSSVVFD
/ITANESRRQLNETFWPVRNLEWYERPHADALEGILPPAIVVDQRPVGGHSRSTVGTM
TDIHSVLRVLFSRHGTPGAGGATAYSFNDPSGMCPGCDGLGRRVQPDMDRILDPARSL
                                                                                                                                                                                                                   /product="dimethylarginine dimethylaminohydrolase"
/protein_id="CAB40668.1"
/bc.xref="GI:4584465"
/db_xref="S-PROT:Q9X7M4"
/translation="MPSKKALVRRPSPRLAEGLVTHVEREKVDHGLALEQWDAYVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADGAVREPPFAAGTWOGOTYTWTEELDTGKPVGDFTAAERAFLARGREGSKVTVSGSG
GTWSTEYEGLADRFERLYLKRDLSGNSERTRDLVNGFDVBARCPDCGGARLNAAALAS
TIDGHSIADCSRWQITDLIAVLNGFDDPVALPVAGAAVAALERVERIGLGYLSLDRET
ATLSGGEGORLKTVRHLGSSLTGMYYTPDEPSYGLHPRDVGRLGDLLIALRDKGNTVL
VVEHDPDVIALADHVVDMGPRAGADGGRVVFEGTPAGLAASDTLTGRCLGRRTAVKDT
                                                                                                                                                                                                                                                                                                                                                                                 GAHGWETLEVDPADDCPDSVEVEDAVVFRNVALITRPGAESRRAETAGVEEAVARLG
CSVNMVWEPGTLDGGDVLKIGDTIYVGRGGRTNAAGVQQLRAAFEPLGARVVAVPVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLHLKSAVTALPDGTVIGHIPLTDVPSLFPRFLPVPEESGAHVVLLGGSRLLMAASAP
TAELLADGGBEVLVDIGBFEKLEGCVTCLSVRLRELYD"
Complement (976, 2324)
/gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRAPTGELWVKGAERHNLREVTVAFPTGVLTAVTGVAGSGKSTLVAELTGAHPDAVVV
DQSAIGISARSTPATYLGIMDTVRKVFARETGAEPGFFSFNSAGACGTCEGRGIIHTD
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ALLDRLVDAGNTVVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
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/gene="SCSF2A.03c"
/note="SCSF2A.03c, probable ABC transporter, len: 544aa;
similar to many involved in antiblotic resistance egs.
                       NG,NG-dimethylarginine dimethylaminohydrolase from Homo sapiens (285 aa) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 aa overlap)." /codon_start=1
(experimental). Similar to TR:D1038106 (EMBL:AB001915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (P-loop). Also contains possible membrane spanning hydrophobic regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transporter, score 35.60, E-value 4e-08." complement(3118. .3141) //gene="SCERA.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1090. .1803)
/gene="SC5F2A.02c"
/note="Pfam match to entry PF00005 ABC_tran, ABC transporter, score 101.40, E-value 1.7e-26."
/gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(976. .3234)
/gene="SC5F2A.02c"
/note="SC5F2A.02c, UvrA-like ABC transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement(2002. .3162)
/gene="SC5F2A.02c"
/note="Pfam match to entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3245. .4879)
/gene="SC5F2A.03c"
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/label=SC5F2A.02c
                                                                                                                                                          /transl_table=11
/label=ddah
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gene

CDS

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/db_xref="Spremal:09x7m6"
/translation="MSTSPTSLTCTSLSFAWPDGTEVFDGLDVAFGPGRTGLVGLNGAGKSTLLKLIAGRLTPADGTVRYAGQYGYLPQNYTLDYALRYDPALRYDBALGIDGRRALLHAIE
AGDVREHFETVGDDMDVERRALATGELGLDHIGLDRYGEVSGGESVLLRLAALLL
RRPDVLLLLDFPTNNLDYYARRRLYAA/BSWPGYWVVYSHDRELLDRYDQIADLRAGSY
TWYGGNLTAYEBALAVEQBABRRNYAVAESDLRRQKRELADAQVVLARRRRYGGKMYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKREPRAVMKLRARTAQÖSAGKYRIMHEEKLAGAKERLDDAVEAVRDDDEIRVDLPYT
YVPORFWYLTLTLAALELAYGARVAGGLDHGPERTALLGKNGAGKTTLLETVAGEELAPV
AGEATAHVPLRFLPORLDVLDDGETVARNARFAPGATNNRTRALLARFLFRGARADO
QAATLSGGERFRAALAMLAEPAPQLLIMLDBPTNNLDMASVRQLTGALEAYEGALLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ñ
TR:054381 (EMBL:X79146) from the lincomycin-production gene cluster of Streptomyces lincolnensis 78-11 (578 aa) fasta scores; opt: 1624, 2-score: 1696.3, E(): 0, (50.3% identity in 541 aa overlap). Contains two Pfam matches to entry PF00005 ABC_tran, ABC transporter, two Prosite matches to PS00017 ATP/CTP-binding site motif & (P-loop) and Prosite match to PS00211 ABC transporters family signature. Also contains a possible colled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4739, .4762)
/gene="SC5F2A.03c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6297 GCGTCTCGTCGCCGCCGCGCGCGTATGCCGAGCATTCCCGCCACCCTGCACTACGACCG 6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ccgggatccctacgcggtgcggatgaccttcc----acctccccggagacgcgcc 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 cgaccgcacggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgagga 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="PS00211 ABC transporters family signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 gagetteetegteteegaggageteteetteaagateeeagtegaactgegataegagae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 tgtgacctgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Pfam match to entry PF00005 ABC_tran, ABC transporter, score 143.80, E-value 3.1e-39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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0; Mismatches 161; Indels
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                                                                                                                                                                                                                                                                                                                                              /product="putative ABC transporter"
/protein_id="CAB40670.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3290. .3787)
/gene="SC5F2A.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4942. .5850
/gene="SC5F2A.04"
4942. .5850
                                                                                                                                                                                                                                                                                                                    /label=SC5F2A.03c
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/transl_table=11
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Local Similarity 53.9%;
les 209; Conservative
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Search completed: July 18, 2002, 11:22:48 Job time: 13778 sec

THIS PACE OF WAR IN THE STORY

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18-APR-2000
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Streptomyces netro Streptomyces grise Streptomyces golde Streptomyces albus Streptomyces albus S. spinosa DNA fra S. spinosa DNA fra Streptomyces clavu Streptomyces clavu
SUMMARIES	AA249731 AA249727 AA249727 AA24720 AA24729 AAF88315 AAF88312 AAF88312 AAD14511
DB	22 22 22 22 22 22 22 22
% Query e Match Length DB	407 407 407 407 407 45624 50000 1227 15079
% Query Match	100.0 73.3 73.3 61.1 55.2 17.4 11.9 13.9
Score	298.2 298.2 298.2 248.6 224.6 70.8 70.8 56.4
Result No.	0 4 5 9 7 8 9 9

(UYLE-) RIJKSUNIV LEIDEN.

1	<u>-</u>		38734	20	AAZ32020	Human METH1 relate
Н	S		38734	22	AAC90077	AL021529 CDNA clon
1			109519	22	AAS08693	Micromonospora DNA
Н	54.		15079	16	AAQ91580	S. clavuligerus cl
1	51.		3241	24	AAS18442	Contig 93 DNA enco
1	51.		65140	22	AAD17184	Streptomyces nours
1	51.	12.7	125401	22	AAD17186	Streptomyces nours
c 1	20	12.4	3957		AAA09686	HSV-2 immediate ea
1	8 50.4	12.4	80161			DNA fragment of Sa
Т	2	12.4	154746		AAD25519	Human herpesvirus
c 5	50	12.4	154746			Human herpesvirus
2		12.3	1761		AAA58473	Nucleotide sequenc
7	49.		2791		AAQ99776	Phosphomycin biosy
2	49.		58857		AAA58471	
2	4	12.0	2249		AAT74283	
2	4		2279		AAT74281	Cellulose binding
7	26 49	12.0	2300	18	AAT74282	Cellulose binding
7	4		3187		AAT10922	Laccase gene. Myc
7	4		3192	18	AAT63318	
7	4		3192	21	AAZ24236	M. thermophila lac
3	4		4213	22	AAD06345	Sorghum dwarfing g
3	4		6827	22	AAD06344	Sorghum full lengt
3	48.		1161	15	AAQ63295	Consensus seguence
3	48.	12.0	3954	23	AAS51481	Pseudomonas aerugi
Э	48	11.9	978	22	AAD14506	S. clavuligerus cl
c 3	48	11.9	3855	12	AAQ13287	P.denitrificans ge
9	48	11.9	11604	22	AAD14501	Streptomyces clavu
С 3	48.		29879	14	AAQ46806	
3	4		44377	18	AAT78508	
3	4		44377	18	AAT80414	Platenolide syntha
4	4		1425	23	AAS54344	
4	47.		2312	14	AAQ35141	srmR coding seguen
4	47.		2799	19	AAV49431	Bovine herpesvirus
4	47.	11.7	3382	14	AAQ48249	Bovine herpesvirus
4	4		3519		AAQ94352	BHV1 gI glycoprote
4	5 47.4	11.6	3192	18	AAT72106	Myceliophthora the

ALIGNMENTS

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mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agent; antagonist; biomass; ds.
                                                                                         ssgA; liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                       1..405
/*tag= a
/label= SsgA_protein
                                                                                                                                                                               Location/Qualifiers
                                                                   Streptomyces netropsis ssgA gene.
  BP.
                                                                                                                                                                                                                                                                                                     98EP-0202148.
                                                                                                                                                                                                                                                                                99WO-NL00395
AAZ49731 standard; DNA; 407
                                            (first entry)
                                                                                                                                                         Streptomyces netropsis.
                                                                                                                                                                                                                                   WO200000613-A1
                                                                                                                                                                                                                                                                               25-JUN-1999;
                                                                                                                                                                                                                                                                                                     26-JUN-1998;
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                                                                                                                                                                                         mat_peptide
                                                                                                                                                                               Key
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Matches
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                                                                                                                              The present sequence is a DNA (ATCC 23940) encoding S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour agents, antimigraine agents, hebbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigratine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ggcgcggaccgcgccctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 acggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctg 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggcgcggaccgcgcctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccggctccaggtg
                                                                        Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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0
                                                                                                                                                                                                                                                                             Length 407;
                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                           Sequence 407 BP; 63 A; 151 C; 131 G; 62 T; 0 other;
WETENSCHAPPELIJK ONDERZO
                                                                                                                                                                                                                                                                             DB 21;
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                                                                                                                                                                                                                                                                           100.0%; Score 407; DB 21, 100.0%; Pred. No. 6.9e-67,
                                                                                                                                                                                                                                                                                                  Mismatches
                     Luiten RGM;
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                                                                                                          60pp; English.
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                                                                                                                                                                                                                                                                                      dest Local Similarity 100. Matches 407; Conservative
                   В,
(NEWE-) NEDERLANDSE ORG
                                          2000-147269/13
                                                                                                          Disclosure; Fig 5;
                                                     P-PSDB; AAY44652
                     Wezel GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour agents, antimigraine agents, herbicides, antiparaslic agents, runniant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%; Score 298.2; DB 21; Length 407; 83.3%; Pred. No. 8.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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/label= SsgA_protein
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                                                Location/Qualifiers
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Streptomyces griseus.
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339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      RIJKSUNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine
                                                                                                                                                                                     mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterotaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; biolinsecticide; receptor agontst; antagonist; biomass; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIJKSUNIV LEIDEN.
NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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Pred. No. 8.4e-47;
                                                                                                                                                                       culture; filamentous bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                     /product= "SsgA protein"
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                                                                                                                                            Streptomyces griseus ssgA gene-1.
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                                                      AAZ49727 standard; DNA; 438 BP
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                                                                                                                                                                                                                                                                                                         31..438
/*tag=
                                                                                                                                                                                                                                                               Streptomyces griseus.
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                                           4A249727
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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, runinant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                            mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 21386; bioinsecticide; receptor agonist; antagonist; biomass; AS.
                          ggcgcggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc
                                                                                                                                                                                                             271 ggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgg
gtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccggctccaggtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhancing fragmentation in filamentous improve their liquid culturing properties
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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/label= SsgA_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasiic agents, runinant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyketide synthase; biosynthesis;
transgenic plant; insect resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atgagetteetegteteegaggagetegeetteegeateeeggtggagetgeggtaegag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcaccctccaggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 accgaccagggettgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctc
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                                    Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                           Score 224.6; DB 21; Length
Pred. No. 3.3e-33;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 407 BP; 57 A; 150 C; 139 G; 61 T; 0 other;
                                                                                           Disclosure; Fig 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. spinosa DNA fragment SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forosamine; trimethylrhamnose; spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.2%;
Best Local Similarity 72.0%;
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
 P-PSDB; AAY44650
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                                                                                                                                                                                                                                              acctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     ggcgcggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc 300
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                                                                                                                                  9.
                                                                                                                                                                   1 atgagetteetegteteggaagaacteteetteegtatteeggtggagetgegttaegag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 3004; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gggagcgaccaggcgatgttccggggtcggcacggcgccgctggtggccttcctggaccgc
                                                                                                                                  atgagetteetegteteegaggageteteetteaagateeeagtegaaetgegataegag
                                                                                                                                                                                                                                                                                   tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac
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                                                                                                                                                                                                                                                                                                                                                                                                gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                                                                                             0;
                                                          Length 407;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 T; 0 other;
                                                        21;
                                                                                             66;
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                                                      Score 248.6; DB
Pred. No. 1.2e-37
                                                                                             Mismatches
 A; 135 C; 145 G;
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SsgA_protein
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1..405
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0
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                                                      61.18;
75.78;
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                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces albus G.
26
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                                                                         Similarity
 BP;
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Sequence 407
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                                                                                           308;
                                                          Query Match
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AAZ49729 RESULT

360

240 240 300 300

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Gaps

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Length 407;

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Eberz G,

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to clentify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylihamnose to a spinosyn or polyketide anglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in forcesamine, trimethylrhamnose and polyketide synthase biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24589 tcggcgtggagctgcggtacgacagccgcaatccgtacgagatctccatgaagctcaacg 24648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzymes for spinosyn biosynthesis, useful for insecticidal spinosyns and their derivatives
                                                                                                   polyketide synthase; biosynthesis;
transgenic plant; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                teceagtegaactgegataegagaeeeegggateeetaegeggtgeggatgaeetteeaee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.8; DB 22;
Pred. No. 6.3e-05;
0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Page 14-31; 354pp; German.
                                                     S. spinosa DNA fragment SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ж,
                                                                                                                              spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
                                                                                                        Forosamine; trimethylrhamnose;
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ilarity 52.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                             99DE-1057268
                                                                                                                                                                                                                                                                                                                                                                                                                 99DE-1040596
  (first entry)
                                                                                                                                                                                                            Saccharopolyspora spinosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moehrle V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-267102/28.
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Best Local Similarity
Matches 181; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-1999;
     28-AUG-2001
                                                                                                                                                                                                                                                                                                             08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contriby, instituting and the properties of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (i) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raises specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of consents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in consemine and trimethylrhamnose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (1) to identify, inactivate or modulate genes involved in the blosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20799 AGCTTGCGGACTTCTTGAACGACACCTACGACGTGGTCGAACCTGGTGATGAACACCGGT 20740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21036 TCGGCGTGGAGCTGCGGTACGACACGCCGAATCCGTACGAGATCTCCATGAAGCTCAACG 20977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20859 TGGTCGTGATCGAGATGAGCTCGCCGTCGGGGCAGGCCTCCTTCGAGGTGAATGCTGACC 20800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20976 TAGGCACGGACGGTCAGGTGGACTGGGTGATCGCCCGCGACCTGCTGGCCGACGGGCTGA 20917
                                                                                                                                                                                                                                                          enzymes for spinosyn biosynthesis, useful for insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 acgiciccaticoggicicoaggigggoggggacogcgccctcitcogigcaggcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 tecceggagaegegeetgtgaeetgggeegtteggeegggagetgetgetegaegggatea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 accgcccgagcggcgacgtccacatcgccccgaccgacccagggcctgtcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 45624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45624 BP; 7933 A; 14913 C; 14940 G; 7838 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20739 GGATGAACGACGACGAGGTGTGAGCCAGCTGCTCGCACAACCT 20694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 tgggtgacttcgaggacagcctggaggccgcgctcggcaagatcct 383
                                                                                                                                                         Salas JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.8; DB 22;
Pred. No. 6.3e-05;
0; Mismatches 162;
                                                                                                                                                         Velten R,
                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 58-74; 354pp; German.
                                                                                                                                                         ж,
                                                                                                                                                         Froede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.4%;
Best Local Similarity 52.3%;
Matches 181; Conservative
99DE-1057268
                                                   99DE-1040596
                                                                                                                                                                                                                                                             New nucleic acid encoding recombinant production of
                                                                                                                                                         Moehrle V,
                                                                                                                                                                                                         WPI; 2001-267102/28.
                                                                                                        (FARB ) BAYER AG.
  29-NOV-1999;
                                                   27-AUG-1999;
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Salas JA;

Velten R,

ä

Gaps 97

3;

Indels

Length 50000;

24766 tggtcgtgatcgagatgagctcgccgtcggggcaggcctccttcgaggtgaatgctgacc 24825

AAF88312 standard; DNA; 50000 BP

AAF88312 RESULT

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AAF88312

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278 cgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggtcaggaacagactc 337

9

338 24886

g ŏ

g

AAD14511

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/*tag= g
/*tag= g
/product= "Clavulanic acid biosynthesis enzyme, CLA"
/product= "Clavulanic acid biosynthesis enzyme, CLA"
/transl_except= (pos:6590..6592, aa:Leu-6lx)
/note= "The CDS corresponds to ORF4 and does not include
                                                                                              969 ggcgggcaaccgggacgagacggtcttccccgacccggaccgggtggacgtggacgcgcga 1028
                                                                                                                                                                         1029 egecegeceatetegeetteggecaeggeatgeaceagtgeetgggecagtggetgge 1088
                                                                                                                                                                                                                                                    1089 ccgggtggagctggaggagatcctcgccggggtgctgcgctggatgcccggtgcccggtt
                                                                                                                                   314
                     909 ggacgiccagcicgacgaigtgictcaiccgggcgggcgagggcgiggiggigcigicgcigic 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clavulanic acid biosynthesis enzyme; antibiotic; infectious disease; broad spectrum beta-lactamase inhibitor; ds.
                                                           gaccgaccccgagggcctgtcggacgtctccatccggctccaggtgggcgcggaccgcgc
                                                                                                                                       cctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgcacggacaagtcggt
                                                                                                                                                                                                              315 gccgctcggtcaggaacagactctgggtgacttcgaggacagcctggaggccgcgctcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Clavulanic acid biosynthesis enzyme" /transl_except= (pos:3932..3934, aa:1le-Glx) /note= "Corresponds to ORF2" 3938..3939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product- "Clavulanic acid biosynthesis enzyme"
/transl_except- (pos:5476..5478, aa:Ala-Glx)
/note- "Corresponds to ORF3"
5482..5653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Clavaminate synthase isozyme (cs2)" /transl_except= (pos:7583..7585, aa:Arg-Glx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product- "Open reading frame (ORF)1 protein"
/transl_except= (pos:112..114, aa:Gly-Glx)
1765..2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces clavuligerus 15 Kb genomic DNA fragment.
   '*tag= d
'note= "Intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= f
/note= "Intergenic region"
5654..6595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "Intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Intergenic region"
                                                                                                                                                                                                                                                                                                                            1149 egeggtgeeettegaggagetggaetteeg 1178
                                                                                                                                                                                                                                                                                         375 caagatcctcgccgaggagcagaacgccgg 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
complement (109..1764)
                                                                                                                                                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                         AAD14499 standard; DNA; 15079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /partial
6596..6610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2216..3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3940..5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..7588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= h
   /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD14499;
                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                     255
                                                           195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to DNA sequences encoding enzymes required for clavulanic acid biosynthesis. Clavulanic acid is a broad spectrum beta-lactamase inhibitor and is an important antibiotic for the treatment of infectious diseases. Also provided in the patent is a 15 Kb genomic DNA fragment downstream to pcbc gene from Streptomyces clavuligerus. The genomic DNA comprises 10 open reading frames (ORFS), eight of which are involved in clavulanic acid biosynthesis. The present sequence is ORFIO DNA from S. clavuligerus genomic DNA.
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24826 agcttgcggacttcttgaacgacacctacgacgtggtcgaacctggtgatgaacacccggt 24885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel enzyme required for clavulanic acid biosynthesis which is useful as broad spectrum beta-lactamase inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgcggtgcggatgaccttccacctcccggagacgcgcctgtgacctgggcgttcggccg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgaggagctgctgcgcttccactccatcgtgcagaacgggctggcccgtgccgcggtgga 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggagetgetgetegaegggateaacegeeegagegaegaeggegaegteeacategeeee 194
                                                                                                                                                                                                                                                                                                                                            Clavulanic acid biosynthesis enzyme; antibiotic; infectious disease; broad spectrum beta-lactamase inhibitor; open reading frame; ORF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Open reading frame (ORF)10 protein"
/transl_except= (pos:1222..1224, aa:Trp-Glx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1227;
                                                                                                                                                                                                                                                                                                         Streptomyces clavuligerus ORF10 DNA downstream to pcbC gene.
                                                                                                ggatgaacgtcgacgaggtgctgagccagctgctctcgcacaacct 24931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1227 BP; 161 A; 439 C; 451 G; 176 T; 0 other;
                                                           tgggtgacttcgaggacagcctggaggccgcgctcggcaagatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56.4; DB 22;
Pred. No. 0.035;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 75-76; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paradkar AS;
                                                                                                                                                                                            BP.
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0
                                                                                                                                                                                         AAD14511 standard; DNA; 1227
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93US-0134018.
95US-0567801.
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ilarity 48.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0385028
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aidoo KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA.
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P-PSDB; AAE07915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  pcbC gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6232106-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1993;
06-DEC-1995;
                                                                                                                                                                                                                                                                   01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jensen SE,
                                                                                                                                                                                                                              AAD14511;
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NAME OF THE PARTY

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The present invention relates to DNA sequences encoding enzymes required for clavulanic acid biosynthesis. Clavulanic acid is a broad spectrum beta-lactamase inhibitor and is an important antibiotic for the treatment of infectious diseases. The present sequence is Streptomyces clavuligerus 15 Kb genomic DNA fragment comprising 10 open reading frames (ORFs), eight of which are involved in clavulanic acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rel enzyme required for clavulanic acid biosynthesis which is useful broad spectrum beta-lactamase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-342772/36.
P-PSDB; AAE07906, AAE07907, AAE07908, AAE07909, AAE07910, AAE07911.
AAE07912, AAE07913, AAE07914, AAE07915.
                                                      /product= "Clavulanic acid biosynthesis enzyme"
/transl_except= (pos:9071..9073, aa:Thr-Glx)
/note= "Corresponds to ORF6"
9077..9240
                                                                                                                                                                                                                                             /product= "Clavulanic acid biosynthesis enzyme"
/transl_except= (pos:11001..11003, aa:Gly-Glx)
// responds to ORF8"
                                                                                                                                                              product= "Clavulanic acid biosynthesis enzyme"
                                                                                                                                                                                                                                                                                                                                                       /product= "Clavulanic acid biosynthesis enzyme"
/transl_except= (pos:12625..12627, aa:Val-Glx)
13366..13768
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ORF10 protein"
/transl_except= (pos:14990..14992, aa:Trp-Glx)
                                                                                                                                                                          'transl_except= (pos:10903..10905, aa:Lys-Glx)
note= "Corresponds to ORF7"
0909..10997
"Corresponds to ORF5"
                                                                                                                                                                                                                                                                                                          /*tag= p
/note= "Intergenic region"
complement (12622..13365)
                                                                                                                          'note= "Intergenic region"
                                                                                                                                                                                                              /*tag= n
/note= "Intergenic region"
complement (10998..12296)
/*tag= o
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= r
/note= "Intergenic region"
13769..14995
                      rote= "Intergenic region"
895..9076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paradkar AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 2; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0134018.
95US-0567801.
                                                                                                                                        241..10908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0385028
'note= "Cor
'589..7894
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aidoo KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYAL-) UNIV ALBERTA
           misc_feature
                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1993;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jensen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
                                             CDS
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Sequence 15079 BP; 2105 A; 5475 C; 5331 G; 2168 T; 0 other;

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                                                                          14737 ggcgggcaaccgggacgagacggtcttccccgacccggaccgggtggacgtggaccgcga 14796
                                                                                                                                                                                                                                                                                                                      14857 ccgggtggagctggaggagatcctcgccgcggtgctgcgctggatgcccggtgcccggct 14916
                                                                                                                                            14677 ggacgtccagctcgacgatgtgctcatccgggcgggcgagggcgtggtggttgctgtcgctgtc 14736
                                                                                                                                                                                                                                                              14797 egecegeceatetegeetteggeeaeggeatgeaecagtgeetgggeeagtggetgge 14856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumatiod arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection;
                                                        75 cgcggtgcggatgaccttccacctcccggagacgcgctgtgacctgggcgttcggccg 134
                                                                                                                                                                                                                                                                                           374
                            Gaps
                                                                                                                135 ggagctgctgctgctggacgggatcaaccgcccgagcggcgacggcgacgtccacatcgccc
                                                                                                                                                                        cctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgcacggacaagtcggt
                                                                                                                                                                                                                                                                                            gccgctcggtcaggaacagactctgggtgacttcgaggacagcctggaggccgcgctcgg
Length 15079;
                            ö
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arterial-venous malformation; immune deficiency; ss.
Score 56.4; DB 22;
Pred. No. 0.031;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 296-321; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                    404
                                                                                                                                                                                                                                                                                                                                                    375 caagatcctcgccgaggagcagaacgccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human METH1 related EST AL021529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iruela-Arispe L, Hastings GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ32020 standard; DNA; 38734
13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US01313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
             Best Local Similarity 48.2
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IRUE/) IRUELA-ARISPE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HASTINGS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-590684/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9937660-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-1998;
28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ32020;
 Query Match
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Crohn's disease; atherosclerosis; birth control;

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meralippincess introduces and meralism minimum and minimum comparison of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rhemmatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, heammadiomas, and arthritis, psoriasis.

They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also used for detection and diagnosis. AA323002 to AA232080, and AA44503 to AA321811 represent sequences given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2516 cggcgccgaggcgttcgcccggctgacctccgacgagggcgccgtcgacgacttcggctt 2575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cccgaccgaccccgagggcctgtcggacgtctccatccggctccaggtgggcgcggaccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgccaaccactccggcaccctgccgctcgacgccctgatgctccaggtggcgctgcacga
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  metalloprotease thrombospondin (METH) proteins METH1 and METH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 56; DB 20; Length 38734; 46.4%; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2876 gcggttgctcggctccggcgaactggtcggcg 2907
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Matches 182;
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The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, renumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic sears, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler Webber syndrome, plaque neovascularisation, telangiectasis, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also eused in birth control. METH can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 cgtctccgaggagctctccttcaagatcccagtcgaactgcgatacgagacccgggatcc 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Trulli SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHI and METH2 polynucleotides and encoded polypeptides, used inhibit anglogensis in the treatment of disorders such as cance rheumatoid arthritis and psoriasis -
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0
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ilarity 46.4%; Pred. No. 0.034;
Conservative 0; Mismatches 210; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38734 BP; 6142 A; 13138 C; 13586 G; 5868 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM, Jonak 2L,
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BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Pages 597-622; 768pp; English.
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                                                                                                                                                                  99US-0144882.
99US-0147823.
99US-0373658.
                                                                                                                                                                                                                                                                 HUMAN GENOME SCI INC
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                                                                                                                        2000WO-US14462
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JONAK Z L.
TRULLI S H.
FORNWALD J A.
                                                                                                                                                                                                                                                                                                                          HASTINGS G A.
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es 182; Conserv
                                                            WO200071577-A1
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                              Unidentified.
                                                                                                                        25-MAY-2000;
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22-FEB-2000;
                                                                                         30-NOV-2000
                                                                                                                                                      25-MAY-1999
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(HAST/)
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/*tag= p 1042411176 /*tag= q	5 . E.	/partial /note= "No start codon" complement (1210813022) /*tag= s	/product= "EvdL" complement (1302713030) /*tag= t complement (1441015363)	/*tag= u //rtag=	<pre>complement (1538015414) /*tag= w / /roduct= "EvrB" //complement 16410 17272</pre>	Comptement 104191/8/3 /*tag= x /product= "EvrC"	Comptement (1707009394) /*tag= y /product= "EvrD" 1937420906	/*tag= z /product= "EvrE"	/*tag= aa . /*tag= "EvrF" /product= "EvrF" 2105622542	/*tag= ab 22748.24172	/rdg= ac /product= EvrG" 2273622740	/*tag= ad complement (2417725223)	/rcay- /product="EvrH" complement (2523025233)	/*tag= af 25550.26626	/_ray= /product= "EvrI" 2668530479	/*tag= ah /product="EvrJ" 2667226676	/*tag= ai complement (3055731876)	/*teg= a) /product= "EvrK" complement (3188531888)	:	/*tag= al /product= "EvrL" complement (3316734405)		comprement (3441434410 /*tag= an complement (3444935210)	/*tag= ao /product= "EvrN"	complement (3521935241) /*tag= ap complement (3529436238)
FT FT CDS	FT CDS . FT FT	FT FT CDS	FT RBS FT CDS	FT FT FT	FT CDS		FT CDS	FT	FT CDS		FT FT RBS		FT FT RBS	FT FT CDS	FT CDS	FT FT FT RBS	υ	FT . FT RBS		FT FT CDS		FT CDS		FT CDS
192 cccgaccgacccgagggcctgtcggacgtctccatccggctccaggtgggggggg	cocctcttccgtgcagcgcccgcgtggtcgcttctcgaccgac	312 ggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctggaggccgcgct 371 	372 cggcaagatcctcgccgaggagcagaacgccg 403 	RESULT 12 AASO8693	AASU8693; AASU8693;		nicromonospoid on encoding prosynchetic ensymmes for Everninomycin. Everninomicin; antibiotic; bottle-neck gene; orthomicin; fermentation; ds.	Micromonospora carbonacea var. africana.	Key Location/Qualifiers CDS complement (1321382)	/product= "EvdA" complement (1389.1394)	CDS	/product= "EvdB" RBS complement (26182622)	CDS	/product= "EvdC" RBS complement (38673870)	CDS		CDS 5309.6235 /*tag= 1	/product= "EvdE" CDS	52	CDS 7272 8327	93	/ ".cg- "		/rtdg= 0 /product= "EvdI" RBS complement (1023210235)

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complement (47156..49234)
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51677..52715
/*tag= bi
/product= "EvsB"
51629..51629
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/product= "EvbB"
complement (55125, 55128)
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complement (56184..56813)
/*tag= aq
/product= "EvrO"
complement (36235..36963)
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complement (43807..43811)
/*tag= bb
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/product= "Evrx"
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complement (56100..56103)
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/product= "Evrs"
complement (40216..40890)
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/product= "EvrU"
complement (41679..42707)
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/product= "EvrV"
complement (42714..42717)
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                                                            /product= "EvrQ"
complement (38072..38566)
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                                            complement (36998..38026)
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/product= "EvsC"
53554..54207
/*tag= bl
/product= "EvbA"
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/product= "EvbC2"
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                                     85 atgacettecacetececeggagaegegeetgtgaeetgggeegtteggeegggagetgetg 144
               Gaps
                                                                                                                                                                                                                                        Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;
Score 55.8; DB 22; Length 109519;
Pred. No. 0.035;
0; Mismatches 147; Indels 0;
                                                                                                                                     /*tag- h
/label- ORF8
complement (12662..13365)
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complement (49..1745)
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//abel= ORF1
/*tag= b
//abel= ORF2
//abel= ORF3
/*tag= d
//abel= ORF4
//abel= ORF4
//orbe= "cla gene"
                                                                                                                                                                                    AAQ91580 standard; DNA; 15079 BP
                                                                                                                                                                                                                            S. clavuligerus cla gene region.
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/label= ORF9
13769..14995
/*tag= j
/label= ORF10
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/label= ORF5
7895..9076
/*tag= 6
/label= ORF6
9241..10908
/*tag= 7
/label= ORF7
 Query Match 13.7%;
Best Local Similarity 49.5%;
Matches 144; Conservative (
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                                                                                                                                                                                                                                                            Streptomyces clavuligerus.
                                                                                                                                                                                                                                                cla gene; ds.
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2126 cettegggacgeggateceggeggege 2152
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  agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Narbonolide polyketide synthase; PKS; narbomycin modification enzyme; erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethymycin;
                                                                                                                                                                                                                                                                                                                                                                                                                             14737 ggcgggcaaccgggacgagacggtcttgcccgacccggaccgggtggacgtggaccgcga 14796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14857 ccgggtggagctggaggagatcctcgccgcggtgctgcgctggatgcccggtgcccggct 14916
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgacgtccacatcgcccc 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaccgaccccgagggcctgtcggacgtctccatccggctccaggtgggcgcggaccgcgc 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgcacggacaagtcggt 314
                                                                                                                                                                                                                                                                                                                                                                                                               75 cgcggtgcggatgaccttccacctccccggagacgcgcctgtgacctgggcgttcggccg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccgctcggtcaggaacagactctgggtgacttcgaggacagcctggaggccgcgctcgg 374
                                                                                                                                                                                                                                                            A library of S. clavuligerus NRRL 5741 genomic DNA fragments (15-22 kb) constructed in cosmid pLARR3 was screened for the cla gene using a probe based on a partial N-terminal sequence from the CLA enzyme. Isolated clone K6L1 included a 15kb fragment having the sequence given in AAQ91580 that included the cla gene (ORF4).
                                                                                                                                                         P-PSDB; AAR77858; AAR77859; AAR77860; AAR77861; AAR77862; AAR77863;
AAR77864; AAR77865; AAR77866; AAR77867.
                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                            Clavulanic acid biosynthesis enzymes and corresp. DNA - useful biosynthesis of the antibiotic in Streptomyces hosts which do naturally produce clavulanate
                                                                                                                                                                                                                                                                                                                                                                   Length 15079;
                                                                                                                                                                                                                                                                                                                                  Sequence 15079 BP; 2097 A; 5488 C; 5324 G; 2170 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contig 93 DNA encoding S. narbonensis polyketide synthase.
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 caagatcctcgccgaggagcagaacgccgg 404
                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                          Paradkar AS;
                                                                                                                                                                                                                                        Disclosure; Fig.2; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   13.5%;
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                                                      93CA-2108113
                                                                             93CA-2108113
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                          Aidoo KA, Jensen SE,
                                                                                                    (UYAL-) UNIV ALBERTA
                                                                                                                                             WPI; 1995-207301/28.
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                      08-OCT-1993;
                                                                            08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-2002
          CA2108113-A.
                                 09-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                          Matches 158;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The present invention relates to recombinant DNA vectors (cosmids) that encode for the narbonolide polyketide synthase (PKS) enzyme and various narbonovicin modification enzymes from Streptonyces narbonensis. The recombinant DNA vectors can be used to produce recombinant ketide synthases and a variety of different polyketides (e.g. erythromycin, rapamycin, tylosin, narbomycin, picromycin, methylmycin and neomethymycin) for use in agriculture, medicine and health. The recombinant vectors may be used to produce polyketides in relatively high yields. AAS18432-AAS18443 represent contig DNA sequences that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1886 cggtgtcccgcaaggtcgccgagaacggcgcggtgctcctgcgcaacgaggccaggccc 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2066 acaccatcaaggcccgcgcgggcgcgggtgcgacggtgacgtacgagacgggtgaggaga 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 tcgaactgcgatacgagacccgggatccctacgcggtgcggatgaccttccacctccccg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding narbonolide polyketide synthases from Streptomyces narbonensis, useful for the recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1946, tgccgctcgccggtgacgccggcaagagcatcgccgtcatcggcccgacggccgtcgacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 gagacgcgcctgtgacctgggcgttcggccgggagctgctgctcgacgggatcaaccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 ccatccggctccaggtgggcgcggaccgccctcttccgtgcaggcgccccgccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3241 BP; 520 A; 1174 C; 1125 G; 422 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51.8; DB 24;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encode for S. narbonensis PKS enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Column 20-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 acttcgaggacagcctggaggccgcgc 370
                                                                                                                                                                                                                                                                                                                                                         (KOSA-) KOSAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.78;
47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyketides, e.g. narbomycin
                                                                                                                                                                                          99US-0434288
                                                                                                                                                                                                                                                       98US-107093P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 155; Conservative
Streptomyces narbonensis
                                                                                                                                                                                                                                                                                                                                                                                                                      McDaniel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-065495/09
                                                                                                                                                                                          05-NOV-1999;
                                                                                                                                                                                                                                                       05-NOV-1998;
27-MAY-1999;
                                                         US6303767-B1
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Gaps

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                                    Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster; antifungal; antibiotic; nysl; ds.
                    Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
                                                                                                                                                                                                                                                                      protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                          t= "NysR4 (short) protein"
"CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                       /note= "CDS does not include start codon" (3765..64961
                                                                                                                                                                                                                                                                                                                                                                 not include start codon"
                                                                                               /product= "NysD2 partial protein"
/note= "CDS does not include stop codon"
complement (1056..2576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
(SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
(ALPH-) ALPHARMA AS.
                                                                                                                                                                                                                                          *tag= g
product= "NysR1 protein"
                                                                                                                                                                                                                                                                                                                                                        /product- "NysR5 protein"
                                                                                                                                                                                                                                                                                                                                                               /note= "CDS does not incl
complement (62551..63615)
                                                                                                                                                                                                                                                                                                    product- "NysR3 protein"
                                                                                                                           /product= "NysD1 protein"
2806..6906
                                                                                                                                                                    *tag= d
product= "NysB protein"
.6550.49840
                                                                                                                                                                                              /product= "NysC protein"
50260..51015
                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= m
/product= "ORF1 protein"
                                                                                                                                                                                                                      product- "NysE protein"
1405..54305
                                                                                                                                                                                                                                                                                                                                                                                      'product= "ORF2 protein"
                                                                                                                                                   /product= "NysA protein"
6952..16530
                                                                          Location/Qualifiers
complement (1..1035)
                                                                                                                                                                                                                                                                             "CDS does
                                                                                                                                                                                                                                                                                                                          'product= "NysR4
                                                                                                                                                                                                                                                                     product= "NysR2
                                                                                                                                                                                                                                                                                    7180..59963
                                                                                                                                                                                                                                                                                                                                  note= "CDS c
                                                                                                                                                                                                                                                       4329..57190
                                                                                                                                                                                                                                                                                                           0415..61047
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2000GB-0008786.
2000GB-0009387.
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       (first entry)
                                                                                                                                                                                                                                                               *tag=
                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINVENT AS.
DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                               note-
                                                           Streptomyces noursel
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200159126-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2000;
10-APR-2000;
14-APR-2000;
      29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DZIE/)
(ZOTC/)
(SEKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SINV-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22015 gcacgacgccggctccttcgacgccgacttcttcgggatgagcccgcgcgaggcgatggc 22074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130,
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135, AAE10136, AAE10137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                            New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 gctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggtcaggaacagactct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 51.8; DB 22; Length 65140; 51.5%; Pred. No. 0.2; Live 0; Mismatches 112; Indels 0;
                                                                                                                  Strom AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22075 caccgaeteceageagegeetgetgetegaacteteetgggaageegtega 22125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;
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                                                                                                                  Brautaset T,
                                                                                                               3, Sekurova ON, Fjaervik E, Brautase
Ellingsen TE, Sletta H, Gulliksen O;
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 116-151; 266pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 18, 2002, 11:38:22
Job time: 11367 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 51.5
Matches 119; Conservative
FJAERVIK E.
BRAUTASET T.
                                                                                                                                                                                                          WPI; 2001-557614/62
                                                       (STRO/) STROM A R.
                                                                                                                      Sotchev SB,
                                                                                                                                                     Valla S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Appl Appl Appl Appl Appl

Appli Appli

Appli Appli Appli Appli Appli Appli Appli Appli

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GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: AAhish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STRATE: D.C.
                                                                Sequence
Sequence
Sequence
Sequence
Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
                                 US-08-387-942C-1
US-08-387-942C-1
US-09-479-409-29
US-09-479-453-29
US-09-105-537-38
US-09-373-816-1
US-09-373-816-2
US-09-385-028-17
US-09-373-816-2
US-09-373-816-2
US-09-373-816-2
US-09-373-816-2
US-09-373-816-2
US-09-373-816-2
US-09-510-6468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION BUNBER:
FILING DATE: 29-JAN-1997
ATTORNEY AGENT INFORMATION:
NAME: D. Douglas Price
REGISTARATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELEFAN: (202 638-6666
TELEFAN: (202 038-6666
TELEFAN: (202) 39305350
TELEFAN: (202) 39305350
TELEFAN: (202) 39305350
TELEFAN: CAN-248593 IDEA UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                US-08-459-595A-6
US-08-459-504B-6
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                                                                                                                                                                                                                                                                                               US-09-231-818-5
US-07-951-715A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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STRANDEDNESS: sing
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; MOLECULE TYPE:
US-09-385-028-23
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                   Query Match
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603.847 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-036-987A-1

US-08-036-987A-1

US-08-036-987A-1

US-08-0314-052-19

US-08-044-052-19

US-08-08-14-052-19

US-08-08-16-037-26

US-08-06-037-26

US-09-083-485-1

US-09-083-485-1

US-09-083-485-1

US-09-083-028-13

US-09-385-028-13

US-09-386-028-13

US-08-804-2276-7

US-08-804-198-1

US-08-804-198-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide &
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnedan ....
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                                                                                                                                  13.9%; Score 56.4; DB 4; Length 15079;
48.2%; Pred. No. 0.0028;
tive 0; Mismatches 171; Indels 0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.30
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                                                            Streptomyces clavuligerus
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APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AuG-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
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Lacroix, Patricia
     DNA (genomic)
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ZIP: 20005-3315
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 ; MOLECULE TYPE: D
; HYPOTHETICAL: NO
ORIGINAL SOURCE:
; ORGANISM: Strei
US-09-385-028-1
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US-08-510-646B-17
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APPLICANT:
APPLICANT:
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                                                            cgcggtgcggatgaccttccacctcccggagacgcgcctgtgacctgggcgttcggccg 134
                                                                                                                                  135 ggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgacgtccacatcgcccc 194
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                         Gaps
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TILLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: The Jenifer Buliding, 400 Seventh Street, N.W. CIIY: Washington
                     171; Indels
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APPLICATION NUMBER: US 08/790,462
APPLICATION NUMBER: US 08/790,462
APPLICATION NUMBER: US 08/790,462
APPLICATION DAME: D. DOUGLAS PLICE
REGISTRATION NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202 638-666
TELEFAX: (202) 3930530
TELEFAX: RCA 248593 IDDA UR
   Pred. No. 0.003;
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1149 CGCGGTGCCCTTCGAGGAGCTGGACTTCCG 1178
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Patent No. 6232106
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   48.28;
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LENGTH: 15079 base pairs
TYPE: nucleic acid
Best Local Similarity 48.2 Matches 159; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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CLASSIFICATION:
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APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
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APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
                    CURRENT APPLICATION NUMBER: US/09/434,288 CURRENT FILING DATE: 1999-11-05 PRICR APPLICATION NUMBER: 60/107,093 PRICR FILING DATE: 1998-11-05
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                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-11
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30062-20030.00
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ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
                                                                                                                   NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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MEDIUM TYPE: Floppy
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US-08-387_942C-7
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STATE: VI
COUNTRY:
                                                                                                                                                                                               LENGTH: 3241
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APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
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                 APPLICATION NUMBER: PCT/FR 93/00923 FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 92/11441 FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgcgctcggcaagatcctcgccgagg 391
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                                                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.6%;
Best Local Similarity 50.3%;
Matches 194; Conservative
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MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: s. virginiae
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 1..2219
; OTHER INFORMATION:
US-08-510-646B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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85 atgacetteceaceteceeggagaegeegeetgtgacetgggegtteggeegggagetgetg 144
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                                                                                                                                                                                                                                                                              Length 80161;
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                                                                                                                                                                                                                                                                              Score 50.4; DB 3;
Pred. No. 0.039;
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Rathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TILE OF INVENTION: Blosynthetic Genes For Spi
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
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                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.4%;
Matches 142; Conservative
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
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                                                                                                                                                                              US-09-036-987A-1
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APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Pred. No. 0.042;
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                               REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 cagginggooggacogcocctctice 262
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Policy
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NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
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       REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-7
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58.8%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 58.89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-036-987A-1
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                     APPLICATION NUMBER: US/08/814,052
FILING DATE: 06-MAR-1997
                                                                                                                                                                                                                                                 Sequence 17, Application US/08814052 Patent No. 6015783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JATE: New York
COUNTRY: U.S.A.
:ZIP: 10174-6401
COMPUTER READALLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: TBM COMPATION
OPERATING SYSTEM: DOS
SOFTWARE: FACATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33,728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17

SEQUENCE CHARACTERISTICS:

LENGTH: 2279 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
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Best Local Similarity 53.1%;
Matches 128; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655
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405 Lexington Avenue, Suite 6400
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265 gcaggcgcccgccgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggt 324
                                                                                                   185 gtgaatgetgaccagettgeggaettettgaacgacacetacgacgtggtegaacetggt 244
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: von der Osten, Claus
APPLICANT: cherry, Joel R.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/814,052
FILING DATE: 06-MAR-1997
                                                                                                                                                                                  245 gatgaacaccggtggatgaacgtcgacgaggtgctg 280
                                                                                                                                          325 caggaacagactctgggtgacttcgaggacagcctg 360
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Pred. No. 0.077
0; Mismatches
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Patent No. 6015783
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 3,728
REFERENCE/DOCKET NUMBER: 466
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TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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INFORMATION FOR SEQ ID NO: 19:
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ilarity 53.1%;
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LENGTH: 2249 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 128; Conserv
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US-08-814-052-19
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Von der Osten, Claus

APPLICANT: Cherry, Joel R.

APPLICANT: Cherry, Joel R.

APPLICANT: Basmussen, Michael Dolberg

APPLICANT: Rasmussen, Michael Dolberg

TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING

TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

* ADDRESSEE: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 2279; 0.077;
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Pred. No. 0.077;
0; Mismatches 110;
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3: No. 59812430 No. 5981243disk of No. 5981243th America, Inc. 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                   OXENB LL, Karen M.
AASLYNG, Dorrit A.
FENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(586..831, 917..994, 1079..1090, 1193..1264, 1337..2308, 2456..2524, 2618..3028)
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Pred. No. 0.076;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 12 PE Floppy disk
COMPUTER: Parentin PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 05/08/939,218A
FILING DATE: 29-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                               ACIDS ENCFODING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                  ; Sequence 1, Application US/08939218A; Patent No. 5981243
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTONNEY/AGENT INFORMATION:
NAME: ROZEK, CATOL E.
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET UNBER: 4184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                  BERKA, Randy Michael
BROWN, Stephen H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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53.1%;
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SCHNEIDER, Palle
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LENGTH: 3183 base pairs
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                     APPLICANT: AASLYNG, DC TITLE OF INVENTION: PT TITLE OF INVENTION: AC NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS ADDRESSEE: NO. 59813
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Matches 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New Yor
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APPLICANT: B
APPLICANT: X
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LOCATION:
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US-08-939-218A-1
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T: 405 Lexington Avenue, Suite 6400
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2015 CGACGACCTGCGCGGGCCGTCTCGGACGCCGACGCCGACCTCGACCTCGCCCTGTGCGC 2074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1789 GCCGGCGTTCGGGTGGTGCTGCCTTCCGGGCCGACAACCCGGGCCCCTGGCTGTT 1848
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                                                                                                                                                                                                     Sequence 18, Application US/08814052
Patent No. 6015783
GENERAL INFORMATION:
APPLICANT: Vond Costen, Claus
APPLICANT: Bjornvad, Mads E.
APPLICANT: Wind, Jesper
APPLICANT: Vind, Jesper
APPLICANT: APPLICANT: Vind, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
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Pred. No. 0.077;
0; Mismatches 110; Indels
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SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,052
FILING DATE: 06-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J
REGISTRATION NUMBER: 33,728
REFERENCE/CDCKET NUMBER: 4684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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53.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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Best Local Similarity 53.1°
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PRO-
TITLE OF INVENTION: OR
TITLE OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 601578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-878-9655
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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US-08-814-052-18
                                                                                                                                                                RESULT 10
US-08-814-052-18
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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PCT-US95-06815-1
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                TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCFODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
join (587..832, 918..995, 1078..1089, 1189..1260,
1333..2304, 2452..2520, 2614..3024)
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06815
FILING DATE: 31-May-1995
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, Suite 6400 COUNTY: U.S.A. ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: FIOPPY disk COMPUTER: IBM PC COMPATER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Myceliophthora thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,781
FILING DATE: 03-June-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          Sequence 1, Application PC/TUS9506815 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,274
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4184
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3187 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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996...1077
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833...917
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CORRESPONDENCE ADDRESS:
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FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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NAME/KEY:
LOCATION:
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LOCATION:
LOCATION:
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PCT-US95-06815-1
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                                                                                             2932 C 2932
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APPLICANT:
                                                             297 c 297
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Patent No. 5770419
GENERAL INFORMATION:
APPLICANT: Wall there, Jul A.
APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
TITLE OF INVENTION: ENHANCED ACTIVITY
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57704190 No. 5770419disk of No. 5770419th America, Inc.
                                                                                                                                                                                                           2688 egceceseaceceseccrecrearesesesecaaccrereresesesesesareresaries 2747
                                                                                                         60 gacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgac 119
                                                           Gaps
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                                                        3;
Length 3187;
Score 49; DB 5; Length 318
Pred. No. 0.076;
0; Mismatches 110; Indels
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REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTR: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,037
FILING DATE: 30-AUG-1996
CLASSIEFCATION: 435
PRIOR APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY APPLICATION UNMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
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TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
  Query Match 12.0%;
Best Local Similarity 53.1%;
Matches 128; Conservative
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LENGTH: 3192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SEE: No. 59481210 No. 5948121d1sk of No. 5948121th America, Inc.: 405 Lexington Avenue New York
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                                                                                                                                                                                                                                                                                               3;
                                                                                                                                           CCATION: Join(586..831, 917..994, 1079..1090, 1193..1264, LOCATION: 1337..2308, 2456..2524, 2618..3028)
                                                                                                                                                                                                                                                     Query Match 12.0%; Score 49; DB 1; Length 3192; Best Local Similarity 53.1%; Pred. No. 0.076; Matches 128; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dorrit Aaslyng
APPLICANT: Sorensen, Niels H.
ATTLE OF INFORTION: Laccases with Improved Dyeing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,485
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFRENCE/POCKET NUMBER: 4639.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09083485 ; Patent No. 5948121
                                                                                   DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3192 base pairs
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                                            single
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                   TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                 MOLECULE TYPE:
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                                                                                                       FEATURE:
NAME/KEY:
                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                     2693 GGCGCGGGACGCGGGCCTGCTGAGCGGGGCCAACCCTGTGCGGCGGGACGTGTCGATGCT 2752
                                                                                                                                                                                                                                                                                                                                    2753 GCCGGCGTTCGGGTGGTGGTGTTCCTTCCGGGCCGACAACCCGGGCGCCTGGTT 2812
                                                                                                                                                                                                                                                                                                                                                                                                           120 ctgggcgttcggccgggagctgctcgacgggatcaaccgcccgagcg---gcgacgg 176
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                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BERKA, Randy Michael
APPLICANT: BROWN, Stephen H.
APPLICANT: XV, Feng
APPLICANT: XCHNEIDER, Palle
APPLICANT: OXENB LL, Karen M.
APPLICANT: AASLYNG, DOITITA.
TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCFODING SAME
                                                                                                                                                                     3;
               join(587..832, 918..995, 1080..1091, 1194..1265, 1338..2309, 2457..2525, 2619..3029)
                                                                                                                           Length 3192;
                                                                                                                     Score 49; DB 1; Length 319
Pred. No. 0.076;
0; Mismatches 110; Indels
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COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,661A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4184.010-US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,146
FILLING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08940661A Patent No. 5795760
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TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                       12.0%;
53.1%;
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TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                     Query Match 12.0%
Best Local Similarity 53.1%
Matches 128; Conservative
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CORRESPONDENCE ADDRESS:
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                 ; LOCATION:
; LOCATION:
US-08-706-037-26
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                                                                               join(586..831, 917..994, 1079..1090, 1193..1264, 1337..2308, 2456..2524, 2618..3028)
                                                                                                                                                             Query Match 12.0%; Score 49; DB 2; Length 3192; Best Local Similarity 53.1%; Pred. No. 0.076; Matches 128; Conservative 0; Mismatches 110; Indels
STRANDEDNESS: single
TOPOLOGX: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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1 atgagcttcctcgtctccga......gaggagcagaacgccggctg 407
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         13736207 seqs, 6748477542 residues
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                                                                             OM nucleic - nucleic search, using sw model
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5: em_gss_lum:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1 1 4 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3	TINOSOTO DIOCONIO	ALUS3013 Drosophil	BI717260 1031018G1	BG858938 1024060E0	BG843065 1024001D0	AL066051 Drosophil	AG075896 Pan trogl	AL056652 Drosophil	AG077010 Pan troql	AU183257 AU183257	AG054664 Pan troql	BG274193 WHE2230_F	BE360790 DG1_67_C1	AG058290 Pan trodl	AL066051 Drosophil	BF292743 WHE2202_C	BF259400 HVSMEf001
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ALIGNMENTS

RESULT 1 CNSO091P LOCUS DEFINITION ACCESSION VERSION VERSION	CNS0091P Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. AL053013 AL053013.1 GI:4934461
SOURCE	Eruit fly. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Peteryota; Neoptera; Endopterayota; Diptera; Brachycera;
REFERENCE AUTHORS TITLE JOURNAL	Genoscope. Direct Submission BP 191 9106 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Razutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's land EST libraries. A more detailed description of the library
FEATURES	and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers 1925 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RRCI-98"

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Local Similarity
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- Web: www.genoscope.cns.fr.

- Olaboration with the Barkeley Drosophila Genome Project (BDGP).

Collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

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Pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                  57 cgagacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcctgt 116
                                                                                                                                                                                                                                                                         560 YGKGCSSGSBSCSCCSSCSCSSCSCCBCCCCCSSSRCCSSBSSKCSSTSBSCSC 619
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 925)
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                                                                                                                                      Query Match 15.2%; Score 61.8; DB 12; Best Local Similarity 11.7%; Pred. No. 0.59; Matches 41; Conservative 177; Mismatches 133;
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                                                172
/clone="BACR19D16"
/note="end : TET3"
61 c 61 g
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Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii

Eukaryota; Viridiplantee; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadceae; Chlamydomonas.

Chlamydomonadceae; Chlamydomonas.

E 1 (bases 1 to 684)

S Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre, P., McDermotti,J.P., Shrager,J., Silfow,C. and Stern,D.

Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031

C unpublished (2001)

Contact: Charles Hauser
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/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
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/hots Stress condition II ilbrary, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
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                                                                                                                                                                                                                   Score 60.4; DB 12;
Pred. No. 0.99;
                                                                                                                                                                                                                                                                      Conservative 162; Mismatches 125;
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
                                                                              : TET3"
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13.0%;
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Query Match
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cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H202 (1, 2, 4 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda 2ap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda APP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806.
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Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 704)
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                                                                                                                                                                                                                                                                                                                                                                                                                   CTACGACATGCCCGAGTCCGACGACAGTCCAAGGGCGAGTCCAAGCACGGCAACGGCGC 483
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                                                                                                                                                                                                                                                                                                                           Length 684;
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Pred. No. 4.9;
0; Mismatches 140; Indels
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Location/Qualifiers
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Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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illarity 50.0%;
Conservative
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Best Local Similarity
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/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
Xho1: This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (accetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA,
synthesized The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN [6', and XhoI [3') sites,
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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/clone_lib="C. reinhardtii CC-1690, normalized, Lambda 2ap
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermctt, J. P., Sliflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydownoas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Compublished (2000)
Contact: Charles Hauser
DCMB Box 91000
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BG843065
BG843065.1 GI:14224249
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Pred. No. 8.1;
0; Mismatches 134; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%; S
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Tel: 919 613 8159
Fax: 919 613 8177
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Matches 135; Conservative
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Query Match
Best Local S
Matches 94
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                                                                                    /note="Vector: pBluescript II SK-; Site_I: ECORI; Site_2:
Xho1; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 58 CO2.
POLYA MRNA was purified from each sample, pooled and cDNA
Synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN (5') and Xho1 (3') sites.
pBluescript II SK- plasmids were exclsed from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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                                               /clone_lib="C. reinhardtii CC-1690, normalized, Lambda 2ap
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Brekeley Drosophila Genome Project (BDGP).
The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Drosophila melanogaster
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AG078896.1 GI:16627698
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-068024.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG075896 816 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-068024.R, genomic survey sequence.
AG075896
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Primates; Catarrhini; Hominidae; Pan.
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BAC Food sequences of Library PTB
Unpublished
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Direct Submission
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
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Mammalia; Eutheria;
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
              Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVVE Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
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/celone_lib="PTB Chimpanzee Male BAC Library"
276 c 418 g 66 t 29 others
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rel:81-45-503-9111, Fax:81-45-503-9170)
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-068024.R"
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Pred. No. 12;
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Location/Qualifiers
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Pan troglodytes
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Pan troglodytes DNA, clone: PTB-071G05.R, genomic survey sequence.
AG077010
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACKIIP16"
/note="end : TET3"
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llarity 14.5%; Pred. No. 19;
Conservative 147; Mismatches 119;
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GSS; GSS (genome survey sequence).
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/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="1560487"
/clone_lib="Rice cDNA from immature leaf including apical
meristem (under short day condition)"
/dcv_stage="1mmature leaf including apical meristem (under short as for 15 g 48 t 1 others
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-040G15.R.
Pan troglodytes
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:si81-45-503-9111, Fax:81-45-503-9170)

Glones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGUS4664 11 DNA linear GSS 02-NOV-2001 Pan troglodytes DNA, clone: PTB-040G15.R, genomic survey sequence.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Pan
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                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                     ; Score 51.8; DB; Pred. No. 23; 0; Mismatches
                                                                                   /organism="Oryza sativa"
                                         Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local Similarity 54.9%;
Matches 101; Conservative
  PROJECT - 'RGP'.
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SM Oryza sativa.

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryzae; Oryzae.

Sasaki,T. and Yamamoto,K.

Rice cDNA from immature leaf including apical meristem (2001)

Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-741
Fax: 81-298-38-7468
Email: tsasakieabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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/clone_lib="PTB Chimpanzee Male BAC Library"
437 c 412 g 28 t 41 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.2; DB 12;
Pred. No. 19;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 957
/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9598"
/clone="PTB-071G05.R"
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R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                             Sequencing: M13Rev
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AU183257.1 GI:13896921
                                                                                                                                                                   tracking errors.
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53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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  Direct Submission
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DG1.67_C10.b2_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA
sequence.
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/organism="Aegilops speltoides"
/cultivar="F2 from 2-12-4-8-1-1-(1) x PI36909-12-811-(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cogaggectgtcggacgtetecatecggetecaggtgggegeggaeegegeetettee 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 GCGAGGGCTCGGAGGCCTTCGCCGCCGCGTGGCGCAGTTCGCGGGGCTCCTGAGCT
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Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50.6;
Pred. No. 35;
                                                                                          /db_xref="taxon:4573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:9302347
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Fax: 706 542 1805
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BE360790
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aegilops speltoides.
Aegilops speltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG274193 469 bp mRNA linear EST 21-FEB-2001 WHE2230_F05_K102S Aegilops speltoides anther cDNA library Aegilops speltoides cDNA clone WHE2230_F05_K10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 aacagactctgggtgacttcgaggacagcctggaggccgcgctcggcaagatcctcgccg 388
                                                                                                                                                                                                                                                                                                                                                                                                                                           cottocacotococogagacgogoctgtgacotgggcgttcggccggggagotgctgctcg 148
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Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 gegeecegeetggtegeetteetegaeegeaeggaeaagteggtgeegeteggteagg
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                                                                                                                                                                                                                                                                                                                         Length 770;
                                                                                                                                                                              BAC Library"
34 others
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                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                        /clone_lib="PTB Chimpanzee Male
428 c 226 g 21 t
         1. .770
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-040G15.R"
                                                                                                                                                                                                                                                                                                                            Score 51.4; I
Pred. No. 26;
                                                                                                                     /sex="male"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG274193.1 GI:13066255
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                                                                                                                                                                                                                                                                                                                         12.6%;
ilarity 46.7%;
Conservative
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Best Local Similarity
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                                                                                                                                                                                                            61
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RESULT 12

g ò g BG274193

LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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source

FEATURES

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GSS 03-JUN-1999
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
  (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
tel:181-45-503-911, Fax:81-45-503-9110)
Clones are derived from the chimpanzee BAC library PTB This BAC en
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSOO6XK
Drosophila melanogaster genome survey sequence 77 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 ccacctccccggagacgcgcctgtgacctggggcgttcggccgggagctgctgctcgacgg 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 agactctgggtgacttcgaggacagcctggaggccgcgctcggcaagatcctcgccgagg 391
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 cccgccgctggtcgccttcct-cgaccgcacggacaagtcggtgccgctcggtcaggaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 gtcggacgtctccatccggctccaggtgggcgcggcgccctcttccgtgcaggcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1434;
                                                                                                                                                                                                                                                                                                                                                                        /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
509 c 521 g 14 t 58 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%; Score 50.6; DB 12;
ilarity 48.2%; Pred. No. 34;
Conservative 0; Mismatches 161;
                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-045C04.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly), genomic survey sequence. AL066051
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                             : pKS145
                                                                                                                                      Sequencing: Ml3Rev
                                                                                           clone tracking errors.
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                                                                                                                                                                                                    R.Site 1
R.Site 2
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                                                                                                                                                        LIBRARY
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VERSION
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TITLE
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-045C04.R.
Pan troglodytes
                                                                                                                                                                          1. .504
//Organism="Sorghum bicolor"
//db_xref="taxon:4558"
//db_cref="taxon:4558"
//clone_lib="Dark Grown 1 (DG1)"
//clone_logan: 5-day-old dark-grown seedlings; Vector:
Lambda Zap: Site_l: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                    to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGUSH290 1434 bp DNA linear GSS 02-NOV-200
Pan troglodytes DNA, clone: PTB-045C04.R, genomic survey sequence.
AG058290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ACCCGGATGCGGCTCAAGTCGCGGGAGCGACGCCTCTAC---ACCAACCGCGCCACCGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 cgatacgagacccgggatccctacgcggtgcggatgaccttccacctcccgggagacgcg 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 octgtgacctgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggc 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 gacggcgacgtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GACACGCTCGCGCTCGACCCGACGCTCCGCGAGGATCCGCGCCCGACCTGCTGCGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50.6; DB 10;
Pred. No. 35;
0; Mismatches 169;
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                                                                                                             High quality sequence stop: 477 POLYA=No.
                                                                                                                                                        Location/Qualiflers
                    Sequences have been trimmed
below Phred quality 16. The
Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                            12.4%;
                                                                                      Seq primer: JEN REV
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                                                                                                                                                                                                                                                                                                                                                        91
                                                                  is 20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pateter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 12.3%; Score 50.2; DB 12; Best Local Similarity 27.4%; Pred. No. 40; Matches 94; Conservative 89; Mismatches 160;
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170 c 16
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Polypeptide sequen Rat RC-9 implicate Rat allograft infl Rat allograft infl Rabbit beta 2 inte Rabbit alpha-d clo Rabbit alpha d prot Rabbit alphad prot Rabbit alphad prot Human polypeptide MEAV vaccine. Syn

Arabidopsis thalia

HSV-2 strain SB5 C HSV-2 strain SB5 C Arabidopsis thalla HSV-2 strain SB5 C Arabidopsis thalia Cellulomonas fimi Neisseria meningit Human ORFX ORF2258 Human glutamate re

Total number of

Database

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Title:

Run on:

Scoring table: Sequence:

C glutamicum prote C. glutamicum SRT S. epidermidis ope Human carbonic anh

Murine Mphi type I C glutamicum prote

Human secreted pro

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SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; mypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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ABB71609
AAG82257
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AAU02198
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AAB59590
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AAB12685
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AAW72840
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AAR58552
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AAY81424
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                      AAB98959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44652 standard; Protein; 135 AA
99WO-NL00395
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                                                                                                                               Streptomyces netropsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-147269/13.
N-PSDB; AAZ49731.
                     WO200000613-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000
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 RESULT
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Arabidopsis thalia
Arabidopsis thalia
Human cytoskeletal
Novel human diagno
Novel human diagno
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Streptomyces golde
Streptomyces albus
                                                                                              (without alignments)
115.010 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                              2. (SIDSS/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. (SIDSS/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. (SIDSS/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4. (SIDSS/gcgdata/geneseqp-embl/AA1981.DAT:*
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1 MSFLVSEELSFKIPVELRYE......FEDSLEAALGKILAEEQNAG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS5/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
                                                                                July 18, 2002, 14:15:03; Search time 130.38 Seconds
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                                    747574 seqs, 111073796 residues
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                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAY77574
ABG05279
ABG20257
                                                          OM protein - protein search, using sw model
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AAY44650
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AAU61464
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Maximum DB seq length: 2000000000
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Match Length
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87.6
78.6
64.5
11.6
11.1
10.7
10.7
10.5
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Score

Result

692 606 544 446 80.5 77 74 74

72.5

S. epidermiuis orc Neisseria gonorrhe

epidermidis ope

Drosophila melanog

Human glutamate Protein encoded

Propionibacterium

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Gaps 9 9

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The present sequence is S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigralne agents, herblcides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is S. goldeniensis SsgA protein, SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths.
                                                                                                                                                                                                                                                                                                                                                              61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
                                                                                                                                                                                                                                                                                                   1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhancing fragmentation in filamentous improve their liquid culturing properties
                                                                                                                                                                                                                  Score 606; DB 21; Length 135;
Pred. No. 1.5e-62;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                      Pred. No. 1.5e
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     goldeniensis SsgA protein.
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85.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Wezel GP, Kraal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing branching and microorganisms used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147269/13.
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                       135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIJKSUNIV
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                                                                                                                                                                                                                                        Best Local Sim
Matches 116;
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                                                                                                                                                                         Sequence
                                                                                                                                                                                                                       Query Match
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                                                                          The present sequence is S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumnour agents, immunosuppressive agents, hypocholesterolaemic agents, immunosuppressive agents, hypocholesterolaemic agents, runninant growth promoters, bioinsecticides, antiparasitic agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
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                                                                                                                                                                                                                                                                                                                                                                     SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antihnigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                       Length 135;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                    Score 692; DB 21;
Pred. No. 1.5e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kraal B, Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY44649 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces griseus SsgA protein.
                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 60pp; English
                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                   Conservative
                                              Fig 5; 60pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces griseus
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                         135 AA;
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maisonneuve J,
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                                                                                                                                                                                                                                                                                           VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
                                                                                                                                                                                   Gaps
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Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypotholesteroleemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                     Length 135;
                                                                                                                                                                                  Indels
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                                                                                                                                                    Score 544; DB 21;
Pred. No. 2.5e-55;
                                                                                                                                                                                  12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44650 standard; Protein; 135 AA.
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                                                                                                                                                  78.6%;
77.8%;
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121 dealdrilaeegnag 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces albus G.
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                                                                                                                                                                  Best Local Similarity
Matches 105; Conserv
                                                                                                        135 AA;
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                                                                                                         Sequence
                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                        61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
                                                                                                                                               Gaps
                                                                                                                                                                                                   1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                        Length 135;
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                                                                                                                                             30; Indels
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                                                                                                          64.5%; Score 446; DB 21;
63.0%; Pred. No. 6.4e-44;
ive 20; Mismatches 30
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Jen S, Carter I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU56775 standard; Protein; 400 AA.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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e J, Zhang Y,
                                                                                     Query Match
Best Local Similarity 63.v.,
And 85; Conservative
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                                                       135 AA;
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              and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; useltis; endopthalmitis; bone; joint, central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                      119 vrftggeplirpslenlvaatstirrtngtppitalttngigldrrvdglveagldrvni 178
                                                                                                                                                                                                                                                                                                                                                    ----- LDRTDK 103
                                                                                                                                                                                                                                                                                                                              12 KIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLD------GINRPSGDGDVH 62
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                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                              Length 400;
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                                                                                                                                                                                                                                                          11.6%; Score 80.5; DB 22; 24.4%; Pred. No. 0.99; iive 19; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                63 IAPTDPEGLSDVSIRLQVGADRALFRA-GAPPLVAF-----
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, Jen S, Carter D;
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L'maisonneuve J, Zhang Y,
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                                                                                                                                                                                                                                                                        Local Similarity 24.4% es 39; Conservative
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                                                                                                                                                                                                          400 AA;
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Matches
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteonyelitis), uveltis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with ache vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequiate expression and activity of P. acnes projections and activity of P. acnes properties and cherefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by colyperties in the sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO at the provint/pub/published_pot_sequences.
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Human cytoskeletal protein, HCYT; cell proliferation; immunological;
reproductive; nervous disorder; cytostatic; immunosuppressive; anti-HIV;
anti-diabetic; antiarteriosclerotic; dermatological; anti-inflammatory;
anti-infertility; vasotropic; cardiant.
 Human cytoskeletal proteins useful for diagnosing, treating preventing cell.proliferative, immunological, reproductive, developmental and nervous disorders
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Claim 20; SEQ ID No 35638; 103pp; English.
 18-FEB-2002
 11-OCT-2001.
 Sequence
 ABG20257;
 Query Match
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 16
 Matches
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 86
 ABG20257
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 10;
 The invention provides human cytoskeletal proteins (HCYT) and nucleic acids encoding the proteins. The HCYT polypeptides can be expressed by standard recombinant methodology. The HCYT polypeptides, modulators and antibodies are useful for treating or preventing a disorder associated with decreased and increased expression or activity of HCYT in mammals. The polypeptides are also useful for diagnosing HCYT activity disorders such as cell proliferative, immunological, reproductive, developmental and nervous disorders. Sequences AAY77569-576 represent HCYT
 ||::| :||||:
494 elkfellekdpyal-----dvpnt-afgrehspygpsplgwpssetraflspptlle 544
 76 IRL-----QVGADRAL-----FRAGAPPLVAF----LDRTDKSVPLGQEQT 112
 Gaps
 545 gplrlspllpggggrgsrgppgnpldhgitnergesscdrltdphrapsdtgslsppwdgd 604
 ---LLLD 50
 -- DVHIAPTDPEGLS--- DVS 75
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 19;
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 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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 polypeptides.
 Homo sapiens
 biodiversity
 13-FEB-2002
 11-OCT-2001.
 Seguence
 ABG05279;
 Query Match
 51
 ABG05279
 qq
셤
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 qq
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 qq
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The invention lighters to isolated polymetractice (1) and isolated polymetrase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The control of (II) is the mapping of the combinant production of (II). The control of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II). (II) is useful for generating partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polymeled and polymelectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and and cand sequences the five invention.

Cand to produce other types of data and products dependent on DNA and cand on a sequence of the invention.

Cand to produce other types of the invention.

Cand to produce other types of the invention.

Cand to produce other types of the invention.

Cand to produce of the invention of mutations and to sequence at for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention of maternal printed or specification, but was obtained in electronic format directly from WIPO at the invention of mutation are specification.
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 ||::| :|||:
507 elkfellekdpyal-----dvpnt-afgrgsrgpgnpldhqitnergesscdrltdp 557
 558 hrapsdtgslsppwdqdrrmmfpppgqsypdsalppgrqdrfcsnsgrlsgpaelrsfnm 617
 Gaps
 HIAPTDPECLS --- DVSIRL ----- QVGADRAL ------FRAGAPPLVAF -- 97
 ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 Length 776;
 Indels
The invention relates to isolated polynucleotide (I) and
 41;
 DB 22;
 ch 10.5%; Score 72.5; D 1. Similarity 29.0%; Pred. No. 21; 42; Conservative 13; Mismatches
 Novel human diagnostic protein #20248.
 ABG20257 standard; Protein; 777 AA.
 psldkmdgsmpsemessrndtkddl 642
 --LDRTDKSVPLGQEQTLGDFEDSL 120
 Tang YT;
 30-MAR-2001; 2001WO-US08631
 31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
 (first entry)
 WPI; 2001-639362/73.
 Drmanac RT, Liu C,
 776 AA;
 (HYSE-) HYSEQ INC.
 WO200175067-A2.
 Homo sapiens.
```

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The present invention describes human secreted proteins obtained from human fetal brain, fetal kidney or adult blood cDNA libraries. The present sequence represents a human secreted protein. The human secreted protein. The human secreted protein, and polynucleotides encoding them, are predicted to have proteins, and polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, arthough no supporting medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, inhibit activity, cedherin/tumour invasion suppressor activity, and tumour continuition activity. The polynucleotides are also stated to be useful
 1100 elkfellekdpyal-----dvpnt-afgrgsrgpgnpldhqitnergesscdrltdp 1150
 Human, secreted protein, antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antitumor; antiulorer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour;
 16 ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
 62 HIAPTDPEGLS---DVSIRL-----QVGADRAL------FRAGAPPLVAF--
 New polynucleotides encoding secreted human proteins potentially useful as, e.g. immunostimulators
 Agostino MJ, Clark HF, Collins-Racie LA, Evans C;
Fechtel K, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
Steininger RJ, Treacy M, Wong GG;
 10.5%; Score 72.5; DB 20; 29.0%; Pred. No. 44; tive 13; Mismatches 41;
 AAU39009 standard; Protein; 1369 AA.
 1211 psldkmdgsmpsemessrndtkddl 1235
 Claim 9; Page 84-89; 99pp; English.
 98 -- LDRTDKSVPLGQEQTLGDFEDSL 120
 Human secreted protein am728_60.
 98WO-US27140.
 98US-0212843
 (first entry)
 (GEMY) GENETICS INST INC.
 Query Match 10.59
Best Local Similarity 29.09
Matches 42; Conservative
 WPI; 1999-395405/33.
 1369 AA;
 for gene therapy
 N-PSDB; AAX80481
 18-DEC-1998;
 16-DEC-1998;
20-DEC-1997;
 16-JAN-2002
 Seguence
 AAU39009
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 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a constitution and an expressing of (II). (II) and sequences are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human considered data for this patent did not appear in the printed setting an electronic format directly from WIPO are the constitution and sequence data for this patent did not appear in the printed appear in the printed are the sequences.
 6
 558 hrapsdtgslsppwdqdrrmmfpppgqsypdsalppqrqdrfcsnsgrlsgpaelrsfnm 617
 Gaps
 16 ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
 62 HIAPTDPEGLS---DVSIRL-----QVGADRAL------FRAGAPPLVAF-- 97
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 cell proliferation; differentiation; immune stimulating; vaccine; suppression; haematopolesis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; cadherin; tumour invasion suppressor;
 49;
 secreted protein; immunostimulator; nutrition; cytokine;
 DB 22; Length 777;
 41; Indels
 at ftp.wipo.int/pub/published_pct_sequences.
 10.5%; Score 72.5; Di
29.0%; Pred. No. 21;
ive 13; Mismatches
 Claim 20; SEQ ID No 50616; 103pp; English.
 AAY24788 standard; Protein; 1369 AA
 98 -- LDRTDKSVPLGQEQTLGDFEDSL 120
 Human secreted protein am728_60.
 tumour inhibition; gene therapy.
 (first entry)
 42; Conservative
 Best Local Similarity
Matches 42; Conserv
 777 AA;
N-PSDB; AAS84444
 biodiversity
 26-AUG-1999
 Homo sapiens
 W09932614-A1
 AAY24788;
 Sequence
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Query Match

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Gaps

41; Indels

Length 1369;

97

01-JUL-1999.

Human;

AAY24788 RESULT

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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation activity or may induce production of other or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immune deficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases inflammation. The proteins are also useful in the treatment of diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and sucrease ergentions, infarction of cardiac and central nervous system, anylotrophic lateral sclerosis, and SNY-brager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin or inhibinin telated activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as decrease for the protein of the invention.
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 graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
 hrapsdtgslsppwdgdrrmmfpppggsypdsalppgrqdrfcsnsgrlsgpaelrsfnm 1210
 1100 elkfellekdpyal-----dvpnt-afgrgsrgpgnpldhqitnergesscdrltdp 1150
 Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke)
 49; Gaps
 ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
 HIAPTDPECLS---DVSIRL-----QVGADRAL------FRAGAPPLVAF-- 97
 Evans C;
Wong GG;
autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
 Length 1369;
 Indels
 Lavallie E, Collins-racie LA, F
7, Steininger RJ, Spaulding V,
Merberg D;
 41;
 DB 22;
 10.5%; Score 72.5; D
29.0%; Pred. No. 44;
:ive 13; Mismatches
 Disclosure; Page 482-487; 619pp; English
 22-MAR-2001; 2001WO-US09369
 30-MAR-2000; 2000US-0539330
04-DEC-2000; 2000US-0729674
 (GEMY) GENETICS INST INC.
 Query Match 10.59
Best Local Similarity 29.09
Matches 42; Conservative
 food supplement; vaccine
 McCoy JM, La
Agostino MJ,
 Fechtel K,
 WPI; 2001-639363/73.
N-PSDB; AAS59227.
 WO200175068-A2
 Homo sapiens.
 11-0CT-2001
 Jacobs K,
Treacy M,
 Clark H,
 Sequence
 1151
 62
 16
 g
 NAMES OF COLUMN
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The present invention provides a number of murine and human Ibal derivatives, which are capable of inhibiting the function of cells with monocyte or macrophage activity. These can be used as immunomodulators to prevent and treat diseases caused by a decrease or increase in the activity or the function of macrophages or an activator or an inhibitor of the function of cells of macrophage type. The present sequence is one
 ö
 81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK------ILAEEQ 132
 69 slkrmleklgvpkthlelkrlirevssgseetf-sysdflrmmlgkrsailrmllmyeek 127
 Gaps
 42 AFG-----RELLLDGINRP-----SGDGD------VHIAPTDPEGLSDVSIRLQV 80
 A macrophage function modifier useful for preventing and treating diseases caused by the increase or decrease in macrophage activity
 12 afgllkaggeerleginkgflddpkysndedlpskleafkvkymefdlngngdidi---m
 Human; mouse; immunomodulatory; monocyte; macrophage; inhibitor.
 33;
 Length 147;
 Indels
 42;
 (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
(MOCH) MOCHIDA PHARM CO LTD.
 10.3%; Score 71.5; DB 22;
 2.9;
 Pred. No. 2.9;
12; Mismatches
 of the function of cells of macropha of the derivatives of the invention.
 1211 psldkmdgsmpsemessrndtkddl 1235
 AAG90040 standard; Protein; 129 AA.
 Ą.
98 -- LDRTDKSVPLGQEQTLGDFEDSL 120
 Claim 10; Page 12; 20pp; Japanese.
 AAB98959 standard; Protein; 147
 99JP-0260793.
 99JP-0260793
 28.1%;
 20-AUG-2001 (first entry)
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 Murine Mphi type IbaI.
 WPI; 2001-313369/33.
 Query Match
Best Local Similarity
 147 AA;
 N-PSDB; AAH25799
 JP2001078775-A.
 14-SEP-1999;
 14-SEP-1999;
 27-MAR-2001.
 34;
 133 N 133
 128 n 128
 Sequence
 AAG90040;
 AAB98959;
 function
 Mus sp.
 14
 Matches
 AAG90040
ID AAG9
 AAB98959
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26-SEP-2001 (first entry)

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
 mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing main o acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
 Yokoi H;
 Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 Claim 17; SEQ ID NO: 3794; 246pp + Sequence Listing; English.
 Mizoguchi H, Ando S, Hayashi M, Ochiai K,
Senoh A, Ikeda M, Ozaki A;
 C glutamicum protein fragment SEQ ID NO: 3794.
 (KYOW) KYOWA HAKKO KOGYO KK
 16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
 18-DEC-2000; 2000EP-0127688
 Corynebacterium glutamicum.
 organic acid synthesis.
 WPI; 2001-376931/40.
N-PSDB; AAH65259.
 Ä
 129
 EP1108790-A2
 20-JUN-2001.
 Nakagawa S,
Tateishi N,
 Seguence
NAME OF THE PROPERTY OF THE PR
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9 16; Gaps DB 22; Length 129; 10.3%; Score 71; DB 22; Length 12: 27.6%; Pred. No. 2.8; Live 23; Mismatches 37; Indels Conservative Query Match Best Local Similarity Matches 29; Conservat

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GAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGKILAEEQNA 134 90

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| |: :|| | || : : | :| || : :| :| idpellrtvdrv---vilgddaqv-dmpesaqgalerwsleepda 106 99

Search completed: July 18, 2002, 14:15:04 Job time: 10334 sec

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Sequence 5, Appli
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Sequence 103, App
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Sequence 103, App
 10, Appl
6, Appli
6, Appli
7, Appli
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 Appli
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 Sequence 93,
 Sequence 10
 Sequence 44
 Sequence 6,
 Description
 Sequence 3
 Sequence
 Sequence
Sequence
 Seguence
 Sequence
 Sequence
 Sequence
 Sequence
 Sequence
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-446-563-10
US-08-081-929-6
US-08-081-929-6
US-08-171-385-5
US-08-171-385-5
US-08-485-618-103
US-08-482-293A-103
US-08-943-363-103
US-08-943-363-103
US-08-943-363-103
 US-09-413-814-44
US-08-015-986A-10
 Total number of hits satisfying chosen parameters:
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US-09-367-206-1
US-09-367-206-21
 US-08-505-860C-2
 JS-08-015-770B-8
 US-09-388-774-1
US-08-436-044-6
 231628 segs, 24425594 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued_Patents_AA:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-749-185-9
 DB
 Length
 Query
 Score
 64.5
64.5
64
 Perfect score:
 Scoring table:
 Sequence:
 Searched:
 Database
 ou:
 Result
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9
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Sequence 5, Appli	US-08-683-458-5	7	337	9.0	62.5	44	
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Sequence 5, Appli	US-08-683-426-5	~	337	9.0	62.5	42.	
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Sequence 5, Appli	US-08-312-387B-5	~	337	9.0	62.5	40	
203,	US-09-430-323-203	4	330	9.0	. 62.5	39	
Sequence 203, App	US-08-854-050-203	4	330	9.0	62.5	38	
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Sequence 24, Appl	PCT-US95-04228-24	Ŋ	1276	9.5	64	31	
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Sequence 6, Appli	US-08-436-054-6	~	987	9.5	64	28	

### ALIGNMENTS

```
APPLICANT: BJOSCKET, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Darndt, Petra
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Heichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REPERBENCE: CTT/US 99/23335
CURRENT APPLICATION NUMBER: US/09/413,814
GURRENT FILING DATE: 1999-10-07
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 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
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 61 VHIA-PTDP----EGLSDVSIRLQVGADRALF-----RAGAPPLVAFLDR 100
 APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
 57; Indels
 Query Match 11.5%; Score 79.5; Di
Best Local Similarity 31.5%; Pred. No. 4.2;
Matches 35; Conservative 8; Mismatches
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 US-09-413-814-80
; Sequence 80, Application US/09413814
; Patent No. 6225064
; GBNERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-93
 EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
US-09-413-814-93
 SEQ ID NO 93
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```

3;

36;

44; Indels

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68 PEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPL-GQEQTLGDFEDSLEA--- 122
 594 LDRRGRRQPPY-----LPG-----ELFLAGDCLARGYLNRPDLTA-LHFVP-N 634
 15 VELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDGDVHIAPTD 67
 GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-GAMMA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
 Pred. No. 2.6; 3; Mismatches
 10-FEB-1993
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 10, Application US/08015986A Patent No. 5532123
29.08; Pt.
 18,872
 REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
 TELEX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
 10.2%;
24.1%;
 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
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 Best Local Similarity 29.09
Matches 38; Conservative
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APPLICATION NUMBER: US,
FILING DATE: 10-FEB-19
CLASSIFICATION: 435
 27; Conservative
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 MOLECULE TYPE: protein
 123 ALGKILAEEQN 133
 690 AAAVVQAESQH 700
 unknown
 Query Match
Best Local Similarity
 amino acid
 STATE: New York COUNTRY: U.S.A.
 STRANDEDNESS:
 10036
 RESULT 4
US-08-015-986A-10
 US-08-015-986A-10
 Matches
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M
 APPLICANT: Mucler, Joachim
APPLICANT: Mucler, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: Heteropolyketide compounds
FILE REFERENCE: PCT/US 99/21535
CURRENT APPLICATION NUMBER: US/09/413,814
EARLIER FILING DATE: 1999-10-07
EARLIER PILING DATE: 1999-10-07
SOFTWARE: PATON NUMBER: DE 198 46 493.2
SOFTWARE: PATON NOS: 107
 APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
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 935 PRVATPEEPFALTEGORAMWLECOKSADGALYNLGRTVRLGAGVDVAALRR 985
 GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Berjer, Stefan
APPLICANT: Beyer, Stefan
APPLICANT: Broecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Cino, Paul M
APPLICANT: Gioloberty, Brian A
APPLICANT: Giolobery, Steven L
 Gesellschaft fuer Biotechnologische Forschung mbH
 57;
 Score 79.5; DB
Pred. No. 4.2;
8; Mismatches
 Bristol-Myers Squibb, Co
 Sequence 44, Application US/09413814 Patent No. 6225064
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US-09-413-814-44
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Best Local Similarity 31.5%;
Matches 35; Conservative
 APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
 Bloecker, Helmut
 NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 881
 APPLICANT: Hofle, Gerhard
 APPLICANT: Hofle, Gerhard
 Stefan
 SEQ ID NO 80
LENGTH: 3079
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 86 PYRLRO-FHL-----HWGSSDDHGSEHTVDGVKYAA---ELHLVHWNPKYNTFKEALKQ 135
 Gaps
 33;
 69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 Length 259;
 34; Indels
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP--
SOFTWARE: PatentIn Release #1.0, Version #1.25
 DB 1;
 ; Score 70.5; D:
; Pred. No. 1.7;
18; Mismatches
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DB 4; Length 881;

10.8%; Score 75;

Query Match

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,986
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leeslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-028
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-8864/9741
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDONUS
STREET: 1155 Avenue of the Americas
 COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, V
 APPLICATION NUMBER: US 08/015,973
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
 US/08/446,363
 APPLICATION NUMBER: US/08/448,164
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
 10.2%;
24.1%;
 Ouery Match
Best Local Similarity 24.19
Matches 27; Conservative
 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 single
 MOLECULE TYPE: protein US-08-446-363-10
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 unknown
 COMPUTER: IBM PC OPERATING SYSTEM:
 amino acid
 New York
: New York
RY: U.S.A.
 FILING DATE: 24 CLASSIFICATION:
 STRANDEDNESS:
 FILING DATE:
 CITY: N
STATE:
 qq
 δλ
 δ
 g
 Gaps
 69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 DB 1; Length 259
 GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
 APPLICANT: SCILESSINGER, JOSEPH
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-GAMMA
NUMBER OF SECUENCES: 14
CORRESPONDENCE ADDRESS:
 Indels
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP--
 STATE: New York
COUNTRY: U.S.A.
2 ID: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/015,973
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
 34;
 ; Score 70.5; DI
; Pred. No. 1.7;
18; Mismatches
 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
 ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
 7683-021
 US-08-446-363-10
Sequence 10, Application US/08446363
Patent No. 5891700
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
 ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTATION UNBER: 18,872
REFERENCE/DOCKET UNBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEFONE: (212)790-9090
TELEFAX: (212)869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
 Sequence 6, Application US/08015973 Patent No. 5604094
 10.2%;
24.1%;
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Query Match 10.2%
Best Local Similarity 24.1%
Matches 27; Conservative
 SEQUENCE CHARACTERISTICS:
 ss: single
unknown
 TOPOLOGY: unknown;
MOLECULE TYPE: protein
US-08-015-973-6
 New York
: U.S.A.
 STREET: 1155 6.
 COUNTRY: UZIP: 10036
US-08-015-973-6
 STATE:
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69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 ; Score 70.5; DB 2; Length 259;
; Pred. No. 1.7;
18; Mismatches 34; Indels 3
 US-08-448-164-6
; Sequence 6, Application US/08448164
; Patent No. 522536
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-BETA
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP--
PatentIn Release #1.0, Version #1.25
 Patentin Release #1.0, Version #1.25
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Query Match
Best Local Similarity
 COMPUTER:
 LIBRARY:
 COUNTRY:
 RESULT 9
US-08-792-013-7
 Matches
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 qq
 οy
 g
 q
 ;
9
 86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAA---ELHLVHWNPKYNTFKEALKQ 135
 Gaps
 69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 Length 259;
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP---
 Indels
 Sequence 6, Application US/08081929
Patent No. 6160090
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Grumet, Martin H.
APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: STRUCTURAL DOMAINS AND LIGANDS
 34;
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/081,929
FILING DATE: 23-UUN-1993
 ; Score 70.5; DB 2;
; Pred. No. 1.7;
18; Mismatches 34;
 STREET: 1155 Avenue of the Americas CITY: New York CUTY: New York COUNTRY: U.S.A. 2IP: 10036
 7683-041-999
 NAME: COCUZZI, LAUTA A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPAN: 212 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 TELEPHONE: (212)790-9090
TELEFAX: (212)869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
 TELECOMMUNICATION INFORMATION:
 Query Match 10.2%;
Best Local Similarity 24.1%;
Matches 27; Conservative 11
 FILING DATE: 23-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
 259 amino acids
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
WOLECULE TYPE: protein
US-08-081-929-6
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
 ; MOLECULE TYPE: protein US-08-448-164-6
 NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & 1
 COMPUTER READABLE FORM:
 RESULT 8
US-08-081-929-6
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 9
 81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK-----ILAEEQ 132
 68 SLKRMLEKLGVPKTHLELKKLIREVSSGSEETF-SYSDFLRMMLGKRSAILRMILMYEEK 126
 ---IAPTDPEGLSDVSIRLQV 80
 11 AFGLLKAQQEERLDGINKHFLDDPKYSSDEDLQSKLEAFKTKYMEFDLNGNGDIDI---M 67
 33;
 33;
 69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 . :|:::| |::| : | |::| 136 RDGIAVIGIFLKIGHENGEFQ-----IFLDALDKIKTKGKEAPFTKFDPS 180
 Length 146;
 Length 259;
 42; Indels
 Indels
 24 PYAVRMTFHLPGDAPVTWA - - - FGRELLLDGINRPSGDGDVHIAPTDP - -
 34;
10.2%; Score 70.5; DB 4; 24.1%; Pred. No. 1.7;
 DB 4;
 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,013
FILING DATE: Filed Herewith
 42 AFG----RELLLDGINRP-----SGDGDVH-----
 18; Mismatches
 APPLICANT: Murry, Lynn E.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYTOKINES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
 Mismatches
 Score 69.5;
Pred. No. 1;
 PF-0205 US
 Sequence 7, Application US/08792013
Patent No. 6204021
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
 13;
 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
 10.0%;
nilarity 27.3%;
Conservative 1:
 E: Diskette
IBM Compatible
 27; Conservative
 STRANDEDNESS: single
 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 TYPE: amino acid
 linear
 Query Match
Best Local Similarity
 Palo Alto
 FILING DATE: FI
 TOPOLOGY: line
IMMEDIATE SOURCE:
 1514969
 USA
 QQ
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81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK------ILAEEQ 132
 69 SIKRMLEKLGVPKTHLELKKLIREVSSGSEETF-SYSDFLRMMLGKRSAILRMILMYEEK 127
 42 AFG----RELLLDGINRP----SGDGDVH-----IAPTDPEGLSDVSIRLQV 80
 Sequence 103, Application US/08485618

Patent No. 5728533

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 572853381 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
 APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
APPLICANT: Ulrus, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
 Length 147;
 42; Indels
 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COREATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janie
 DB 3;
 13; Mismatches
 Score 69.5;
 Pred. No.
 NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
TELEPHONE: 617/542-8906
 27.3%;
 LENGTH: 147 amino acids
 STATE: Illinois
COUNTRY: United States
 TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Conservative
 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 COMPÚTER READABLE FORM
 Query Match
Best Local Similarity
Matches 33; Conserva
 amino acid
 RY: USA
02110-2804
GENERAL INFORMATION:
 Boston
 US-08-485-618-103
 TOPOLOGY:
 US-08-361-441B-5
 STATE: M
COUNTRY:
 133; N 133
 128'N 128
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 81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK------ILAEEQ 132
 69 SIKRMLEKIGVPKTHIELKKITREVSSGSEETF-SYSDFLRMMLGKRSAILRMILMYBEK 127
 33;
 DB 1; Length 147;
 Indels
 Sequence 5, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: MATY E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
 42;
 10.0%; Score 69.5; DE ilarity 27.3%; Pred. No. 1; Conservative 13; Mismatches
 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55X
OPERATING SYSTEM: MS-DOS (Version 5.0)
 05433/006001
 42 AFG-----SGDGDVH--
 SOFTWARE: WORDFRIECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
 US-08-361-441B-5; Sequence 5, Application US/08361441B; Patent No. 6077948
 ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGIGSTRATFON NUMBER: 34,819
REFRENCE/COCKET NUMBER: 0543:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 Massachusetts
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 CLASSIFICATION: 514
 amino acid
 ; TOPOLOGY: linear
US-08-171-385-5
 Query Match
Best Local Similarity
Matches 33; Conserv
 STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02110-2804
 Boston
 STRANDEDNESS
 FILING DATE:
 128 N 128
 133 N 133
 133 N 133
 127 N 127
 US-08-171-385-5
 LENGTH:
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Matches
 QQ
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 7;
 123 TLLVGLSLELTVTVTVRNEGEDSYGTAITLYYPAGL------SYRRVSGOTQP 169
 61 ----VHIA----PIDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRIDKSVPLGQEQT 112
 170 WQRPLHLACEAVPTESEGLRSTS----CSVNHPIFQGGAQG--TFVVKFDVS----SKAS 219
 2 SFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD- 60
 Sequence 103, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 Indels 37;
 DB 1; Length 494;
 E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 54;
 Ouery Match 10.0%; Score 69.5; DB Best Local Similarity 23.4%; Pred. No. 5.3; Matches 33; Conservative 17; Mismatches
 REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEBHONE: 312-474-6300
TELERA: 312-474-0448
TELEX: 26-2005
 FILING DATE:
CLASSIFICATION: 435
PLOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
 TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
TOPOLOGY: linear
COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/M-19PHYRE: Patonia-
 220 LGD----RLLMGASASSENN 235
 113 LGDFEDSLEAALGKILAEEQN 133
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 COUNTRY: United States
ZIP: 60606-6402
 MOLECULE TYPE: protein US-08-485-618-103
 CITY: Chicago
STATE: Illinois
 ADDALL ZOURTHEET: ZOURTHEET: ZOURTHEET
 RESULT 13
US-08-605-672-103
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61 ----VHIA----PTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQT 112
 2 SFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD- 60
 Patent No. 3031021.
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: 103
 Length 494;
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
 . 2; DB 2; 5.3;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 17; Mismatches
 10.0%; Score 69.5; 23.4%; Pred. No. 5.
 FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTONNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
 27866/32684
 US/08/482,293A
APPLICATION NUMBER: US/08/605,672
 FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
TIME DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
 Sequence 103, Application US/08482293A Patent No. 5831029
 REFERENCE/DOCKET NUMBER: 27. TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEFAX: 312-474-0448
 220 LGD-----RLLMGASASSENN 235
 113 LGDFEDSLEAALGKILAEEQN 133
 33; Conservative
 STATE: Illinois
COUNTRY: United States
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-103
 CLASSIFICATION: 530
 APPLICATION NUMBER:
 Query Match
Best Local Similarity
 60606-6402
 US-08-482-293A-103
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----VHIA----PIDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQT 112
 170 WQRPLHLACEAVPTESEGLRSTS----CSVNHPIFQGGAGG--TFVVKFDVS----SKAS 219
 123 TLLVGLSLELTVTVTVTVRNEGEDSYGTAITLYYPAGL------SYRRVSGOTQP 169
 Indels 37; Gaps
 2. SFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD- 60
 DB 2; Length 494;
 Query Match
10.0%; Score 69.5; DE
Best Local Similarity 23.4%; Pred. No. 5.3;
Matches 33; Conservative 17; Mismatches
 Search completed: July 18, 2002, 14:16:09 Job time: 9699 sec
 US 08/362,652
 REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEFRAX: 312-474-6300
TELEFRAX: 312-474-6448
FREEX: 25-3856
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENTH: 494 amino acids
TYPE: amino acid
 NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
 | | | | : | : | LGD-----RLLMGASASSENN 235
 113 LGDFEDSLEAALGKILAEEQN 133
 FILING DATE: 21-DEC-1994 ATTORNEY/AGENT INFORMATION:
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-103
 APPLICATION NUMBER:
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 Sequence 103, Application US/08943363

Patent No. 5337478

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
CORRESPONDENCE: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STAFE: Illinois
COUNTRY: United States
COMPUTER: Illopy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
 170 WQRPLHLACEAVPTESEGLRSTS----CSVNHPIFQGGAQG--TFVVKFDVS----SKAS 219
 61 ----VHIA, ----PIDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQT 112
 2 SFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD- 60
 54; Indels 37;
 17; Mismatches
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 28,659

REFERENCE/DOCKET NUMBER: 27866/32684

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SOID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 494 amino acids
 PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
 220 LGD----RLLMGASASSENN 235
 113 LGDFEDSLEAALGKILAEEQN 133
 Query Match
Best Local Similarity 23.4%;
Matches 33; Conservative 1:
 ; MOLECULE TYPE: protein US-08-482-293A-103
 linear
 CLASSIFICATION:
 FILING DATE:
 US-08-943-363-103
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Copyright (c) 1993 - 2000 Compugen Ltd.
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July 18, 2002, 14:17:37; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec Run on:

US-09-749-185-9

692 1 MSFLVSEELSFKIPVELRYE......FEDSLEAALGKILAEEQNAG 135 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	Description	rotalizat ofdedova				amidophosphoribosy	carbonate dehydrat	endoglucanase C (E	hypothetical prote	amidophosphoribosy	conserved hypothet	probable ClpA/B-ty	translation initia	carbonate dehydrat	hypothetical prote	conserved hypothet	penicillin-binding	penicillin binding	conserved hypothet	carbonate dehydrat	probable alcohol d	hypothetical prote	_	끄	hypothetical prote	ч	Д	hypothetical prote	MHC class I RT1.C-	glycosyl hydrolase
SUMMARIES	ID	т37179	436147	T35247	T35319	G81935	A22612	S15271	H84169	A81170	F87327	G83635	S12566	152551	н70678	AD3237	G97472	AC2691	B87500	A43641	н69789	B90668	E85518	AE0358	C70963	B64993	G91017	A85862	169009	E75484
	DB		,	7	7	~	7	7	7	7	7	7	7	7	7	~	~	~	~	7	Н	7	7	~	N	7	~	N	N	0
	Length	136	142	138	142	514	259	1101	313	514	818	902	611	260	291	408	757	757	347	260	346	732	732	891	265	1337	1534	1534	343	657
d	Query Match	79.2	34.2	23.0	19.1	11.6	11.5	11.4	11.1	11.0	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.6	10.6	10.6	10.6	10.6	10.5	10.5	10.5	10.5	10.5	10.5
	Score	874	237	159	132.5	80	79.5	79	76.5	92	75.5	75.5	7.5	74.5	74.5	74.5	74.5	74.5	74	73.5	73.5	73.5	73.5	73.5			73	^	72.5	72.5
	Result No.	-	2	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable oxidoredu probable secreted	transcription regu hypothetical prote carbonate dehydrat	probable secreted laminin alpha 5 ch	<pre>UDP-N-acetylmuramo v-type ATP synthas ionized calcium bi</pre>	allograft inflamma hexokinase (EC 2.7 hypothetical prote	pyruvate dehydroge hypothetical cytos aldehyde dehydroge
D64754 T36609	B90719 C85569 CRHU3	T44873 T10053	AD0068 D75487 JC4902	I55617 S68694 E70747	F83676 AE3254 AC3043
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732	225 225 260	3635	458 690 146	147 484 626	328 389 505
10.5 10.3	10.2 10.2 10.2	10.2	10.1	10.0	10.0 10.0
72.5	70.5	70.5	70 70 69.5	69 69.5 69.5	69 69
30 31	3 8 8 2 8 4	392	37 38 39.	4 4 4 4 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	6 4 4 4 6 4 4 5

#### ALIGNMENTS

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probable regulator - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Dec-1999 #text_change 03-Dec-1999 C; Accession: T37179 C; Accession:
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Gaps ö Length 136; Indels 79.2%; Score 548; DB 2; L4 77.8%; Pred. No. 1.1e-46; Live 14; Mismatches 16; Query Match
Best Local Similarity 77.8%
Matches 105; Conservative

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2 MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGD 61 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60 δλ g

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121 EAALGKILAEEQNAG 135 ò

: || :||||||||| 122 DEALDRILAEEQSAG 136 g

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A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
 Query Match
Best Local Similarity 30.64
Matches, 37; Conservative
 1 MSFLVSEELSFKIPV-----
 Query Match 11.69
Best Local Similarity 23.09
Matches 50; Conservative
 69 E----
 140 A 140
 122 A 122
 C; Genetics:
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 probable regulator - Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Accesion: T35247
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Oliver, K.; Harris, Data Library, April 1999
A;Reference number: Z21573
A;Accession: T35247
A;Accession: T35247
A;Accession: T35247
A;Accession: T35247
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A;Accession: T35
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C; Daces (5. Nov-1999) #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C; Accession: T35319
R; Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A; Reference number: 221575
A; Reference number: 221575
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A;Molecule type: DNA
A;Residues: 1-142 <oli>A;Acls <oli>A;Cross-references: EMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
A;Experimental source: strain A3(2)
 ö
 3;
 61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
 ----TDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 Gaps
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
 Gaps
 13 IPVELRYETRDPYAVRMTFHLPG---DAPVTWAFGRELLLLDGINRPSGDGDVHIAP---- 65
 .;
0
 26;
A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
 Length 142;
 Length 138;
 Indels
 42;
 26;
 34.2%; Score 237; DB 2;
39.7%; Pred. No. 4.1e-16;
iive 20; Mismatches 56
 Query Match 23.0%; Score 159; DB 2; Best Local Similarity 33.1%; Pred. No. 1.8e-08; Matches 40; Conservative 13; Mismatches 42
 probable regulator - Streptomyces coelicolor
 Query Match
Best Local Similarity 39.78
Matches 50; Conservative
 137 AELLAR 142
 121 EAALGK 126
 120 L 120
 L 130
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 130
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 11;
 Gaps
 71 LSDVSIRLQVGAD-----RALFRAGAPPLVAFLDRTDKSVPLGQEQT-LGDFEDSLE 121
 404 EVRYPNVYGIDMPTREELIANGRSAAEIAAEIGADGIVFQDLGDLEAVVKALNPKIESF- 462
 11 FKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEG 70
 -----ELRYETRDPYA-----VRMTFHLP 34
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C;Superfamily: amidophosphoribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase
F;2-514/Product: amidophosphoribosyltransferase #status predicted <MAT>
F;2/Active site: Cys #status predicted
 -GLSDVSIRLQVGAD-----RALFRAGAPPLVAFL
 35 GDA------PVTWAF-GRELLL--DGI------NRPSGDGDVHIAPTDP
 11;
 90:
 Length 142;
 DB 2; Length 514;
 Indels
 53; Indels
19.1%; Score 132.5; DB 2; 30.6%; Pred. No. 7.6e-06; ive 21; Mismatches 52;
 99 DRIDKSVPLGQEQTLGDFEDSLEAALGKILAEEQNAG 135
 11.6%; Score 80; DB 223.0%; Pred. No. 5.1; ive 24; Mismatches
 A22612
carbonate dehydratase (EC 4.2.1.1) III - horse
Alternate names: carbonate dehydratase III
C;Species: Equus caballus (domestic horse)
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aminophosylutionary integrated are the control of t
 amidophosphoribosyltransferase (EC 2.4.2.14) NMB0690 [similarity] – Neisseria meningi
 Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Fing, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Las,
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 1276-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M
A;Acterscion: H84169
A;Accession: H84169
A;Status: preliminary
A;Molecule type: Dana
 A; Cross-references: GB: AE004437; NID: 910579744; PIDN: AAG18724.1; GSPDB: GN00138 C; Genetics:
 MGVSLAEKIKRELPVDGIDVVMPIPDTSRPSAMELAVHLDKPYREGLIKNRYIGRTFIMP 343
 11 FKIPVELRYET------RDPYAVRMTFHLPGDAPVTWAFGRELLLD--GINRPS 56
 -----VRMTFHLP 34
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;Reywords: glycosyltransferase; pentosyltransferase
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;2/Active site: Cys #status predicted
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 Length 313;
 11.0%; Score 76; DB 2; Length 514; llarity 23.0%; Pred. No. 13; Conservative 23; Mismatches 54; Indels
 98 LDRTDKSVPLGQEQTLGDFEDSLEAAL------GKILAEEQNAG 135
 224 -DRVREQVEAGSEEVGEDAYNLAELGIGTNVAVTELVGSVLLDEKAAG 270
 55;
 DB 2;
 19; Mismatches
 11.1%; Score 76.5; 24.4%; Pred. No. 6.2
 57 GD-----GDVHIAPTDPEG-
 1 MSFLVSEELSFKIPV----
 41; Conservative
 Query.Match
Best Local Similarity
Matches 41; Conserv
 Local Similarity
tes. 50; Conserv
 A; Molecule type: DNA
A; Residues: 1-313 <STO>
 A; Gene: VNG0096C
 Query Match
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 endoquacanase C (EC 3.2.1.-) - Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 01-Dec-2000
C;Accession: S15271; A43636
R;Coutinho, J.B.; Moser, B.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Mol. Microbiol. 5, 1221-1233, 1991
A;Title: Nucleotide sequence of the endoqlucanase C gene (cenC) of Cellulomonas fimi, it
A;Reference number: S15271; MUID:92065819
A;Recession: S15271
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A;Molecule type: DNA
A;Residues: I-1101 <COU>
A;Rossion: S15271
A;Status: preliminary
A;Note: the authors translated the codon GAC for residues 361, 380, 400, 550, 670, and 8
B;Moser, B.; Gillses, N.R.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Appl. Environ. Microbiol. 55, 2480-2487, 1989
A;Title: Purification and characterization of endoglucanase C of Cellulomonas fimi, clon
A;Reference number: A43636; MUID:90103465
A;Status: preliminary
A;Status: preliminary
 4
 Š,
22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 25-Apr-1997
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAP-----TDPEG 70
 19 YETRDPYAV -- RMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSI 76
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C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Superfamily: carbonate dehydratase; carbon-oxygen lyase; hydro-lyase; zinc
E;4-258/Domain: carbonic anhydrase homology <CAH>
F;1-258/Domain: carbonic anhydrase homology CAH>
F;1/Modified site: acetylated amino end (Ala) #status predicted
 Residues: 1.64,'W' <MOS>
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 Length 259;
 Length 1101;
 71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 Riwendorff, K.M.; Nishita, T.; Jabusch, J.R.; Deutsch, H.F.
J. Biol. Chem. 260, 6129-6132, 1985
A.Title: The sequence of equine muscle carbonic anhydrase.
A.Reference number: A22612; MUID:85207593
 ;
;
 ;;
 DB
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 Mismatches
 DB
 Score 79;
Pred. No.
 12;
 RVLVGEGGGAYRTAFEQGSAPL 277
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 A;Gene: cenC
A;Start codon: GTG
C;Keywords: glycosidase; hydrolase
 11.5%;
26.6%;
 11.4%;
 Conservative
 Conservative
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 Query Match
Best Local Similarity
Matches 25; Conserv
 Query Match
Best Local Similarity
Matches 29; Conserv
 Molecule type: DNA
 Accession: A22612
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Genetics:

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RESULT

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QY         35 GDAPVTWAF-GRELLLDGINRPSGDGDVHIAPTDP 68           Db         344 GQATRKKSVRQKLSPMETEFAGKSVLLVDDSIVRGTTSREIVEMVRAAGARKVYIASAAP 403           QY         69 E	Query Match  Query Match  10.9%; Score 75.5; DB 2; Length 902;  Best Local Similarity 24.6%; Pred. No. 28;  Matches. 35; Conservative 18; Mismatches 46; Indels 43; Gaps 6;  Qy .7 EELSFKIPVELRYETROPAVRMTFHLEGDAPVTWAFGRELLLDGINRPSGGDVHIAPT 66     : ::
F87337  Conserved hypothetical protein CC0633 [imported] - Caulobacter crescentus C.Species: Caulobacter crescentus	Qy 105 VPLGQEQTLGDFEDSLEAALGK 126                       Db 315 VGAGGAAGTGDAANLLKPALAR 336
C; Accession: F87327 R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A; Reference number: A87249; MUID:21173698; PMID:11259647	RESULT 12 \$12566 translation initiation factor eIF-4B - human C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999 C;Accession: \$1256 R;Milburn, S.C.; Hershey, J.W.B.; Davies, M.V.; Kelleher, K.; Kaufman, R.J. FMRO 1, 9, 2783-2790, 1990
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-818 <sto> A;Cross-references: GB:AE005673; NID:g13421844; PIDN:AAK22618.1; GSPDB:GN00148 C;Genetics: A;Gene: CC0633</sto>	A; Title: Cloning and expression of eukaryotic initiation factor 4B cDNA: sequence det A; Reference number: \$12566; MUID:90360989 A; Accession: \$12566 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecu
Query Match  10.9%; Score 75.5; DB 2; Length 818; Best Local Similarity 27.2%; Pred. No. 25; Matches 41; Conservative 17; Mismatches 50; Indels 43; Garches 22 RDPYAVR	or eIF- sis; RN yy <rrm< td=""></rrm<>
1QALKFMLGFLKGFAVGADRALFRA :       HYAAPIAAPITL-PA DSLEAALG	Query Match  10.8%; Score 75; DB 1; Length 611; Best Local Similarity 25.0%; Pred. No. 19; Matches 39; Conservative 15; Mismatches 38; Indels 64; Ga  14 PVELRYETRDPYAVRMTFHLECDAPVTWAFGRELLLDGINRPSGDGDVHIAP
Db 253 AQPQFLGHYQPRLPADLGFYDLRQREVLAQQ 283  RESULT 11	Db 37 PVSWADETDDLEGDVSTTWHSNDDDVYRAPPIDRSILP 74 Qy 66 TDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSV
probable ClpA/B-type chaperone PA0090 [imported] - Pseudomonas aeruginosa (strain PAO1) C.Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa C.Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C.Accession: 683635	Qy 106PLGQEQTLGDFEDSLEAALGKILAEEQNAG 135 10
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho A; Reference number: A82950; MUID:20437337	ISSULT. 13 IS2551 carbonate dehydratase (EC 4.2.1.1) III - rat N;Alternate names: carbonic anhydrase III C;Species: Rattus norvegicus (Orvewy rat)
A Status: preliminary A Molecule type: DNA A; Residues: 1-902 <stoo 1-902="" 99945902;="" <stoo="" a;="" aag03480.1;="" ae004091;="" ae004447;="" atp-binding="" c;="" chain<="" clp="" cross-references:="" endopeptidase="" experimental="" gb:="" gene:="" genetics:="" gn001="" gspdb:="" nid:="" pa0090="" pao1="" pidn:="" residues:="" source:="" strain="" superfamily:="" td=""><td></td></stoo>	
	A;Residues: 1-260 <res></res>

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C;Accession: AD3237
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 conserved hypothetical protein Atu6078 [imported] - Agrobacterium tumefaciens (strain
 Aftitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AREINE AREINE NUMBER: AREINE NUMBER: AREINE NUMBER: AREINE NUMBER: ALEINE NUMBER: ALEINE NUMBER: ALEINE ALUGORE
A.REFERENCE NUMBER: ALUGORE NUMBER: A
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C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 ----PPLVAFLDRTDKSVPLGQEQ 111
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 PSG-----DGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLG 108
 30. TFHLPGDAPVTWAF-----GRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQV--GA
 24, TGYLPDTATATAVFLADRLGKPLLVEG - - - PAGVGKTELARAVAQATGSGLVRLQCYEGV
 Length 408;
 Indels
 61;
 5;
 DB
 10.8%; Score 74.5; D
Llarity 25.5%; Pred. No. 13;
Conservative 19; Mismatches
 12. KIPVELRYETRDPYAVRMTFHLPGDAPVTWA----
 109 QEQTLGDFEDSLEAALGKILA--EEQNAG 135
 PIIVCRDTDQEAQEYYGAIVAAVEQRNVG 315
 completed: July 18, 2002, 14:17:38
he: 9548 sec
 83 D--RALF------RAGA----
 112 TLGDFEDSLEAALGKILAE 130
 141 DKADIE--IEGLLLEVLSD 157
 Local Similarity
hes 38; Conserv
 A; Genome: plasmid
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Matches 38
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Job time:
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 A; Molecule type: protein
A; Residues: 19-28, 'X', 30-33 <NAG>
A; Residues: 19-28, 'X', 30-33 <NAG>
B; Experimental Source: Long Evens Cinnamon
B; Chai, Y. C.; Jung, C.H.; Lii, C.K.; Ashraf, S.S.; Hendrich, S.; Wolf, B.; Sies, H.; Thc
Arch. Blochem. Blophys. 284, 270-278, 1991
A; Title: Identification of an abundant S-thiolated rat liver protein as carbonic anhydra
A; Reference number: $13896; MUID:91112820
 A; Molecule fype: profein
A; Molecule fype: profein
A; Residues: 25, X',27-34,38,'T',40-42,'XX',45-46,'S',48-51,'X',53-56,'RVV',74,'XXTFX',86
C; Superfamily: carbonate dehydratase; carbonic anhydrase homology
C; Keywords: blocked amino end; carbon-oxygen lyase; hydro-lyase
F;5-259/Domain: carbonic anhydrase homology <CAH>
 hypothetical protein Rv2426c - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Saccession: H70678
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID:98295987
A; Reference number: A70500; MUID:98295987
A; Accession: H70678
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A; Accession: H70678
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 87 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTSEEALKQPDG 139
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 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAP-----TDPEG 70
A;Cross-references: GB:M22413; NID:g203224; PIDN:AAA40846.1; PID:g203225 R;Lynch, C.J.; Brennan, W.A.J.; Vary, T.C.; Carter, N.; Dodgson, S.J. Mn. J. Physiol. 264, E621-E630, 1993 A;Title: Carbonic anhydrase Ill in obese Zucker rats. A;Reference number: A48856; MUID:93236031
 27;
 43;
 Length 260;
 Length 291;
 71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 Indels
 Indels
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 39;
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 DB 2;
 Score 74.5; DB
 14; Mismatches
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 A; Reference number: A61530; MUID: 92070082
 A;Experimental source: strain H37Rv C;Genetics:
 10.8%;
26.6%;
 Query Match
Best Local Similarity 25.99
Matches 36; Conservative
 Conservative
 Best Local Similarity
 Status: preliminary
 A; Accession: A48856
 A; Accession: B61530
 A; Accession: S13896
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 Query Match
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2002, 14:31:56; Search time 45.63 Seconds (without alignments) 114.555 Million cell updates/sec Run on:

US-09-749-185-9 692 1 MSFLVSEELSFKIPVELRYE......FEDSLEAALGKILAEEQNAG 135 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	P07450 equus cabal	P14090 cellulomona	P23588 homo sapien		P16015 mus musculu	P71930 mycobacteri	P77489 escherichia	033517 rhodobacter	P07451 homo sapien	_	Q9rwh3 deinococcus		P95522 phormidium		Q10966 mycobacteri	_			P43928 haemophilus	_	Q27575 drosophila	P96889 mycobacteri	•	Q14202 homo sapien	P46696 mycobacteri	Q49608 mycobacteri	_	P57145 buchnera ap	P11205 newcastle d	P95119 mycobacteri	_	093869 neurospora	P39925 saccharomyc
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SUMMARIES	ID	CAH3_HORSE	GUNC_CELFI	IF4B_HUMAN	CAH3_RAT	CAH3_MOUSE	YQ31_MYCTU	YAGR_ECOLI	SECD_RHOCA	CAH3_HUMAN	LMA5_MOUSE	VATI_DEIRA	AIF1_RAT	CYF_PHOLA	HXK1_SCHPO	YT17_MYCTU	EXON_HSV2	ENDA_HALVO	GLN1_STRVR	RF3_HAEIN	E2K3_MOUSE	PS73_DROME	YW84_MYCTU	KDPE_ECOLI	Z261_HUMAN	SYH_MYCLE	GYRA_MYCKA	EPB4_MOUSE	RPOC_BUCAI	RRPL_NDVB	UNG_MYCTU	YW40_PSEAE	GYS_NEUCR	AFG3_YEAST
	DB	; ⊣	<b>.</b>	-	Н	Н	-	Н	_	_	Н	7	_	-	-	_	Н	-	_	1	Н	Н	7	_	-	-	Н	Н	П	٦	П	7	_	~
	Query Match Length 1	259	1101	611	259	259	432	732	554	259	3718	069	147	338	484	602	620	339	469	527	1114	252	143	225	1370	427	549	987	1407	2204	227	285	206	761
d	Query Match	11.5	11.4	10.8	10.8		10.5	10.5	10.3		10.2	10.1	10.0	10.0	10.0	10.0	10.0	9.9	6.6	8.6	8.6			•		•			•			9.5	•	9.5
	Score	79.5	79	75	74.5	73.5	73	72.5	71	70.5	70.5	70	69.5	69.5	69.5	69.5	69	68.5	68.5	68	67.5	29	66.5	66.5	66.5	99	99	99	99	99	65.5	65.5	65.5	65.5
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Q8ywh5 anabaena sp P51537 nordotis ma	P14432 mus musculu P34536 caenorhabdi O53189 mvcobacteri		P96981 rhodobacter P51198 porphyra pu		-
MOAE_ANASP MYG_NORMA	HAIT_MOUSE YNC3_CAEEL TIG MYCTH	LIGC_TRAVE	GLO2_RHOCA ACCD_PORPU	KPYK_METEX GYRA MYCGO	SYFB_THETH
	~ ~ ~		п п	1	-
165	384	372	256 288	483	785
0 0 4 4	0 0 0 4 4 4		0.0	9.5	9.5
65 65	655	64.5	64	64	64
34 35	36 37.	96.0	41.	43. 443.	45

## ALIGNMENTS

RESULT CAH3_H ID C	RESULT 1 CARJ-MORSE STANDARD: PRT: 259 AA.	
AC P	Control Control	
담	(Rel. 07, Creat (Rel. 07, Last	
DE DE	16-OCT-2001 (Rel. 40, Last annotation update) Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-	
DE		
os	s caballus (Horse).	
88	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Perissodactvla: Equidae: Equus.	
o X	)=9796;	
N I	[1]	
R R	SEQUENCE. MEDLINE-85207593: PubMed=3922970:	
RA	rff K.M., Nishita T., Jabusch J.R., Deutsch H	
RI	e sedneuce c	
3 5	J. Biol. Chem. 260:6129-6132(1985). pinctine brurbstrir underthy de cappon dioxide	
ខ្លួ		
ပ္ပ		
ပ္ပင္ပ	-1- SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE	
ט ני	FAMILIA PITD: x07613	
DR DR	FIK; AZZOLZ; AZZOLZ. HSSP: P00918: 1BV3.	
DR	InterPro; IPR001148; Carb_anhydrase.	
DR	Pfam; PF00194; carb_anhydrase; 1.	
DR G	ProDom; PD000865; Carb_anhydrase; 1.	
Z 3	TYPOTIE'S PINC. PINC. COLAMNIUMASE, I.	
E E		
FT	93 93 ZINC	
FT	95 ZINC	
FT	118 118 ZINC (CATALYTIC).	
og S	SEQUENCE 259 AA; 29380 MW; B3EECDFF89BFEDUZ CRC64;	
N W W	Query Match 11.5%; Score 79.5; DB 1; Length 259; Best Local Similarity 26.6%; Pred. No. 0.9; Matches 29; Conservative 16; Mismatches 37; Indels 27; Gaps 5	5,
ò	PYAVBMTFHI.DGDADVTWAFGRELIT.DGTNRPSGDGDVHTAPTDPE	
5		
g	86 PYRLRQ-FHLHWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTYGGALKQPDG 138	
Qy	71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119	
q	::   ::  ::   ::  ::  :  :  :  :  :  :	
RESULT GUNC_C	CELFI	
AC D	GUNC_CELFI STANDARD; PRT; 1101 AA. P14090;	

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EMBL; M29708; AAA23088.1; ALT_SEQ

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 Coutinho J.B., Moser B., Kilburn D.G., Warren R.A.J., Miller R.C. Jr.; "Nucleotide sequence of the endoglucanase C gene (cenc) of Cellulomonas fini, its high-level expression in Escherichia coli, and characterization of its products."; Mol. Microbiol. 5:1221-1233(1991).
 (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 SEQUENCE OF 1-64 FROM N.A., AND SEQUENCE OF 625-641.
SEQUENCE OF 1-64 FROM N.A., AND SEQUENCE OF 625-641.
MEDLINE-90103465; PubMed-2604391;
MOSET B., Gilkes.N.R., Kilburn D.G., Warren R.A.J., Miller R.C. Jr.;
"Purification and characterization of endoglucanase C of Cellulomonas fimi, cloning of the gene, and analysis of in vivo transcripts of the
 MEDLINE-92269585; PubMed-1375311;
Coutinho J.B., Gilkes N.R., Warren R.A.J., Kilburn D.G.,
Miller R.C. Jr.;
"The binding of Cellulomonas fimi endoglucanase C (CenC) to cellulose and Sephadex is mediated by the N-terminal repeats.";
Mol. Microbiol. 6:1243-1252(1992).
 MEDLINE-97074498; PubMed-8916925;
Johnson P.E., Joshi M.D., Tomme P., Kilburn D.G., McIntosh L.P.;
"Structure of the N-terminal cellulose-binding domain of Cellulomonas
 fini cenc determined by nuclear magnetic resonance spectroscopy.";
Biochemistry 35:14381-14394(1996).
-!- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
(1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
(2) EXOCELLOBIOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 linkages in cellulose.
 01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endoglucanase C precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase C)
 HYDROLASES).
SIMILARITY: CONTAINS 2 CELLULOSE-BINDING DOMAIN (CBD) REMOTELY
 Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas.
NCBI_TaxID=1708;
 IDENTIFICATION OF IG-LIKE DOMAINS.
MEDLINE-97035265; PubMed-8860921;
Bateman A., Eddy S.R., Chothia C.;
"Members of the immunoglobulin superfamily in bacteria.";
Protein Sci. 5:1939-1942(1996).
 RELATED TO BACTERIAL-TYPE CBD'S. SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE DOMAINS.
 Appl. Environ. Microbiol. 55:2480-2487(1989).
[3]
CELLULOSE-BINDING DOMAINS.
 FROM N.A., AND SEQUENCE OF 33-42.
 STRAIN=ATCC 484;
MEDLINE=92065819; PubMed=1956299;
 Created)
 STRUCTURE BY NMR OF 33-184
01-JAN-1990 (Rel. 13, 01-MAR-1992 (Rel. 21, 16-OCT-2001 (Rel. 40,
 Cellulomonas fimi
 (Cellulase C).
 SEQUENCE
 -

 [5]
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EMBL; X57858; CAA40993.1; -. EMBL; M29707; AAA23087.1; ALT_TERM.

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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90360989; PubMed-2190971;
Milburn S.C., Hershey J.W.B., Davies M.V., Kelleher K., Kaufman R.J.;
"Cloning and expression of eukaryotic initiation factor 4B cDNA:
sequence determination identifies a common RNA recognition motif.";
 Gaps
 19 YETRDPYAV--RMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSI 76
 Methot N., Pause A., Hershey J.W., Sonenberg N.; "The translation initiation factor eIF-4B contains an RNA-binding region that is distinct and independent from its ribonucleoprotein
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 10;
 PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; FALSE_NEG.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat; Immunoglobulin domain; 3D-structure.
 DB 1; Length 1101;
 35; Indels
 1FBAD189CC5F8B5D CRC64;
 Eukaryotic translation initiation factor 4B (eIF-4B).
EIF4B.
 ENDOGLUCANASE C.
CELLULOSE-BINDING 1.
CELLULOSE-BINDING 2.
CATALYTIC.
IG-LIKE DOMAIN 1.
IG-LIKE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 11.4%; Score 79; DB 1
30.5%; Pred. No. 5.7;
ive 12; Mismatches
 611 AA
PIR; $15271; $15271.
PDB; IULO; OLARR-97.
PDB; IULO; OLARR-97.
INTERPO; IPR001305; CBD_6.
INTERPO; IPR001701, Glyco_hydro_9.
INTERPO; IPR001701, Glyco_hydro_9.
INTERPO; IPR001806; Ig_MHC.
INTERPO; IPR004197; cebb_N.
PFam; PP02201; CBD_6; 2.
Pfam; PP02201; CBD_6; 2.
Pfam; PP02927; celb_N; 1.
Pfam; PP03927; celb_N; 1.
Pfam; PP03927; celb_N; 1.
Pfam; PP03927; celb_N; 1.
Pfam; PP03927; celb_N; 1.
 Mol. Cell. Biol. 14:2307-2316(1994).
 CHARACTERIZATION.
MEDLINE-94187701; PubMed-8139536;
 115216 MW;
 77 RLQV----GADRALFRAGAPPL 94
 EMBO J. 9:2783-2790(1990).
 Conservative
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 1101
173
318
880
1006
1097
 consensus sequence."
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 Local Similarity
 1101
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64
212
329
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918
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831
831
 25;
 IF4B_HUMAN
 ACT_SITE
ACT_SITE
SEQUENCE
 Query Match
Best Local 5
 ACT_SITE
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 SIGNAL
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 DOMAIN
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 DOMAIN
 RESULT 3
IF4B_HUMAN
 CHAIN
 256
 Matches
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 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=Wister: TISSUB-Liver;

X MEDLINE-20361776; Pubmed-10900145;

A Ikeda M., Ishii Y., Kato H., Akazawa D., Hatsumura M., Ishida T.,

A Matsusue K., Yamada H., Oguri K.;

Matsusue K., Yamada H., Oguri K.;

A Matsusue K., Yamada H., Oguri R.;

A Matsusue K., Yamada H., Oguri R.;

T "Suppression of carbonic anhydrase III in rat liver by a dioxin-related toxic compound, coplanar polychlorinated biphenyl,

T 3,3',4,4' 5-pentachlorobiphenyl.";

Arch Biochem Biophys. 380:159-164(2000).

C -: FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.

C -: CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.

C -: SINGLELLULAR LOCATION: Cytoplasmic.

C -: SINILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE

C -: FAMILK.
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAP------TDPEG 70
 CAH3_MOUSE STANDARD; PRT; 259 AA.
P16015;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
11 (CCT-2001 (Rel. 40, Last annotation update)
11 (EC 4.2.1.1) (Carbonate dehydratase III) (CA-III)
 Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A.; "cDNA sequence of rat liver carbonic anhydrase III."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
 10.8%; Score 74.5; DB 1; Length 259; 26.6%; Pred. No. 2.8;
 71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 Indels
 ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
A -> G (IN REF. 1).
FG -> SE (IN REF. 1).
KL -> NV (IN REF. 1).
 14; Mismatches
 Pfam; PF00194; carb_anhydrase; 1.
Probom; PD000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc.
 HSSP; P00918; ICIM.
InterPro; IPR001148; Carb_anhydrase.
 EMBL, AF037072; AAB92558.1; -. EMBL, AB030829; BAB08111.1; -. HSSP; P00918; 1CIM.
 MM.
 Biosci. Rep. 8:401-406(1988).
 EMBL; M22413; AAA40846.1;
 29300
 Conservative
 223
259 AA;
 Similarity
 SEQUENCE FROM N.A.
 TISSUE-Liver;
 29;
 INIT_MET
METAL
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 METAL
CONFLICT
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 CAH3_MOUSE
 Matches
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 6
 Methot N., Song M.S., Sonenberg N.;

"A region rich in aspartic acid, arginine, tyrosine, and glycine (Brg3) mediates eukaryotic initiation factor 4B (eIF4B) self-association and interaction with eIF3.";

Mol. Cell. Biol. 16:5128-5334(1996).

- FUNCTION: REQUIRED FOR THE BINDING OF MRNA TO RIBOSOMES. FUNCTIONS IN CLOSE ASSOCIATION WITH EIF4-F AND EIF4-A. BINDS NEAR THE 5'-TEMMINAL CAP OF MRNA IN PRESENCE OF EIF-4F AND ATP. PROMOTES THE ATPASE ACTIVITY AND THE ATP-DEPENDENT RNA UNWINDING ACTIVITY OF
 75 TAPRAAREPNI-----DRSRL-PKSPPYTAFLGNLPYDVTEESIKEFFRGLNISAVRLP 127
 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 14 PVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVH-----IAP 65
 37 PVSWADETDD------LEGDVSTTW-------HSNDDDVYRAPPIDRSILP 74
 15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
 SEQUENCE FROM N.A.

BEDLINE-SB166882. PubMed-2852973;
Kelly C.D., Carter N.D., Jeffery S., Edwards Y.H.;
"Characterisation of cDNA clones for rat muscle carbonic anhydrase
 SUBUNIT: SELF ASSOCIATES AND INTERACTS WITH EIF3 P170 SUBUNIT. SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 10.8%; Score 75; DB 1; Length 611; 25.0%; Pred. No. 7; tive 15; Mismatches 38; Indels
 5EAD0891694D00D9 CRC64;
 66 TDPEGLSDVSIRLQVGADRALFRAGAPPLVAFL----DRTDKSV---
 PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
Protein biosynthesis; Initiation factor; RNA-binding.
 --PLGQEQTLG----DFEDSLEAALGKILAEEQNAG 135
 128 REPSNPERLKGFGYAEFED-LDSLLSALSLNEESLG 162
 259 AA
 RNA-BINDING
 DRYG
 MEDLINE-96413282; PubMed-8816444;
 CAH3_RAT STANDARD; P
P14141: 054961;
01-JAN-1990 (Rel. 13, Created)
15-UUL-1999 (Rel. 38, Last sequ)
01-MAR-2002 (Rel. 41, Last anno
 611 AA; 69224 MW;
 EMBL; X55733; CAA39265.1; -. PIR; S12566; S12566.
MIM; 603928; -.
 BOTH EIF4-A AND EIF4-F.
 InterPro; IPR000504; RRM. Pfam; PF00076; rrm; 1. SMART; SMO0360; RRM; 1.
 Conservative
 Rattus norvegicus (Rat).
 Local Similarity
nes 39; Conserv
 Query Match
Best Local Si
Matches 39,
 SEQUENCE
 DOMAIN
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5;

Gaps

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NCBI_TaxID=562;
[1]
 TIGR; MT2707;
 YAGR_ECOLI
P77489;
 Bishai W.;
 Query Match
 YAGR_ECOLI
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 'n
 86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPRYNTFGEALKQPDG 138
 27; Gaps
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAP-----TDPEG 70
 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 Biochem. Genet. 27:17-30(1989).
-!- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-!- CATALYTIC ACTIVITY: H(2)C0(3) = CO(2) + H(2)O.
-!- SUBCELLULAR LOCATION: CYLOPIASMic.
-!- SIMILARITY: BELONGS TO THE EUKARYOFIC-TYPE CARBONIC ANHYDRASE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Tweedie S., Edwards Y.;
"Mouse carbonic anhydrase III: nucleotide sequence and expression
 Length 259;
 Indels
 Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS
 E35B5CDDC4A54A93 CRC64;
 39;
 DB 1;
 ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
 0.1007-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 45.6 kDa protein Rv2631.
RV2631 OR MT2707 OR MTCX441.01.
 432 AA
 10.6%; Score 73.5; Di
26.6%; Pred. No. 3.5;
 Conservative 14; Mismatches
 HSSP, P00918; ICIM.
SWISS-2DPAGE; P16015; MOUSE.
MGD; MGI 88270; Car3.
InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
Pr0Dom; P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc.
 MEDLINE-89227981; PubMed-2496681;
 STRAIN=H37RV;
MEDLINE=98295987; PubMed=9634230;
 29397 MW;
 EMBL; M27796; AAA37355.1; -. PIR; A43641.
 STANDARD;
 musculus (Mouse)
 259 AA;
 Local Similarity
hes 29; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=1773;
 FAMILY.
 YQ31_MYCTU
P71930;
 INIT_MET
 SEQUENCE
 Query Match
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 9
 METAL
 YO31_MYCTU
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 Ω.
 SEQUENCE FROM N.A.
STRANG-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 ŝ
 Gaps
 24 PYAVRMTFHLPGDAPVTWAFG-----RELLLDGINRPSGDGDVHIAPTDPEGLSDVS 75
 10' PGIVRASYAMP---DVHWGYGFPIGGVAATDVDNDGVVSPGGVG------FDIS 54
 "Whole genome comparison of Mycobacterium tuberculosis clinical and
 Harris
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Susten S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
 Escherichia coli.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
 30;
 10.5%; Score 73; DB 1; Length 432; 28.9%; Pred. No. 7.3; ive 14; Mismatches 25; Indels
 Propriet is a series of the proteome. The protection of the protec
 76 -- IRLQV--GADRALFRAGAPPLVAFLDRTDKSVPLG 108
 88
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yagR.
 732
 EMBL; 280225; CAB02365.1; ALT_FRAME.
 PRT;
 FRAMESHIFT IN POSITION 257.
 TubercuList; Rv2631; -.
InterPro; IPR001233; UPF0027.
 Pfam; PF01139; UPF0027; 1.
PROSITE; PS01288; UPF0027; 1.
 EMBL; AE007103; AAK47022.1;
 Best Local Similarity 28.99
Matches 28; Conservative
 Nature 393:537-544(1998).
 STANDARD;
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58943 MW;
 Conservative
 STANDARD;
 412
455
511
536
 392
435
491
516
554 AA;
 SEQUENCE FROM N.A.
 Similarity
 SEQUENCE FROM N.A.
 41;
 RESULT 9
CAH3_HUMAN
ID CAH3_HUMAN
 TRANSMEM
TRANSMEM
 TRANSMEM
TRANSMEM
 Query Match
Best Local &
 SEQUENCE
 P07451
 Matches
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 5,
 D.,
 Gaps
 32 HLPGDAPVTWAFGRELLLDGINRPSG------DGDVHIAPTDPEGLSDVSIRLQVGA 82
SEQUENCE FROM N.A.
STRAINKIZ, MG165;
STRAINKIZ, MG165;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
 K.,
Lin I
 "Molecular and immunological analysis of an ABC transporter complex
 Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: YAGR, YAGS AND YAGT COULD BE THREE SUBUNITS OF A DEHYDROGENASE.
 13;
 Goldman B.S., Beckman D.L., Bali A., Monika E.M., Gabbert K.K.,
 Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 5
 Length 732;
 SIMILARITY: TO VERTEBRATE XANTHINE DEHYDROGENASES AND TC
R.PALUSTRIS 4-HYDROXYBENZOYL-COA REDUCTASE SUBUNIT HBAC.
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 Indels
 Pfam; PF01315; Ald_Xan_dh_C; 1.
Pfam; PF02738; Ald_Xan_dh_C2; 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
SEQUENCE 732 AA; 78088 MW; AF198715794F0138 CRC64;
 27;
 DB 1;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
 Score 72.5; DB Pred. No. 15; 10; Mismatches
 554 AA.
 required for cytochrome c biogenesis.";
J. Mol. Biol. 268:724-738(1997).
 Protein-export membrane protein secD
 EMBL; U73857; AAB18013.1; -. EcoGene; EG13557; yagR.
InterPro; IPR000674; Aldxan_dh_C.
 MEDLINE=97318920; PubMed=9175857;
 10;
 EMBL; AE000136; AAC73387.1; -.
 10.5%;
 Conservative
 STANDARD;
 DELAEKAGIDPV 377
 83 DRALFRAGAPPL 94
 Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1061;
 STRAIN-SB100
 Rhodobacter.
 Kranz R.G.;
 22;
 SECD_RHOCA
033517;
 Query Match
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Matches
 SECD_RHOCA
 366
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 GLSDVSIRLQVGADRAL--FRAG--APPLVAFLDRTDKSVPLGQEQTLG------DF 116
 295 GAPAVSFRFNVSGARAFGDYTAGHIGEPFAIVLDGKVISAPTIQAHIAGGSGIITGRFSI 354
 237 KLTFHPVLSTTSNPNAPV--ASGNELLPDAERQGLYHLLDEVPVVTGDDLTDARPTTDDN 294
FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
WHICH COMPRISE SECA, SECB, SECB, SECE, SECG AND SECY
 (BY SIMILARITY).
SUBCELULAR LOCATION: Integral membrane protein (By similarity).
SIMILARITY: BELONGS TO THE SECD/SECF FAMILY. SECD FAMILY.
 Gaps
 28.RMTFH-----LPGDAPVTWAFGREL------LLDGINRPSGDGDVHIAP-TDPE 69
 01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-0CT-2001 (Rel. 40, Last andtation update)
carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
 MEDLINE=87092290; PubMed=3099285; Wade:R., Gunning.P., Eddy R., Shows T., Kedes L.; Wade:R., Gunning.P., Eddy R., Shows T., Kedes L.; Woclectide sequence, tissue-specific expression, and chromosome location of human carbonic anhydrase III: the human CAIII gene is located on the same chromosome as the closely linked CAI and CAII genes.";
 Homo.sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 42;
 MEDLINE=86221704; PubMed=3086182;
Lloyd J., McMillan S., Hopkinson D., Edwards Y.H.;
"Nucleotide sequence and derived amino acid sequence of a cDNA
encoding human muscle carbonic anhydrase.";
Gene.41:233-239(1986).
 Protein transport; Translocation; Transmembrane; Membrane.
TRANSMEM 10 30 POTENTIAL.
 DB 1; Length 554;
16;
 55; Indels
 DF2CBEEBA9F69EDF CRC64;
 259 AA.
 10; Mismatches
 10.3%; Score 71; 27.7%; Pred. No.
 POTENTIAL
 POTENTIAL
 POTENTIAL
 POTENTIAL
 117 EDSLEAAL-----GKILAEEQNAG 135
 EEATDLALLLRAGALPAGMTFLEERTIG 382
 PRT;
 EMBL; U69979; AAB62801.1; -.
InterPro; IPR003335; Secb_SecF.
Pfam; PF02355; Secb_SecF; 1.
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Mon Jul

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REVISIONS.
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 9
 86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAA---ELHLVHWNPKYNTFKEALKQ 135
 Lloyd J., Brownson C., Tweedie S., Charlton J., Edwards Y.H.; "Human muscle carbonic anhydrase: gene structure and DNA methylation patterns in fetal and adult tissues."; Genes Dev. 1:594-602(1987).
 Gaps
 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP------- 68
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
 -i- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-i- CATALITIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-i- SUBCELLULAR LOCATION: CYPOPLASMIC.
-i- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
-i- SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
 33;
 69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 136 RDGIAVIGIFLKIGHENGEFQ-----IFLDALDKIKTKGKEAPFTKFDPS 180
 10.2%; Score 70.5; DB 1; Length 259; 24.1%; Pred. No. 7;
 Indels
 BY SIMILARITY.

ZINC (CATALYTIC).

ZINC (CATALYTIC).

ZINC (CATALYTIC).

I -> V (IN REF. 2).

W; EFBC56CF7721E4E CRC64;
 34;
Proc. Natl. Acad. Sci. U.S.A. 83:9571-9575(1986)
 061001; 099H06;
01-NOV-1997 (Rel. 35, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
Laminin alpha-5 chain precursor.
 18; Mismatches
 PRT; 3718 AA
 Pfam; PF00194; carb_anhydrase.
Probom; P000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc.
 R PIR; A25850; -; NOT_ANNOTATED_CDS.
R PIR; A25850; A25850.
PIR; A26690; A26690.
HSSP; P00918; 1CIM.
HSC-2DPAGE; P07451; HUMAN.
INFORMATION PORTION PO
 interPro; IPR001148; Carb_anhydrase.
 MEDLINE-88056301; PubMed-2824285;
 30 I
29440 MW;
 SEQUENCE OF 1-92 FROM N.A. Timpl R., Sasaki T.;
 PARTIAL SEQUENCE FROM N.A.
 Conservative
 STANDARD;
 Mus musculus (Mouse)
 0
93
95
118
30
259 AA;
 Query Match
Best Local Similarity
Matches 27; Conserv
 LMA5_MOUSE
Q61001; Q9J
 FAMILY
 NIT MET
 CONFLICT
 SEQUENCE
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RT Completion of the Niterminal sequence of the murine Laminin alpha 5 (Pahin.) in closed to the Niterminal sequence of the murine Laminin alpha 5 (Pahin.) in the Subalited (JUL-2000) to the EMB/Canbank/DDBJ databases.

RESIDENCE-CSPE. OR 84-718 FROM NA Shares 1.R.;

RECORDER-CSPE. OR 84-718 FROM NA Shares 1.R.;

RECORDER-CSPE. OR 86-718 FROM NA Shares 1.R.;

REVERSION CONTROL FOR STATE
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3129 MTFHGHGFLPLALPDVAPIT----EVVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLREG 3183
 VATI_DEIRA STANDARD; PRT; 690 AA.
09RWH3;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
ATPI OR DR0695
 MTFH-----LPGDAPVTWAFGRELLLDGIN-RPSGDGDVHIAPTDPEGLSDVSIR-- 77
 STRAIN=R1.
STRAIN=R1.
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Möffat K.S., Qin H., Jiang L., Pemphile W., Crosby M., Shen M.,
 INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
N-LINKED (GLCNAC. . .) (POTENTIAL).
 (POTENTIAL).
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 ; Score 70.5; DB 1; Length 3718;
; Pred. No. 1.7e+02;
10; Mismatches 25; Indels 25;
 group; Deinococcales; Deinococcus
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 78 -----LOVGADRALFRAGAPPLVAE 97
:| | | | | | | | | | | 3110
3184 HVTLRFMNQEVETQR-VFADGAPHYVAF 3210
 Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
 10.2%;
31.8%;
 Conservative
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Best Local Similarity
Matches 28; Conserv
 1973
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Biophys. Res. Commun. 224:855-862(1996).
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 .;
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 Gaps
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 34 PGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVG-ADRALFRAGAP 92
 STRAIN-WISTAR; TISSUE-Testis; MEDLINE-96311378; PubMed-8713135; Imai Y., Ibata I., Ito D., Ohsawa K., Kohsaka S.; Tto D., Ohsawa K., Kohsaka S.; A novel gene ibal in the major histocompatibility complex class III region encoding an EF hand protein expressed in a monocytic
 InterPro; IPR003490; V_ATPase_sub_a.
Pfam; PF01496; V_ATPase_sub_a; 1.
Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
SEQUENCE 690 AA; 75223 WW; 30D7785EFF388EA2 CRC64;
 Utans U., Arceci R.J., Yamashita Y., Russell M.E.; "Cloning and characterization of allograft inflammatory factor-1: novel macrophage factor identified in rat cardiac allografts with
 CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
 01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Allograft inflammatory factor-1 (AFF-1) (Ionized calcium-binding adapter molecule 1) (Microglia response factor) (MFF-1).
AIR OR IBAI OR MRF1.
 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 radiodurans R1.";
Science 286:1571-1577(1999).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 14;
 "Genome sequence of the radioresistant bacterium Deinococcus
 Length 690;
 37;
 DB 1;
 93 PLVAFLDRTDK--SVP--LGQEQTLGDFEDSLEAALG 125
 147 AA
 10.1%; Score 70; DB 29.9%; Pred. No. 25; Live 17; Mismatches
 Clin. Invest. 95:2954-2962(1995)
 STRAIN-LEWIS; TISSUE-Heart;
MEDLINE-95286865; PubMed-7769138;
 P55009; P70491;
01-OCT-1996 (Rel. 34, Created)
 EMBL; AE001926; AAF10273.1; -.
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 EXPRESSION PEAKS AT DAY 7.

-! INDUCTION: BY INTERFORM GAMMA.

-! SIMILARITY: SOME, TO EF-HAND CALCIUM BINDING PROTEINS.

-! SIMILARITY: STRONG, TO BALLOON ANGIOPLASTY RESPONSIVE TRANSCRIPT 1.
81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK-----ILAEEQ 132
 69 SLKRMLEKLGVPKTHLELKKLIREVSSGSEETF-SYSDFLRMMLGKRSAILRMILMYEEK 127
 Gaps
 42 AFG----RELLLDGINRP-----SGDGDVH-----IAPTDPEGLSDVSIRLQV 80
 12 AFGLLKAQQEERLDGINKHFLDDPKYSSDEDLQSKLEAFKTKYMEFDLNGNGDIDI---M 68
 33;
 REF. 2).
 DB 1; Length 147;
 42; Indels
 ANCESTRAL CALCIUM SITE.
MSQSKDLQG -> MKPEEISR (IN
76EAIDAC977A71DA CRC64;
 Bacteria; Cyanobacteria; Oscillatoriales; Phormidium.
 EF-HAND (POTENTIAL)
 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
 10.0%; Score 69.5; Di
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 PRT;
 SEQUENCE FROM N.A.
MEDLINE-97009001; Pubmed-8856106;
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 InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 1.
 EMBL; U17919; AAA80105.1; -.
 EMBL; AB000818; BAA19189.1;
HSSP; P02593; 1AK8.
 147 AA; 16827
 Apocytochrome F precursor
 Conservative
 105
 D82069; BAA11533
 Phormidium laminosum
 Query Match
Best Local Similarity
Matches 33; Conserv
 NCBI_TaxID=32059;
 Calcium-binding.
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Hexokinase 1 (EC 2.7.1.1). HXK1 OR SPAC24H6.04.
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 -:- SUBURIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING
CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN.
-:- SUBCELLULAR LOCATION: THYLAKOID MEMBRARE (PROBABLE).
-:- SIMILARITY: BELONGS TO THE CYTOCHROWE C FAMILY.

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 8
Wagner M.J., Packer J.C.L., Howe C.J., Bendall D.S.; "Some characteristics of cytochrome f in the cyanobacterium Phormidium laminosum: its sequence and charge properties in the reaction with
 cyanobacterium Phormidium laminosum.";
Blochemistry 38:9590-9599(1999).
-!- FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAKOID MEMBRANE AND TRANSFERS ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM II. IT RECEIVES ELECTRONS FROM THE RIESKE IRON-SULFUR PROTEIN AND PASSES THEM TO PLASTOCYANIN; THIS FUNCTION IS VERY SIMILAR TO THAT OF MITOCHONDRIAL CYTOCHROME C1.
 133 RIPEEMKEEVGPSYLFQPYADDKQNIVLVGPLPGDQYEEIVFPVLSPNPATNKSVAFGKY 192
 47 LLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTD---- 102
 193 SIHLGANRGRG----QIYPTGEK-----SNNAVYNASAAGVITAIAKADDGSA 236
 61; Gaps
 12 KIPVELRYETR-----DPYA-----VRMTFHLPGDA------PV------TWAFGRE 46
 MEDLINE-99352179; PubMed-10423236;
Carrell C.J., Schlarb B.G., Bendall D.S., Howe C.J., Cramer W.A.,
 DB 1; Length 338;
 Smith J.L., structure of the soluble domain of cytochrome f from the "Structure" of the soluble domain of cytochrome f
 48; Indels
 Pfam; PF01333; Apocytochrome_F; 1.
PRINTS; PR00610; CYTOCHROMEF.
PROSITE; PS00190; CYTOCHROME_C; 1.
Electron transport; Heme; Photosynthesis; Photosystem I;
 103 ------KSVPLGQEQTLGDFEDSLEAALGKILAEEQNAG 135
 237 EVKIRTEDGTTIVDKIPAGPELIVSEGE---EVAAGAALTNNPNVG 279
 APOCYTOCHROME F.
IRON (HEWE AXTAL LIGAND).
HEME (COVALENT).
HEME (COVALENT).
IRON (HEME AXIAL LIGAND).
 ON (HEME AXIAL LIGAND). BD3D52036181FB50 CRC64;
 X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 46-295
 Created)
Last sequence update)
Last annotation update)
 484 AA
 Pred. No. 12;
; Mismatches
 Biochim. Biophys. Acta 1276:246-252(1996).
 Score 69.5;
 InterPro; IPR002325; Apocyt_F.
InterPro; IPR000345; CytC_heme_bind.
 Photosystem II; Signal; 3D-structure
 20;
 66 HI
69 HI
70 II
36069 MW;
 EMBL; Y09612; CAA70824.1; -.
 10.0%;
 22.3%;
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 STANDARD;
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 PDB; 1CI3; 31-MAY-00.
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Matches 37; Conserv
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 plastocyanin.
 01-NOV-1995
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15-JUL-1998
 HXK1_SCHPO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 57.GDGDVHIAPTDPEGLSDVSI-----RLQVGADRALFRAGAPPLVAFLDRTDKSVPL 107
 Gaps
 -i- FUNCTION: HAS LOW AFFINITY FOR GLUCOSE AND SOME OF ITS ANALOGS.
-i- CATALYITIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-i- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
-i- SUBUNIT: MONOMER.
 MEDLINE-96140736; PubMed-8549830;
Petit T., Blazquez M.A., Gancedo C.;
"Schizosaccharomyces pombe possesses an unusual and a conventional
hexokinase: blochemical and molecular characterization of both
 8 ELSFKIPVELRYETRDPYAVRMTFHL---PGDAPV--TWAFGRELLLDGINRPS----
 35 EEQFTIPTELLHRVTDRFVSELYKGLTTNPGDVPMVPTWIIGTP---DGNEHGSYLALDL
 Transferase; Kinase; Glycolysis; ATP-binding; Multigene family.
BINDING 115 115 ATP (BY SIMILARITY).
DOMAIN 154 180 GLUCOSE-BINDING (POTENTIAL).
SEQUENCE 484 AA; 53597 WW; 165500F19E6BBB0F CRC64;
 27;
 Length 484;
 Indels
 Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
 10.0%; Score 69.5; DB 1; 1
26.2%; Pred. No. 19;
Live 14; Mismatches. 52;
 Y117_MYCTU STANDARD; PRT; 602 AA. 010966, 210967; Created)
16-OCT-1996 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
18-OCT-2010 (Rel. 40, Last annotation update)
 Barrell B.G., Rajandream M.A., Walsh S.V.;
 InterPro; IPR001312; Hexokinase.
Pfam; PF00349; hexokinase; 1.
PRINTS; PR00475; HEXOKINASE.
PRODO; PD001109; Hexokinase; 1.
PROSITE; PS00378; HEXOKINASES; 1.
 EMBL; X92894; CAA63487.1; -.
 FEBS Lett. 378:185-189(1996)
 Query Match
Best Local Similarity 26.2%
Matches 33; Conservative
 EMBL; Z54142; CAA90848.1;
HSSP; P19367; 1HKC.
 Schizosaccharomyces
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=4896;
 108 GQEQTL 113
 148 GKSQNL 153
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Job time: 946 sec
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 7;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Shelton S., Squares S., Squares R., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
 STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 148 VRTEARKTLVVFDEIHHGGDAK-TWGDAIREAFGDATRRLALTGTPFRSDDSPIPFVSYQ 206
 PEGLSDVSIRLQV----GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAA 123
 23; Gaps
 17 LRYETRDPYAVRMTFHLPGDAPVTW-----AFG---RELLLDGINRPSGDGDVHIAPTD 67
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
 Bishal W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: STRONG, TO M.LEPRAE ML1624.
 EMBL; ALC.

TIGR: MT2985; -.

A TUBCCULIST: RV2917; -.

R InterPro; IPR001410; DEAD.

DR SMART; SM00382; AAA; 1.

DR SMART; SM00487; DEXDC: 1.

W Hypotherical protein; Complete proteome.

W Hypotherical protein; Complete proteome.

TOTAL NO. STORY STOR
 10.0%; Score 69.5; DB 1; Length 602; 30.5%; Pred. No. 24;
 Query Match 10.0%; Score 69.5; DB 1; Length 6(Best Local Similarity 30.5%; Pred. No. 24; Matches 40; Conservative 11; Mismatches 57; Indels
 EMBL; 274697; CAA98979.1; ALT_INIT.
EMBL; AE007120; AAK47311.1; -.
 MEDLINE=98295987; PubMed=9634230;
 Mycobacterium tuberculosis
 LGEPLSAEQTA 268
 124 LGKILAEEQNA 134
 SEQUENCE FROM N.A.
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Search completed: July 18, 2002, 14:31:57

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OM protein

Run on:

Sequence:

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SEQUENCE FROM N.A.

van Wezel G.P., Rousseau C., Kraal B.;

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";

submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF195772: AAG28483.1; -

SEQUENCE 145 AA; 15838 MM; 92AC0F30DF3D2620 CRC64;
 Streptoverticillium netropsis (Streptoverticillium flavopersicus).
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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 Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 8.3e-62;
ive 0; Mismatches 0;
 145 AA
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 Q9BLC7
Q9K0C4
Q9KKD0
Q9AAG7
Q9EX45
Q9L218
Q91218
Q99L19
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 PRT;
(TrEMBLrel. 16, TrEMBLrel. 16, TrEMBLrel. 18,
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Matches 135; Conservative
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 MSFLVSEELSFKIPVELRYE.....FEDSLEAALGKILAEEQNAG 135
 July 18, 2002, 14:30:57; Search time 140.15 Seconds
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Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 562222 seqs, 172994929 residues
 SUMMARIES
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Copyright (c) 1993 - 2000
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Q9F9B5
P95753
Q9X9U2
Q9F9B7
Q9L268
Q9SZF7
Q9FCO7
Q9Y7M1
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sp_bacteria:*
sp_fung::*
sp_human:*
sp_invertebrate:*
sp_mammal:*
 sp_unclassified:*
 sp_virus:*
sp_vertebrate:*
 sp_organelle:*
sp_phage:*
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 Scoring table:
 Score
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Length 145; 0; Indels 61. VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120 71 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLQQEQTLGDFEDSL 130

121 EAALGKILAEEQNAG 135

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O9jvc9 r O9ckd1 p O9hss8 b

Q9ACY2 Q9JLM4 Q9JVC9 Q9CKD1 Q9HSS8

Result Š halobacteri

1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60

11. MSFLVSEELSFKIPVELRYETRDPYAVRMFFHLPGDAPVTWAFGRELLLDGINRPSGDGD

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Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J., Klassih H., Hopwood D.A.;

*Klassih H., Hopwood D.A.;

*A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

*Mol. Microbiol. 21:77-96(1996).

*EMBL; AL096823; CA846664.1;

*SEQUENCE 136 AA; 14920 MW; 4B67CIFIEOBECC88 CRC64;
 Streptomycineae; Streptomycetaceae; Streptomyces
 J., Barrell B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases
 the EMBL/GenBank/DDBJ databases
 STRAIN-A3(2);
MEDLINE-97000351; Pubmed-8843436;
 (TrEMBLrel. 16, (TrEMBLrel. 16, ICTEMBLrel. 16, ICTEMBLrel. 16, ICTEMBLrel. 16, ICTEMBLrel. 16, ICTEMBLRER
 Streptomyces goldeniensis.
 Matches 105; Conservative
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 121 EAALGKILAEEQNAG 135
 PRELIMINARY;
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 STRAIN=A3(2);
Seeger K., Harris D.;
Submitted (JUL-1999)
 STRAIN=A3(2);
James K.D., Parkhill
Submitted (JUL-1999)
 Best Local Similarity
Matches 105; Conserva
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 SEQUENCE FROM N.A.
 Local Similarity
 NCBI_TaxID=1902;
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 61
 Gaps
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
 STRAIN=B2682;
Shinichi K., Ensign J.;
"Cloning and characterization of a gene involved in sporulation and
cell division of Streptomyces griseus.";
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 Kawamoto S., Ensign J.C.;
"Cloning and characterization of a gene involved in regulation of
"Sporulation and cell division of Streptomyces griseus.";
Nippon Hosenkin Gakkaishi 9:136-151(1995).
 STRAIN=B2682;
Kawamoto S., Ensign J.C.;
"Isolation of mutants of Streptomyces griseus that sporulate in nutrient rich media.";
 ;
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 MEDLINE-97286526; PubMed-9141673; Kawamoto S., Watanabe H., Hesketh A., Ensign J.C., Ochi K.; "Expression analysis of a ssgA gene product associated with sportulation and cell division in Streptomyces griseus."; Microbiology 143.1077-1086(1997).

EMBL; D50051; BAA21558.1; -. SEQUENCE 136 AA; 14783 MW; C6A28A7823AD7C8B CRC64;
 Length 136;
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Pred. No. 3.2e-53;
7; Mismatches 12; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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 136 AA
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 Nippon Hosenkin Gakkaishi 9:124-135(1995)
 Created)
 PRT;
 87.68;
85.98;
 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
 Query Match
Best Local Similarity 85.99
Matches 116; Conservative
 CLC-2001 (TrEMBLrel.
PUTATIVE REGULATOR.
SCQ11.09.
 EAALGKILAEEQNAG 135
 PRELIMINARY;
 Streptomyces griseus.
 [1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1911;
 STRAIN-B2682;
 Q9X9U2
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SEQUENCE FROM N.A.
van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195770; AAC28481.1. ..
 61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
 : 61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
 Gaps
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
 2 MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGD 61
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. NCBI_TaxID=121022;
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD
 .;
0
 Length 136;
 Length 135;
79.2%; Score 548; DB 2; Length 13 ilarity 77.8%; Pred. No. 2.1e-47; Conservative 14; Mismatches 16; Indels
 18; Indels
 Last sequence update)
Last annotation update)
 78.6%; Score 544; DB 2; 77.8%; Pred. No. 5.3e-47;
 135 AA.
 12; Mismatches
 Created)
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MEDLINE=97000351; PubMed=8843436;
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61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
 Gaps
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
 Streptomyces albus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces albus ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195771; AAG28482.1; -.
SEQUENCE 135 AA; 14735 MW; 0FCBF4BDB2BA201B CRC64;
 ;
 64.5%; Score 446; DB 2; Length 135; 63.0%; Pred. No. 3.6e-37; Live 20; Mismatches 30; Indels
 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 D.; to the EMBL/GenBank/DDBJ databases
 Last sequence update)
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 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
 (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16,
 Conservative
 121 EAALGKILAEEQNAG 135
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121 DDALNRSLAEEQSAG 135
 PRELIMINARY;
 EAALGKILAEEQNAG 135
 PRELIMINARY;
 STRAIN=A3(2);
Seeger K.J., Harris D
Submitted (JAN-2000)
 PUTATIVE REGULATOR.
 Local Similarity
nes 85; Conserv
 [1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1902;
 NCBI_TaxID=1888;
 STRAIN=A3(2);
 STRAIN=A3(2);
 01-MAR-2001
01-MAR-2001
 01-MAR-2001
 Query Match
Best Local Si
Matches 85;
 Q9F9B6;
 Q9L268;
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL, AL096852; CAB51005.1; -. SEQUENCE 142 AA; 15364 MW; 857862390AA51CCB CRC64;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL137778; CAB70943.1;
EMBL, AL137778; CAB70943.1;
EMBLGOBIOCE 159 AA: 17472 MW; BA41013F940D7315 CRC64;
 61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
 61: VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
 Gaps
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
 33 LRLVVSSESSLPVPAGLRYDTADPYAVHATFHTGAEETVEWVFARDLLAEGLHRPTGTGD 92
 Gaps
 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. NCBI_TaxID=1902;
 ;
 Redenbach M., Kieser H.M., Denapaite D., Elchner A., Cullum J., Kinashi H., Hopwood D.A.;
 ..
 Length 142;
 Length 159;
 Ouery Match 34.2%; Score 237; DB 2; Length 14 Best Local Similarity 39.7%; Pred. No. 3.5e-16; Matches 50; Conservative 20; Mismatches 56; Indels
 Indels
 Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 James K.D., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
 Last sequence update)
Last annotation update)
 55;
 Query Match 35.5%; Score 246; DB 2; Best Local Similarity 43.1%; Pred. No. 5.1e-17; Matches; 56; Conservative 15; Mismatches 55
 142 AA
 Created)
 PRT;
 STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
 01-MAY-2000 (TremBlrel. 13, 01-MAY-2000 (TremBlrel. 13, 01-MAY-2000 (TremBlrel. 13, PUTATIVE REGULATOR.
 PRELIMINARY;
 Streptomyces coelicolor
 121 EAALGKILAE 130
 149 DQELSHILAE 158
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN=A3(2);
 STRAIN=A3(2);
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01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
 PUTATIVE REGULATOR.
SC5H1.03.
Streptomyces coelicolor.
 PRELIMINARY;
 STRAIN-A3(2);
Oliver K., Harris D.;
Submitted (MAY-1999)
 SEQUENCE FROM N.A.
 FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-A3(2);
 STRAIN-A3(2);
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 130 L 130
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77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLGIDDGL 136
 MEDITINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for
 GLSDVSIRLQVGA--DRALFRAGAPPLVAFLDRTDKSVPLGQEQT-LGDFEDSLEAALGK 126
 ----TAWLOVNAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLG-----TDAFLSK 146
 Gaps
 13 IPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHI.---APTDPE 69
 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 16;
 24.3%; Score 168; DB 2; Length 156; 38.1%; Pred. No. 3.3e-09; Live 15; Mismatches 47; Indels
 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL, A191041; CACOL575.1: -
SEQUENCE 156 AA; 17188 MW; 7181972EE7F33FB0 CRC64;
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 156 AA
 138 AA
 Created)
 Created)
 Q9X7M8;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
PUTATIVE REGULATOR.
 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
 Conservative
 Streptomyces coelicolor.
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
Matches 48; Conserv
 PUTATIVE REGULATOR
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1902;
 121 EAALGK 126
 137 AELLAR 142
 127 ILAEEO 132
 LFDEPE 152
 STRAIN=A3(2);
 STRAIN-A3(2);
 STRAIN=A3(2)
 SC8A11.03.
 SC5F2A.05C
 Q9FC07
 Q9X7M8
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 RESULT
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 09X7M8
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STRAIN=A3(2);
MEDLINE-97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Klasshi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
 83 RTVLEFHAPEGTAVIHVR-----SGELRRFLQAAGELVPVGLEHLQLDLDHD 129
 -----TDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
 for
 Gaps
 13 IPVELRYETRDPYAVRMTFHLPG---DAPVTWAFGRELLLDGINRPSGDGDVHIAP---- 65
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood DA.;
"A set of ordered cosmids and a detailed genetic and physical map
A set of ordered cosmids and a Metailed genetic and physical map
Mol. Microbiol. 21:77-96(1996).
EMBL; ALO49863; CAB42928.1; --
 26;
 Length 138;
 Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 42; Indels
Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
 STRAIN-A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
 to the EMBL/GenBank/DDBJ databases
 138 AA; 15261 MW; F531BA295144ABA5 CRC64;
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049587; CAB40672.1; -.
 Last sequence update)
Last annotation update)
 Ouery Match 23.0%; Score 159; DB 2; Best Local Similarity 33.1%; Pred. No. 2.2e-08; Matches 40; Conservative 13; Mismatches 42;
 Created)
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RESULT Q9RKC9

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Scheer M.P., van der Maarel S., Kuebart S., Schulz A., Wirth J., Schweiger S., Ropers H.-H., Nothwang H.G.; "DXS6673E Encodes a Predominantly Nuclear Protein, and Its Mouse Ortholog DXHXS6673E Is Alternatively Spliced in a Developmental and Tissue-Specific Manner.";
 23 DPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGA 82
 Streptomyces coelicolor.

acteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBL_TaxID=1902;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 Redenbach M., Ikeda K., Yamasaki M., Kinashi H.;
Cloning and physical mapping of the EcoRI fragments of the giant
linear plasmid SCP1 ".
J. Bacteriol. 180:2796-2799(1998).
BmBL; ALSO90463; CAC36690.1; -.
InterPro; IPRO10687; PTP_GTP_A.
SEQUENCE 537 AA; 58705 MW; 638BBF89EB02D821 CRC64;
 Score 81; DB 2; Length 537;
Pred. No. 8.8;
5; Mismatches 33; Indels
 STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 Brown S.P., Murphy L.D., Harris D.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE ATP/GTP-BINDING PROTEIN.
 Created)
Last sequence update)
Last annotation update)
 83 DRALFRAGAPPLV--AFLDRTDK----SVPL--GQEQTLG 114
 Æ
 PRT; 1370
 TISSUE=BRAIN;
MEDLINE=20130120; Pubmed=10662551;
 STRAIN=A3(2);
MEDLINE=98241550; PubMed=9573173;
 152878 MW;
 Genomics 63:123-132(2000).
EMBL; AF156605; AAF37800.1; -.
MGD; MGI:1927231; Zfp261.
SEQUENCE 1370 AA: 152878 MW;
 11.78;
36.08;
 01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2000 (TrEMBLrel, 15, 01-JUN-2001 (TrEMBLrel, 17, DXHXS6673E PROTEIN.
 Query Match
Best Local Similarity 36.0°
Matches 36; Conservative
 PRELIMINARY;
 ZFP261 OR DXHXS6673E.
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-A3(2);
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 RESULT
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 "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MAO1. Microbiol. 21:77-96(1996).
EMBL; AL132674; CAB59654.1; -.
 71 LSDVSIRLQVGAD-----RALFRAGAPPLVAFLDRTDKSVPLGQEQT-LGDFEDSLE 121
 Gaps
 11 FKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEG 70
 31; Gaps
 13 IPVELRYETR-DPYAVRMTFHLPG-----DAPVTWAFGRELLLDGINRPSGDGDVHIAPT 66
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID-1902;
 11;
 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
 Length 126;
 Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 Length
 Indels
 Indels
 STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein.
SEQUENCE 126 AA; 13742 MW; D54A8574D28B4D69 CRC64;
 GRVQAVVEFHSPQGCSVVQFE----NKALIR-----FLRRT 116
15741 MW; E24AA52C00AF40F1 CRC64;
 67 ------DPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRT 101
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 15.0%; Score 103.5; DB 2; 33.3%; Pred. No. 0.0074; tive 10; Mismatches 29;
 19.1%; Score 132.5; DB 2; 30.6%; Pred. No. 1.1e-05; Live 21; Mismatches 52;
 126 AA
 PRT;
 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
 HYPOTHETICAL 13.7 KDA PROTEIN.
 Query Match
Best Local Similarity 33.3%;
Matches 35; Conservative 1
 Conservative
 PRELIMINARY;
 Streptomyces coelicolor.
AA;
 Query Match
Best Local Similarity
Matches 37; Conserv
 SEQUENCE FROM N.A.
 [2]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-A3(2);
 140 A 140
 122 A 122
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Gaps

26;

E9270E68366E46F1 CRC64;

537 AA

PRT;

PRELIMINARY;

RESULT 12 Q9ACY2 ID Q9ACY2

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 SEQUENCE FROM N.A.
STRAIN-ZA91/ SEROROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
MEDLINE-2022556; PubMed-10761919;
Rales S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamilin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spraft B.G., Barrell B.G.;
meningitidis 22491.
 72 SDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLG--DFEDSLEAALG---- 125
 Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 20 LAGDLPVDMEFGEDLLESQTAPSRGWAPPGPSPSSGALDLLDTPSG-----LEKDPGGV 73
 Gaps
 ------LDGINRPSGDGDVHIAPTDPEGL 71
 -----ELRYETRDPYA------VRMTFHLP 34
 35 GDA------PVTWAF-GRELLL--DGI------NRPSGDGDVHIAPTDP 68
 ---GLSDVSIRLQVGAD------RALFRAGAPPLVAFL 98
 90;
 Length 1370;
 Length 514;
 ..
<u>..</u>
 Indels
 Indels
 PROSITE; PS00443; GATĀSE_IYPE_II; UNKNOWN_1.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 514 AA; 56010 MW; 57188EF89EAGE9E4 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14).
 37;
 53;
 -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
EMB.; ALL62754; CAB84172.1; -. HSSP: P00496; 1ECB.
 DB 11;
30;
 11.6%; Score 80; DB 16; 23.0%; Pred. No. 10; iive 24; Mismatches 53;
 514 AA
 11.7%; Score 81; DB 26.9%; Pred. No. 30; ive 14; Mismatches
 MENOCO:
InterPro; IPR000583; GATASe_2.
InterPro; IPR000836; Pribosyltran.
InterPro; IPR002375; Pur_pyr_pr_transf.
 Created)
 33 LPGDAPVTWAFGRELL------
 Pfam; PF00310; GATase_2; 1.
Pfam; PF00156; Pribosyltran; 1.
 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
 Conservative
 Conservative
 1 MSFLVSEELSFKIPV-----
 PRELIMINARY;
 Nature 404:502-506(2000)
 123 EVMPPDPGAG 132
Query Match
Best Local Similarity
Matches 35; Conserv
 126 KILAEEQNAG 135
 Local Similarity
nes 50; Conserv
 NCBI_TaxID=65699;
 MEROPS; C44.UNW;
 PURF OR NMA0892
 Query Match
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404 EVRYPNVYGIDMPTREELIANGRSAAEIAAEIGADGIVFQDLGDLEAVVKALNPKIESF- 462
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24) (PORPHOBILINOGEN
 25 YAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDP----EGLSDVSIRLQV 80
 May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V., "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S. A. 98:3460-3465(2001).
-I- CATALYTIC ACTIVITY: 2 5-AMINOLEVULINATE - PORPHOBILINOGEN + 2
 14;
 Pasteurella multocida.
Bacteria: Proteobacteria: gamma subdivision; Pasteurellaceae;
 -i- PATHWAY: SECOND STEP IN PORPHYRIN AND HEME BIOSYNTHESIS.
-i- SUBUNIT: HOMOCTAMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ALADH FAMILY.
EMBL; AE006205; A80776.1; -.
EMSSP; P15002; 184E.
 11.4%; Score 79; DB 16; Length 341; 29.9%; Pred. No. 7.7; tive 12; Mismatches 42; Indels
 PRODOM: PROD14: DALDHYDRTASE.
PRODOM: PD002304; D_ala_dehydrtse; 1.
PROSTITE; PS00169; D_ala_Dehydrstrarses: 1.
COMPLETE PROTECTION: D_ALA_DEHYDRATASE.
POTOHACE PROTECTION: J9389; POTPHYIN blosynthesis.
SEQUENCE 341 AA; 38389 WW; E28FA4503960A587 CRC64;
 253 GADMVWVKPGMPYLDLVYRVKTHFGVPTFAYQVSGEY 289
 81 GADRALFRAGAPPL-VAFLDRTDKSVPLGQEQTLGDF 116
 341 AA.
 Interpro; IPR001731; D_ala_dehydratase.
Pfam; PF00490; ALAD; 1.
 01-JUN-2001 (TrEMBLrel. 17, Created)
 PRT;
 STRAIN-PM70;
MEDLINE-21145866; Pubmed-11248100;
 Conservative
 PRELIMINARY;
 Query Match
Best Local Similarity
Matches 29; Conserv
 SYNTHASE) (ALADH).
HEMB OR PM1692.
 SEQUENCE FROM N.A.
 NCBI_TaxID=747;
 Pasteurella
 Q9CKD1;
 Q9CKĎ1
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